

PCTWORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 7 : C12N 15/31, 15/11, 15/10, C07K 14/245		A2	(11) International Publication Number: WO 00/44906
			(43) International Publication Date: 3 August 2000 (03.08.00)
(21) International Application Number: PCT/US00/02200		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: 27 January 2000 (27.01.00)		Published <i>Without international search report and to be republished upon receipt of that report.</i>	
(30) Priority Data: 60/117,405 27 January 1999 (27.01.99) US			
(71) Applicant: ELITRA PHARMACEUTICALS, INC. [US/US]; Suite A, 3510 Dunhill Street, San Diego, CA 92121 (US).			
(72) Inventors: ZYSKIND, Judith; 8514 La Jolla Scenic Drive, La Jolla, CA 92047 (US). OHLSEN, Kari, L.; 3560 Vista De La Orilla, San Diego, CA 92117 (US). TRAWICK, John; 7210 Baldrich Street, La Mesa, CA 91942 (US). FORSYTH, R., Allyn; 1135 Beryl Street, San Diego, CA 92109 (US). FROELICH, Jamie, M.; 5057 35th Street, San Diego, CA 92116 (US). CARR, Grant, J.; 2210 Sunrise Glen, Escondido, CA 92029 (US). YAMAMOTO, Robert, T.; 3725 Norte Dame Avenue, San Diego, CA 92131 (US). XU, H., Howard; 11142 Ivy Hill Drive, San Diego, CA 92131 (US).			
(74) Agent: REISMAN, Joseph, M.; Knobbe, Martens, Olson & Bear, LLP, 16th Floor, 620 Newport Center Drive, Newport Beach, CA 92660 (US).			
(54) Title: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN <i>ESCHERICHIA COLI</i>			
(57) Abstract			
<p>The sequences of nucleic acids encoding proteins required for <i>E. coli</i> proliferation are disclosed. The nucleic acids can be used to express proteins or portions thereof, to obtain antibodies capable of specifically binding to the expressed proteins, and to use those expressed proteins as a screen to isolate candidate molecules for rational drug discovery programs. The nucleic acids can also be used to screen for homologous genes that are required for proliferation in microorganisms other than <i>E. coli</i>. The nucleic acids can also be used to design expression vectors and secretion vectors. The nucleic acids of the present invention can also be used in various assay systems to screen for proliferation required genes in other organisms as well as to screen for antimicrobial agents.</p>			

ATTORNEY DOCKET NUMBER: 10182-016-999
SERIAL NUMBER: 10/032,585
REFERENCE: CA

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TC	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

Description

5

10

15

20

25

30

35

40

45

50

55

**GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
*ESCHERICHIA COLI***

BACKGROUND OF THE INVENTION

Since the discovery of penicillin, the use of antibiotics to treat the ravages of bacterial infections has saved millions of lives. With the advent of these "miracle drugs," for a time it was popularly believed that humanity might, once and for all, be saved from the scourge of bacterial infections. In fact, during the 1980s and early 1990s, many large pharmaceutical companies cut back or eliminated antibiotics research and development. They believed that infectious disease caused by bacteria finally had been conquered and that markets for new drugs were limited. Unfortunately, this belief was overly optimistic.

The tide is beginning to turn in favor of the bacteria as reports of drug resistant bacteria become more frequent. The United States Centers for Disease Control announced that one of the most powerful known antibiotics, vancomycin, was unable to treat an infection of the common *Staphylococcus aureus* (staph). This organism is commonly found in our environment and is responsible for many nosocomial infections. The import of this announcement becomes clear when one considers that vancomycin was used for years to treat infections caused by stubborn strains of bacteria, like staph. In short, the bacteria are becoming resistant to our most powerful antibiotics. If this trend continues, it is conceivable that we will return to a time when what are presently considered minor bacterial infections are fatal diseases.

There are a number of causes for the predicament in which practitioners of medical arts find themselves. Over-prescription and improper prescription habits by some physicians have caused an indiscriminate increase in the availability of antibiotics to the public. The patient is also partly responsible, for even in instances where an antibiotic is the appropriate treatment, patients will often improperly use the drug, the result being yet another population of bacteria that is resistant, in whole or in part, to traditional antibiotics.

The bacterial scourges that have haunted humanity remain, in spite of the development of modern scientific practices to deal with the diseases that they cause. Drug resistant bacteria are now advancing on the health of humanity. A new generation of antibiotics to once again deal with the pending health threat that bacteria present is required.

Discovery of New Antibiotics

As more and more bacterial strains become resistant to the panel of available antibiotics, new compounds are required. In the past, practitioners of pharmacology would have to rely upon traditional methods of drug discovery to generate novel, safe and efficacious compounds for the treatment of disease. Traditional drug discovery methods involve blindly testing potential drug candidate-molecules, often selected at random, in the hope that one might prove to be an effective treatment for some disease. The process is painstaking and laborious, with no guarantee of success. Today, the average cost to discover and develop a new drug is nearly US \$500 million, and the average time is 15 years from laboratory to patient. Improving this process, even incrementally, would represent a huge advance in the generation of novel antimicrobial agents.

Newly emerging practices in drug discovery utilize a number of biochemical techniques to provide for directed approaches to creating new drugs, rather than discovering them at random. For example, gene sequences and proteins encoded thereby that are required for the proliferation of an organism make for excellent targets since exposure of bacteria to compounds active against these targets would result in the inactivation of the organism. Once a target is identified, biochemical analysis of that target can be used to discover or to design molecules that interact with and alter the functions of the target. Using physical and computational techniques, to analyze structural and biochemical targets in order to derive compounds that interact with a target is called rational drug design and offers great future potential. Thus, emerging drug discovery practices use molecular modeling techniques, combinatorial chemistry approaches, and other means to produce and screen and/or design large numbers of candidate compounds.

Nevertheless, while this approach to drug discovery is clearly the way of the future, problems remain. For example, the initial step of identifying molecular targets for investigation can be an extremely time consuming task. It may also be difficult to design molecules that interact with the target by using computer modeling techniques. Furthermore, in cases where the function of the target is not known or is poorly understood, it may be difficult to design assays to detect molecules that interact with and alter the functions of the target. To improve the rate of novel drug discovery and development, methods of identifying important molecular targets in pathogenic microorganisms and methods for identifying molecules that interact with and alter the functions of such molecular targets are urgently required.

Escherichia coli represents an excellent model system to understand bacterial biochemistry and physiology. The estimated 4288 genes scattered along the 4.6×10^6 base pairs of the *Escherichia coli* (*E. coli*) chromosome offer tremendous promise for the understanding of bacterial biochemical processes. In turn, this knowledge will assist in the development of new tools for the diagnosis and treatment of bacteria-caused human disease. The entire *E. coli* genome has been sequenced, and this body of information holds a tremendous potential for application to the discovery and development of new antibiotic compounds. Yet, in spite of this accomplishment, the general functions or roles of many of these genes are still unknown. For example, the total number of proliferation-required genes contained within the *E. coli* genome is unknown, but has been variously estimated at around 200 to 700 (Armstrong, K.A. and Fan, D.P. Essential Genes in the *metB-malB* Region of *Escherichia coli* K12, 1975, J. Bacteriol. 126: 48-55).

Novel, safe and effective antimicrobial compounds are needed in view of the rapid rise of antibiotic resistant microorganisms. However, prior to this invention, the characterization of even a single bacterial gene was a painstaking process, requiring years of effort. Accordingly, there is an urgent need for more novel methods to identify and characterize bacterial genomic sequences that encode gene products required for proliferation and for methods to identify molecules that interact with and alter the functions of such genes and gene products.

SUMMARY OF THE INVENTION

One embodiment of the present invention is a purified or isolated nucleic acid sequence consisting essentially of one of SEQ ID NOs: 1-81, 405-485, wherein said nucleic acid inhibits microorganism proliferation. The nucleic acid sequence may be complementary to at least a portion of a coding sequence of a gene whose expression is required for

microorganism proliferation. The nucleic acid sequence may comprise a fragment of one of SEQ ID NOs: 1-81, 405-485, said fragment selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 1-81, 405-485. The nucleic acid sequence may be complementary to a coding sequence of a gene whose expression is required for microorganism proliferation.

Another embodiment of the present invention is a vector comprising a promoter operably linked to a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs: 1-81, 405-485. The promoter may be active in an organism selected from the group consisting of *Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

Another embodiment of the present invention is a host cell containing the vectors described above.

Another embodiment of the present invention is a purified or isolated nucleic acid consisting essentially of the coding sequence of one of SEQ ID NOs: 82-88, 90-242. One aspect of this embodiment is a fragment of the nucleic acid comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 82-88, 90-242.

Another embodiment of the present invention is a vector comprising a promoter operably linked to the nucleic acids of the preceding embodiment.

Another aspect of the present invention is a purified or isolated nucleic acid comprising a nucleic acid sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding region, or 3' noncoding region within an operon encoding a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs: 243-357, 359-398.

Another embodiment of the present invention is a purified or isolated nucleic acid comprising a nucleic acid having at least 70% homology to a sequence selected from the group consisting of SEQ ID NOs 1-81, 405-485, 82-88, 90-242 or the sequences complementary thereto as determined using BLASTN version 2.0 with the default parameters. The nucleic acid may be from an organism selected from the group consisting of *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, and *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

Another embodiment of the present invention is a purified or isolated nucleic acid consisting essentially of a nucleic acid encoding a polypeptide having a sequence selected from the group consisting of SEQ ID NOs.: 243-357, 359-398.

Another embodiment of the present invention is a vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide having a sequence selected from the group consisting of SEQ ID NOs.: 243-357, 359-398.

Another embodiment of the present invention is a host cell containing the vector of the preceding embodiment.

Another embodiment of the present invention is purified or isolated polypeptide comprising the sequence of one of SEQ ID NOs: 243-357, 359-398.

Another embodiment of the present invention is purified or isolated polypeptide comprising a fragment of one of the polypeptides of SEQ ID NOs. 243-357, 359-398, said fragment selected from the group consisting of fragments comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the polypeptides of SEQ ID NOs.: 243-357, 359-398.

Another embodiment of the present invention is an antibody capable of specifically binding the polypeptide of the preceding embodiment.

Another embodiment of the present invention is method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide having a sequence selected from the group consisting of SEQ ID NOs. 243-357, 359-398 into a cell. The method may further comprise the step of isolating said protein.

Another embodiment of the present invention is a method of inhibiting proliferation comprising inhibiting the activity or reducing the amount of a polypeptide having a sequence selected from the group consisting of SEQ ID NOs. 243-357, 359-398 or inhibiting the activity or reducing the amount of a nucleic acid encoding said polypeptide.

Another embodiment of the present invention is method for identifying compounds which influence the activity of a polypeptide required for proliferation comprising:

contacting a polypeptide comprising a sequence selected from the group consisting of 243-357, 359-398 with a candidate compound; and

determining whether said compound influences the activity of said polypeptide.

The activity may be an enzymatic activity. The activity may be a carbon compound catabolism activity. The activity may be a biosynthetic activity. The activity may be a transporter activity. The activity may be a transcriptional activity. The activity may be a DNA replication activity. The activity may be a cell division activity.

Another embodiment of the present invention is a compound identified using the above method.

Another embodiment of the present invention is method for assaying compounds for the ability to reduce the activity or level of a polypeptide required for proliferation, comprising:

providing a target, wherein said target comprises the coding sequence of a sequence selected from the group consisting of SEQ ID NOs. 82-88, 90-242;

contacting said target with a candidate compound; and
measuring an activity of said target.

The target may be a messenger RNA molecule transcribed from a coding region of one of SEQ ID. NOs.: 82-88, 90-242 and said activity is translation of said messenger RNA. The target may be a coding region of one of SEQ ID. NOs. 82-88, 90-242 and said activity is transcription of said messenger RNA.

Another embodiment of the present invention is a compound identified using the method above.

Another embodiment of the present invention is a method for identifying compounds which reduce the activity or level of a gene product required for cell proliferation comprising the steps of:

expressing an antisense nucleic acid against a nucleic acid encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;

contacting said sensitized cell with a compound; and

determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

The cell may be selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells. The cell may be an *E. coli* cell. The cell may be from an organism selected from the group consisting of *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, and *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species. The antisense nucleic acid may be transcribed from an inducible promoter. The method may, further comprise the step of contacting said cell with a concentration of inducer which induces said antisense nucleic acid to a sublethal level. The sub-lethal concentration of said inducer may be such that growth inhibition is 8% or more. The inducer may be isopropyl-1-thio- β -D-galactoside. The growth inhibition may be measured by monitoring optical density of a culture growth solution. The gene product may be a polypeptide. The gene product may be an RNA. The gene product may comprise a polypeptide having a sequence selected from the group consisting of SEQ ID NOs.: 243-357, 359-398.

Another embodiment of the present invention is a compound identified using the method above.

Another embodiment of the present invention is a method for inhibiting cellular proliferation comprising introducing a compound with activity against a gene corresponding to one of SEQ ID NOs.: 82-88, 90-242 or with activity against the product of said gene into a population of cells expressing a gene. The compound may be an antisense oligonucleotide comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-81, 405-485, or a proliferation-inhibiting portion thereof. The proliferation inhibiting portion of one of SEQ ID NOs. 1-81, 405-485

5 may be a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 1-81, 405-485. The compound may be a triple helix oligonucleotide.

10 5 Another embodiment of the present invention is a preparation comprising an effective concentration of an antisense oligonucleotide comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-81, 405-485, or a proliferation-inhibiting portion thereof in a pharmaceutically acceptable carrier. The proliferation-inhibiting portion of one of SEQ ID NOs. 1-81, 405-485 may comprise at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 1-81, 405-485.

15 10 Another embodiment of the present invention is a method for inhibiting the expression of a gene in an operon required for proliferation comprising contacting a cell in a cell population with an antisense nucleic acid, said cell expressing a gene corresponding to one of SEQ ID NOs.: 82-88, 90-242, wherein said antisense nucleic acid comprises at least a proliferation-inhibiting portion of said operon in an antisense orientation that is effective in inhibiting expression of said gene. The antisense nucleic acid may be complementary to a sequence of a gene comprising one or more of SEQ ID NOs.: 82-88, 90-242. The antisense nucleic acid may be a sequence of one of SEQ ID NOs.: 1-81, 20 405-485, or a portion thereof. The cell may be contacted with said antisense nucleic acid by introducing a plasmid which expresses said antisense nucleic acid into said cell population. The cell may be contacted with said antisense nucleic acid by introducing a phage which expresses said antisense nucleic acid into said cell population. The cell may be contacted with said antisense nucleic acid by introducing a sequence encoding said antisense nucleic acid into the chromosome of said cell into said cell population. The cell may be contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population. The cell may be contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme is complementary to said antisense oligonucleotide. The cell may be contacted with said antisense nucleic acid by introducing a liposome comprising said antisense oligonucleotide into said cell. The cell may be contacted with said antisense nucleic acid by electroporation. The antisense nucleic acid may be a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 82-88, 90- 25 242. The antisense nucleic acid may be an oligonucleotide.

30 25 Another embodiment of the present invention is a method for identifying bacterial strains comprising the steps of:

40 providing a sample containing a bacterial species; and

30 identifying a bacterial species using a species specific probe having a sequence selected from the group consisting of SEQ ID NOs. 1-81, 405-485, 82-88, 90-242.

45 Another embodiment of the present invention is a method for identifying a gene in a microorganism required for proliferation comprising:

- 50 (a) identifying an inhibitory nucleic acid which inhibits the activity of a gene or gene product required for proliferation in a first microorganism;
- 35 (b) contacting a second microorganism with said inhibitory nucleic acid;

(c) determining whether said inhibitory nucleic acid from said first microorganism inhibits proliferation of said second microorganism; and

(d) identifying the gene in said second microorganism which is inhibited by said inhibitory nucleic acid.

Another embodiment of the present invention is a method for assaying a compound for the ability to inhibit proliferation of a microorganism comprising:

(a) identifying a gene or gene product required for proliferation in a first microorganism;

(b) identifying a homolog of said gene or gene product in a second microorganism;

(c) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said second microorganism;

(d) contacting said second microorganism with a proliferation-inhibiting amount of said inhibitory nucleic acid, thus sensitizing said second microorganism;

(e) contacting the sensitized microorganism of step (d) with a compound; and

(f) determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism.

The step of identifying a gene involved in proliferation in a first microorganism may comprise:

introducing a nucleic acid comprising a random genomic fragment from said first microorganism operably linked to a promoter wherein said random genomic fragment is in the antisense orientation; and

comparing the proliferation of said first microorganism transcribing a first level of said random genomic fragment to the proliferation of said first microorganism transcribing a lower level of said random genomic fragment, wherein a difference in proliferation indicates that said random genomic fragment comprises a gene involved in proliferation.

The step of identifying a homolog of said gene in a second microorganism may comprise identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a database using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default parameters. The step of identifying a homolog of said gene in a second microorganism may comprise identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide by identifying nucleic acids which hybridize to said first gene. The step of identifying a homolog of said gene in a second microorganism may comprise expressing a nucleic acid which inhibits the proliferation of said first microorganism in said second microorganism. The inhibitory nucleic acid may be an antisense nucleic acid. The inhibitory nucleic acid may comprise an antisense nucleic acid to a portion of said homolog. The inhibitory nucleic acid may comprise an antisense nucleic acid to a portion of the operon encoding said homolog. The step of contacting the second microorganism with a proliferation-inhibiting amount of said nucleic acid sequence may comprise directly contacting said second microorganism with said nucleic acid. The step of contacting the second microorganism with a proliferation-inhibiting amount of said nucleic acid sequence may comprise expressing an antisense nucleic acid to said homolog in said second microorganism.

Another embodiment of the present invention is a compound identified using the method above.

Another embodiment of the present invention is a method of assaying a compound for the ability to inhibit proliferation comprising:

- (a) identifying an inhibitory nucleic acid sequence which inhibits the activity of a gene or gene product required for proliferation in a first microorganism;
- (b) contacting a second microorganism with a proliferation-inhibiting amount of said inhibitory nucleic acid, thus sensitizing said second microorganism;
- (c) contacting the proliferation-inhibited microorganism of step (b) with a compound; and
- (d) determining whether said compound inhibits proliferation of said sensitized second microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized second microorganism.

The inhibitory nucleic acid may be an antisense nucleic acid which inhibits the proliferation of said first microorganism. The inhibitory nucleic acid may comprise a portion of an antisense nucleic acid which inhibits the proliferation of said first microorganism. The inhibitory nucleic acid may comprise an antisense molecule against the entire coding region of the gene involved in proliferation of the first microorganism. The inhibitory nucleic acid may comprise an antisense nucleic acid to a portion of the operon encoding the gene involved in proliferation of the first microorganism.

Another embodiment of the present invention is a compound identified using the method above.

Another embodiment of the present invention is a method for assaying compounds for activity against a biological pathway required for proliferation comprising:

- sensitizing a cell by expressing an antisense nucleic acid against a nucleic acid encoding a gene product required for proliferation in a cell to reduce the activity or amount of said gene product;
- contacting the sensitized cell with a compound; and
- determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

The cell may be selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells. The cell may be an *E. coli* cell. The cell may be an organism selected from the group consisting of *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, and *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species. The antisense nucleic acid may be transcribed from an inducible promoter. The method may further comprise contacting the cell with an agent which induces expression of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is expressed at a sublethal level. The sublethal level of said antisense nucleic acid

5 may inhibit proliferation by 8% or more. The agent may be isopropyl-1-thio- β -D-galactoside (IPTG). The inhibition of proliferation may be measured by monitoring the optical density of a liquid culture. The gene product may comprise a polypeptide having a sequence selected from the group consisting of SEQ ID NOs: 243-357, 359-398.

Another embodiment of the present invention is a compound identified using the method above.

10 5 Another embodiment of the present invention is a method for assaying a compound for the ability to inhibit cellular proliferation comprising:

contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell;

15 contacting said cell with said compound; and

10 determining whether said compound reduces proliferation to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent.

20 The agent which reduces the activity or level of a gene product required for proliferation of said cell may comprise an antisense nucleic acid to a gene or operon required for proliferation. The agent which reduces the activity or level of a gene product required for proliferation of said cell may comprise an antibiotic. The cell may contain a temperature sensitive mutation which reduces the activity or level of said gene product required for proliferation of said cell. The antisense nucleic acid may be directed against the same functional domain of said gene product required for proliferation of said cell to which said antisense nucleic acid is directed. The antisense nucleic acid may be directed against a different functional domain of said gene product required for proliferation of said cell than the functional domain to which said antisense nucleic acid is directed.

20 Another embodiment of the present invention is a compound identified using the method above.

30 Another embodiment of the present invention is a method for identifying the pathway in which a proliferation-required nucleic acid or its gene product lies comprising:

expressing a sublethal level of an antisense nucleic acid directed against said proliferation-required nucleic acid in a cell;

35 25 contacting said cell with an antibiotic, wherein the a biological pathway on which said antibiotic acts is known; and

determining whether said cell has a substantially greater sensitivity to said antibiotic than a cell which does not express said sublethal level of said antisense nucleic acid.

40 30 Another embodiment of the present invention is a method for determining the pathway on which a test compound acts comprising:

45 (a) expressing a sublethal level of an antisense nucleic acid directed against a proliferation-required nucleic acid in a cell, wherein the biological pathway in which said proliferation-required nucleic acid lies is known,

(b) contacting said cell with said test compound; and

35 (c) determining whether said cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid.

The method may further comprise:

(d) expressing a sublethal level of a second antisense nucleic acid directed against a second proliferation-required nucleic acid in said cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

(e) determining whether said cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid.

Another embodiment of the present invention is a purified or isolated nucleic acid consisting essentially of one of SEQ ID NOs: 358, 399-402.

Another embodiment of the present invention is a purified or isolated nucleic acid comprising a sequence selected from the group consisting of 1-81, 405-485, 82-88, 90-242, 358, 399-402.

Another embodiment of the present invention is a compound which interacts with the gene or gene product of a nucleic acid comprising a sequence of one of SEQ ID NOs: 82-88, 90-242 to inhibit proliferation.

Another embodiment of the present invention compound which interacts with a polypeptide comprising one of SEQ ID NOs. 243-357, 359-398 to inhibit proliferation.

Another embodiment of the present invention is a compound which interacts with a nucleic acid comprising one of SEQ ID NOs: 358, 399-402 to inhibit proliferation.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is an IPTG dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing either an antisense clone to the *E. coli* ribosomal protein rplW (AS-rplW) which is required for protein synthesis and essential cell proliferation, or an antisense clone to the *elaD* (AS-*elaD*) gene which is not known to be involved in protein synthesis and which is also essential for proliferation.

Figure 2A is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to rplW(AS-rplW) in the presence of 0, 20 or 50 μ M IPTG.

Figure 2B is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to *elaD* (AS-*elaD*) in the presence of 0, 20 or 50 μ M IPTG.

Figure 3 is a graph showing the fold increase in tetracycline sensitivity of *E. coli* transfected with antisense clones to essential ribosomal proteins L23 (AS-rplW) and L7/L12 and L10 (AS-rplLrplJ). Antisense clones to genes known not to be involved in protein synthesis (atpB/E(AS-atpB/E), *visC* (AS-*visC*, *elaD* (AS-*elaD*), *yohH* (AS-*yohH*) are much less sensitive to tetracycline.

Definitions

By "biological pathway" is meant any discrete cell function or process that is carried out by a gene product or a subset of gene products. Biological pathways include enzymatic, biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such cell walls. Biological pathways that are usually required for proliferation of microorganisms include, but are not limited to, cell division, DNA synthesis & replication,

RNA synthesis (transcription), protein synthesis (translation), protein processing, protein transport, fatty acid biosynthesis, cell wall synthesis, cell membrane synthesis & maintenance, etc.

By "inhibit activity against a gene or gene product" is meant having the ability to interfere with the function of a gene or gene product in such a way as to decrease expression of the gene or to reduce the level or activity of a product of the gene. Agents which have activity against a gene include agents that inhibit transcription of the gene and agents that inhibit translation of the mRNA transcribed from the gene. In microorganisms, agents which have activity against a gene can act to decrease expression of the operon in which the gene resides or alter the processing of operon RNA such as to reduce the level or activity of the gene product. The gene product can be a non-translated RNA such as ribosomal RNA, a translated RNA (mRNA) or the protein product resulting from translation of the gene mRNA. Of particular utility to the present invention are anti-sense RNAs that have activities against the operons or genes to which they specifically hybridize.

By "activity against a gene product" is meant having the ability to inhibit the function or to reduce the level or activity of the gene product in a cell.

By "activity against a protein" is meant having the ability to inhibit the function or to reduce the level or activity of the protein in a cell.

By "activity against nucleic acid" is meant having the ability to inhibit the function or to reduce the level or activity of the nucleic acid in a cell.

As used herein, "sublethal" means a concentration of an agent below the concentration required to inhibit all cell growth.

DETAILED DESCRIPTION OF THE INVENTION

The present invention describes a group of *E. coli* genes and gene families required for growth and/or proliferation. A proliferation-required gene or gene family is one where, in the absence of a gene transcript and/or gene product, growth or viability of the microorganism is reduced or eliminated. Thus, as used herein the terminology "proliferation-required" or "required for proliferation" encompasses sequences where the absence of a gene transcript and/or gene product completely eliminates cell growth as well as sequences where the absence of a gene transcript and/or gene product merely reduces cell growth. These proliferation-required genes can be used as potential targets for the generation of new antimicrobial agents. To achieve that goal, the present invention also encompasses novel assays for analyzing proliferation-required genes and for identifying compounds which interact with the gene products of the proliferation-required genes. In addition, the present invention contemplates the expression of genes and the purification of the proteins encoded by the nucleic acid sequences identified as required proliferation genes and reported herein. The purified proteins can be used to generate reagents and screen small molecule libraries or other candidate compound libraries for compounds that can be further developed to yield novel antimicrobial compounds. The present invention also describes methods for identification of homologous genes in organisms other than *E. coli*.

The present invention utilizes a novel method to identify proliferation-required *E. coli* sequences. Generally, a library of nucleic acid sequences from a given source are subcloned or otherwise inserted into an inducible expression

vector, thus forming an expression library. Although the insert nucleic acids may be derived from the chromosome of the organism into which the expression vector is to be introduced, because the insert is not in its natural chromosomal location, the insert nucleic acid is an exogenous nucleic acid for the purposes of the discussion herein. The term expression is defined as the production of an RNA molecule from a gene, gene fragment, genomic fragment, or operon. Expression can also be used to refer to the process of peptide or polypeptide synthesis. An expression vector is defined as a vehicle by which a ribonucleic acid (RNA) sequence is transcribed from a nucleic acid sequence carried within the expression vehicle. The expression vector can also contain features that permit translation of a protein product from the transcribed RNA message expressed from the exogenous nucleic acid sequence carried by the expression vector. Accordingly, an expression vector can produce an RNA molecule as its sole product or the expression vector can produce a RNA molecule that is ultimately translated into a protein product.

Once generated, the expression library containing the exogenous nucleic acid sequences is introduced into an *E. coli* population to search for genes that are required for bacterial proliferation. Because the library molecules are foreign to the population of *E. coli*, the expression vectors and the nucleic acid segments contained therein are considered exogenous nucleic acid.

Expression of the exogenous nucleic acid fragments in the test population of *E. coli* containing the expression vector library is then activated. Activation of the expression vectors consists of subjecting the cells containing the vectors to conditions that result in the expression of the exogenous nucleic acid sequences carried by the expression vector library. The test population of *E. coli* cells is then assayed to determine the effect of expressing the exogenous nucleic acid fragments on the test population of cells. Those expression vectors that, upon activation and expression, negatively impact the growth of the *E. coli* screen population were identified, isolated, and purified for further study.

A variety of assays are contemplated to identify nucleic acid sequences that negatively impact growth upon expression. In one embodiment, growth in *E. coli* cultures expressing exogenous nucleic acid sequences and growth in cultures not expressing these sequences is compared. Growth measurements are assayed by examining the extent of growth by measuring optical densities. Alternatively, enzymatic assays can be used to measure bacterial growth rates to identify exogenous nucleic acid sequences of interest. Colony size, colony morphology, and cell morphology are additional factors used to evaluate growth of the host cells. Those cultures that failed to grow or grow with reduced efficiency under expression conditions are identified as containing an expression vector encoding a nucleic acid fragment that negatively affects a proliferation-required gene.

Once exogenous nucleic acid sequences of interest are identified, they are analyzed. The first step of the analysis is to acquire the nucleic acid sequence of the nucleic acid fragment of interest. To achieve this end, the insert in those expression vectors identified as containing a sequence of interest is sequenced, using standard techniques well known in the art. The next step of the process is to determine the source of the nucleic acid sequence.

Determination of sequence source is achieved by comparing the obtained sequence data with known sequences in various genetic databases. The sequences identified are used to probe these gene databases. The result of this

5 procedure is a list of exogenous nucleic acid sequences corresponding to a list that includes novel bacterial genes required for proliferation as well as genes previously identified as required for proliferation.

5 The number of DNA and protein sequences available in database systems has been growing exponentially for years. For example, at the end of 1998, the complete sequences of *Caenorhabditis elegans*, *Saccharomyces cerevisiae* and nineteen bacterial genomes, including *E. coli* were available. This sequence information is stored in a number of databanks, such as GenBank (the National Center for Biotechnology Information (NCBI), and is publicly available for searching.

10 A variety of computer programs are available to assist in the analysis of the sequences stored within these databases. FastA, (W. R. Pearson (1990) "Rapid and Sensitive Sequence Comparison with FASTP and FASTA" Methods in Enzymology 183:63- 98), Sequence Retrieval System (SRS), (Etzold & Argos, SRS an indexing and retrieval tool for flat file data libraries. Comput. Appl. Biosci. 9:49-57, 1993) are two examples of computer programs that can be used to analyze sequences of interest. In one embodiment of the present invention, the BLAST family of computer programs, which includes BLASTN version 2.0 with the default parameters, or BLASTX version 2.0 with the default parameters, is used to analyze nucleic acid sequences.

15 BLAST, an acronym for "Basic Local Alignment Search Tool," is a family of programs for database similarity searching. The BLAST family of programs includes: BLASTN, a nucleotide sequence database searching program, BLASTX, a protein database searching program where the input is a nucleic acid sequence; and BLASTP, a protein database searching program. BLAST programs embody a fast algorithm for sequence matching, rigorous statistical methods for judging the significance of matches, and various options for tailoring the program for special situations. Assistance in using the program can be obtained by e-mail at blast@ncbi.nlm.nih.gov.

20 Bacterial genes are often transcribed in polycistronic groups. These groups comprise operons, which are a collection of genes and intergenic sequences. The genes of an operon are co-transcribed and are often related functionally. Given the nature of the screening protocol, it is possible that the identified exogenous nucleic acid sequence corresponds to a gene or portion thereof with or without adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a sequence spanning at least a portion of two or more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual sequence that is required for bacterial proliferation. Accordingly, determining which of the genes that are encoded within the operons are individually required for proliferation is often desirable.

25 In one embodiment of the present invention, an operon is dissected to determine which gene or genes are required for proliferation. For example, the RegulonDB DataBase described by Huerta et al. (*Wucl. Acids Res.* 26:55-59, 1998), which may also be found on the website http://www.cifn.unam.mx/Computational_Biology/regulondb/, may be used to identify the boundaries of operons encoded within microbial genomes. A number of techniques that are well known in the art can be used to dissect the operon. In one aspect of this embodiment, gene disruption by homologous recombination is used to individually inactivate the genes of an operon that is thought to contain a gene required for proliferation.

30 Several gene disruption techniques have been described for the replacement of a functional gene with a mutated, non-functional (null) allele. These techniques generally involve the use of homologous recombination. The

method described by Link et al. (J. Bacteriol 1997 179:6228; incorporated herein by reference in its entirety) serves as an excellent example of these methods as applicable to disruption of genes in *E. coli*. This technique uses crossover PCR to create a null allele with an in-frame deletion of the coding region of a target gene. The null allele is constructed in such a way that sequences adjacent to the wild type gene (ca. 500 bp) are retained. These homologous sequences surrounding the deletion null allele provide targets for homologous recombination so that the wild type gene on the *E. coli* chromosome can be replaced by the constructed null allele.

The crossover PCR amplification product is subcloned into the vector pK03, the features of which include a chloramphenicol resistance gene, the counter-selectable marker *sacB*, and a temperature sensitive autonomous replication function. Following transformation of an *E. coli* cell population with such a vector, selection for cells that have undergone homologous recombination of the vector into the chromosome is achieved by growth on chloramphenicol at the non-permissive temperature of 43°C. Under these conditions, autonomous replication of the plasmid cannot occur and cell are resistant to chloramphenicol only if the chloramphenicol resistance gene has been integrated into the chromosome. Usually a single crossover event is responsible for this integration event such that the *E. coli* chromosome now contains a tandem duplication of the target gene consisting of one wild type allele and one deletion null allele separated by vector sequence.

This new *E. coli* strain containing the tandem duplication can be maintained at permissive temperatures in the presence of drug selection (chloramphenicol). Subsequently, cells of this new strain are cultured at the permissive temperature 30°C without drug selection. Under these conditions, the chromosome of some of the cells within the population will have undergone an internal homologous recombination event resulting in removal of the plasmid sequences. Subsequent culturing of the strain in growth medium lacking chloramphenicol but containing sucrose is used to select for such recombinative resolutions. In the presence of the counter-selectable marker *sacB*, sucrose is rendered into a toxic metabolite. Thus, cells that survive this counter-selection have lost both the plasmid sequences from the chromosome and the autonomously replicating plasmid that results as a byproduct of recombinative resolution.

There are two possible outcomes of the above recombinative resolution via homologous recombination. Either the wild type copy of the targeted gene is retained on the chromosome or the mutated null allele is retained on the chromosome. In the case of an essential gene, a single copy of the null allele would be lethal and such cells should not be obtained by the above procedure when applied to essential genes. In the case of a non-essential gene, roughly equal numbers of cells containing null alleles and cells containing wild type alleles should be obtained. Thus, the method serves as a test for essentiality of the targeted gene: when applied to essential genes, only cells with a wild type allele on the chromosome will be obtained.

Other techniques have also been described for the creation of disruption mutations in *E. coli*. For example, Link et al. also describe inserting an in-frame sequence tag concomitantly with an in-frame deletion in order to simplify analysis of recombinants obtained. Further, Link et al. describe disruption of genes with a drug resistance marker such as a kanamycin resistance gene. Arigoni et al., (Arigoni, F. et al. A Genome-based Approach for the

5 Identification of Essential Bacterial Genes, Nature Biotechnology 16: 851-856, the disclosure of which is incorporated herein by reference in its entirety) describe the use of gene disruption combined with engineering a second copy of a
10 5 test gene such that the expression of the gene is regulated by and inducible promoter such as the arabinose promoter to test the essentiality of the gene. Many of these techniques result in the insertion of large fragments of DNA into the gene of interest, such as a drug selection marker. An advantage of the technique described by Link et al. is that it
15 10 does not rely on an insertion into the gene to cause a functional defect, but rather results in the precise removal of the coding region. This insures the lack of polar effects on the expression of genes downstream from the target gene.

Recombinant DNA techniques can be used to express the entire coding sequences of the gene identified as required for proliferation, or portions thereof. The over-expressed proteins can be used as reagents for further study. The
15 10 identified exogenous sequences are isolated, purified, and cloned into a suitable expression vector using methods well known in the art. If desired, the nucleic acids can contain the sequences encoding a signal peptide to facilitate secretion of the expressed protein.

Expression of fragments of the bacterial genes identified as required for proliferation is also contemplated by the present invention. The fragments of the identified genes can encode a polypeptide comprising at least 5, at least 10, at
15 15 least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 75, or more than 75 consecutive amino acids of a gene complementary to one of the identified sequences of the present invention. The nucleic acids inserted into the expression vectors can also contain sequences upstream and
20 25 downstream of the coding sequence.

When expressing the coding sequence of an entire gene identified as required for bacterial proliferation or a fragment thereof, the nucleic acid sequence to be expressed is operably linked to a promoter in an expression vector using
20 30 conventional cloning technology. The expression vector can be any of the bacterial, insect, yeast, or mammalian expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon usage
35 25 and codon bias of the sequence can be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, et al., U.S. Patent No. 5,082,767, incorporated herein by this reference. Fusion protein expression systems are also contemplated by the present invention.

Following expression of the protein encoded by the identified exogenous nucleic acid sequence, the protein is
40 30 purified. Protein purification techniques are well known in the art. Proteins encoded and expressed from identified exogenous nucleic acid sequences can be partially purified using precipitation techniques, such as precipitation with polyethylene glycol. Chromatographic methods usable with the present invention can include ion-exchange chromatography, gel filtration, use of hydroxyapatite columns, immobilized reactive dyes, chromatofocusing, and use of
45 50 high-performance liquid chromatography. Electrophoretic methods such one-dimensional gel electrophoresis, high-resolution two-dimensional polyacrylamide electrophoresis, isoelectric focusing, and others are contemplated as purification methods.

Also, affinity chromatographic methods, comprising antibody columns, ligand presenting columns and other affinity chromatographic matrices are contemplated as purification methods in the present invention.

The purified proteins produced from the gene coding sequences identified as required for proliferation can be used in a variety of protocols to generate useful antimicrobial reagents. In one embodiment of the present invention, antibodies are generated against the proteins expressed from the identified exogenous nucleic acid sequences. Both monoclonal and polyclonal antibodies can be generated against the expressed proteins. Methods for generating monoclonal and polyclonal antibodies are well known in the art. Also, antibody fragment preparations prepared from the produced antibodies discussed above are contemplated.

Another application for the purified proteins of the present invention is to screen small molecule libraries for candidate compounds active against the various target proteins of the present invention. Advances in the field of combinatorial chemistry provide methods, well known in the art, to produce large numbers of candidate compounds that can have a binding, or otherwise inhibitory effect on a target protein. Accordingly, the screening of small molecule libraries for compounds with binding affinity or inhibitory activity for a target protein produced from an identified gene sequence is contemplated by the present invention.

The present invention further contemplates utility against a variety of other pathogenic organisms in addition to *E. coli*. For example, the invention has utility in identifying genes required for proliferation in prokaryotes and eukaryotes. For example, the invention has utility with protists, such as *Plasmodium* spp.; plants; animals, such as *Entamoeba* spp. and *Contracaecum* spp.; and fungi including *Candida* spp., (e.g., *Candida albicans*), *Saccharomyces cerevisiae*, *Cryptococcus neoformans*, and *Aspergillus fumigatus*. In one embodiment of the present invention, monera, specifically bacteria are probed in search of novel gene sequences required for proliferation. This embodiment is particularly important given the rise of drug resistant bacteria.

The numbers of bacterial species that are becoming resistant to existing antibiotics are growing. A partial list of these organisms includes: *Staphylococcus* spp., such as *S. aureus*; *Enterococcus* spp., such as *E. faecalis*; *Pseudomonas* spp., such as *P. aeruginosa*; *Clostridium* spp., such as *C. botulinum*; *Haemophilus* spp., such as *H. influenzae*; *Enterobacter* spp., such as *E. cloacae*; *Vibrio* spp., such as *V. cholera*; *Moraxella* spp., such as *M. catarrhalis*; *Streptococcus* spp., such as *S. pneumoniae*; *Neisseria* spp., such as *N. gonorrhoeae*; *Mycoplasma* spp., such as *Mycoplasma pneumoniae*; *Salmonella typhimurium*; *Helicobacter pylori*; *Escherichia coli*; and *Mycobacterium tuberculosis*. The sequences identified as required for proliferation in the present invention can be used to probe these and other organisms to identify homologous required proliferation genes contained therein.

In one embodiment of the present invention, the nucleic acid sequences disclosed herein are used to screen genomic libraries generated from bacterial species of interest other than *E. coli*. For example, the genomic library may be from *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium*

5 *tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*,
10 *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any
15 of the above species. Standard molecular biology techniques are used to generate genomic libraries from various
microorganisms. In one aspect, the libraries are generated and bound to nitrocellulose paper. The identified exogenous
nucleic acid sequences of the present invention can then be used as probes to screen the libraries for homologous
sequences. The homologous sequences identified can then be used as targets for the identification of new, antimicrobial
compounds with activity against more than one organism.

For example, the preceding methods may be used to isolate nucleic acids having a sequence with at least
97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% identity to a nucleic acid sequence
selected from the group consisting of one of the sequences of SEQ ID NOS. 1-81, 405-485, 82-88, 90-242, fragments
comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases thereof, and
the sequences complementary thereto. Identity may be measured using BLASTN version 2.0 with the default
parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search
Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by reference in its
entirety). For example, the homologous polynucleotides may have a coding sequence which is a naturally occurring
allelic variant of one of the coding sequences described herein. Such allelic variants may have a substitution, deletion
or addition of one or more nucleotides when compared to the nucleic acids of SEQ ID NOS: 1-81, 405-485, 82-88, 90-
242 or the sequences complementary thereto.

Additionally, the above procedures may be used to isolate nucleic acids which encode polypeptides having at
least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, or at least 40%
identity or similarity to a polypeptide having the sequence of one of SEQ ID NOS: 243-357, 359-398 or fragments
comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined
using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity
may be identified using BLASTP with the default parameters, BLASTX with the default parameters, or TBLASTN with
the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database
Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by
reference in its entirety).

Alternatively, homologous nucleic acids or polypeptides may be identified by searching a database to identify
sequences having a desired level of homology to a nucleic acid or polypeptide involved in proliferation or an antisense
nucleic acid to a nucleic acid involved in microbial proliferation. A variety of such databases are available to those
skilled in the art, including GenBank and GenSeq. In some embodiments, the databases are screened to identify
nucleic acids or polypeptides having at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, at least
70%, at least 60%, or at least 50%, at least 40% identity or similarity to a nucleic acid or polypeptide involved in
proliferation or an antisense nucleic acid involved in proliferation. For example, the database may be screened to
identify nucleic acids homologous to one of SEQ ID Nos. 1-81, 405-485, 82-88, 90-242 or polypeptides homologous

to SEQ ID NOs. 243-357, 359-398. In some embodiments, the database may be screened to identify homologous nucleic acids or polypeptides from organisms other than *E. coli*, including organisms such as *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

In another embodiment, gene expression arrays and microarrays can be employed. Gene expression arrays are high density arrays of DNA samples deposited at specific locations on a glass chip, nylon membrane, or the like. Such arrays can be used by researchers to quantify relative gene expression under different conditions. Gene expression arrays are used by researchers to help identify optimal drug targets, profile new compounds, and determine disease pathways. An example of this technology is found in U.S. Patent No. 5807522, which is hereby incorporated by reference.

It is possible to study the expression of all genes in the genome of a particular microbial organism using a single array. For example, the arrays from Genosys consist of 12 x 24 cm nylon filters containing PCR products corresponding to 4290 ORFs from *E. coli*. 10 ngs of each are spotted every 1.5 mm on the filter. Single stranded labeled cDNAs are prepared for hybridization to the array (no second strand synthesis or amplification step is done) and placed in contact with the filter. Thus the labeled cDNAs are of "antisense" orientation. Quantitative analysis is done by phosphorimager.

Hybridization of cDNA made from a sample of total cell mRNA to such an array followed by detection of binding by one or more of various techniques known to those in the art results in a signal at each location on the array to which cDNA hybridized. The intensity of the hybridization signal obtained at each location in the array thus reflects the amount of mRNA for that specific gene that was present in the sample. Comparing the results obtained for mRNA isolated from cells grown under different conditions thus allows for a comparison of the relative amount of expression of each individual gene during growth under the different conditions.

Gene expression arrays may be used to analyze the total mRNA expression pattern at various time points after induction of an antisense nucleic acid against a proliferation-required gene. Analysis of the expression pattern indicated by hybridization to the array provides information on whether or not the target gene of the antisense nucleic acid is being affected by antisense induction, how quickly the antisense is affecting the target gene, and for later timepoints, what other genes are affected by antisense expression. For example, if the antisense is directed against a gene for ribosomal protein L7/L12 in the 50S subunit, its targeted mRNA may disappear first and then other mRNAs may be observed to increase, decrease or stay the same. Similarly, if the antisense is directed against a different 50S subunit ribosomal protein mRNA (e.g. L25), that mRNA may disappear first followed by changes in mRNA expression that are similar to those seen with the L7/L12 antisense expression. Thus, the mRNA expression pattern observed

5 with an antisense nucleic acid against a proliferation required gene may identify other proliferation-required nucleic acids in the same pathway as the target of the antisense nucleic acid. In addition, the mRNA expression patterns observed with candidate drug compounds may be compared to those observed with antisense nucleic acids against a proliferation-required nucleic acid. If the mRNA expression pattern observed with the candidate drug compound is similar to that observed with the antisense nucleic acid, the drug compound may be a promising therapeutic candidate. Thus, the assay would be useful in assisting in the selection of candidate drug compounds for use in screening methods such as those described below.

10 In cases where the source of nucleic acid deposited on the array and the source of the nucleic acid being hybridized to the array are from two different organisms, gene expression arrays can identify homologous genes in the two organisms.

15 The present invention also contemplates additional methods for screening other microorganisms for proliferation-required genes. In this embodiment, the conserved portions of sequences identified as proliferation-required can be used to generate degenerate primers for use in the polymerase chain reaction (PCR). The PCR technique is well known in the art. The successful production of a PCR product using degenerate probes generated from the sequences identified herein would indicate the presence of a homologous gene sequence in the species being screened. This homologous gene is then isolated, expressed, and used as a target for candidate antibiotic compounds. In another aspect of this embodiment, the homologous gene is expressed in an autologous organism or in a heterologous organism in such a way as to alter the level or activity of a homologous gene required for proliferation in the autologous or heterologous organism. In still another aspect of this embodiment, the homologous gene or portion is expressed in an antisense orientation in such a way as to alter the level or activity of a nucleic acid required for proliferation of an autologous or heterologous organism.

20 The homologous sequences to proliferation-required genes identified using the techniques described herein may be used to identify proliferation-required genes of organisms other than *E. coli*, to inhibit the proliferation of organisms other than *E. coli* by inhibiting the activity or reducing the amount of the identified homologous nucleic acid or polypeptide in the organism other than *E. coli*, or to identify compounds which inhibit the growth of organisms other than *E. coli* as described below.

25 In another embodiment of the present invention, *E. coli* sequences identified as required for proliferation are transferred to expression vectors capable of function within non-*E. coli* species. As would be appreciated by one of ordinary skill in the art, expression vectors must contain certain elements that are species specific. These elements can include promoter sequences, operator sequences, repressor genes, origins of replication, ribosomal binding sequences, termination sequences, and others. To use the identified exogenous sequences of the present invention, one of ordinary skill in the art would know to use standard molecular biology techniques to isolate vectors containing the sequences of interest from cultured bacterial cells, isolate and purify those sequences, and subclone those sequences into an expression vector adapted for use in the species of bacteria to be screened.

30 Expression vectors for a variety of other species are known in the art. For example, Cao et al. report the expression of steroid receptor fragments in *Staphylococcus aureus*. J. Steroid Biochem Mol Biol. 44(1):1-11

(1993). Also, Pla et al. have reported an expression vector that is functional in a number of relevant hosts including: *Salmonella typhimurium*, *Pseudomonas putida*, and *Pseudomonas aeruginosa*. J. Bacteriol. 172(8):4448-55 (1990). These examples demonstrate the existence of molecular biology techniques capable of constructing expression vectors for the species of bacteria of interest to the present invention.

Following the subcloning of the identified nucleic acid sequences into an expression vector functional in the microorganism of interest, the identified nucleic acid sequences are conditionally transcribed to assay for bacterial growth inhibition. Those expression vectors found to contain sequences that, when transcribed, inhibit bacterial growth are compared to the known genomic sequence of the pathogenic microorganism being screened or, if the homologous sequence from the organism being screened is not known, it may be identified and isolated by hybridization to the proliferation-required *E. coli* sequence interest or by amplification using primers based on the proliferation-required *E. coli* sequence of interest as described above.

The antisense sequences from the second organism which are identified as described above may then be operably linked to a promoter, such as an inducible promoter, and introduced into the second organism. The techniques described herein for identifying *E. coli* genes required for proliferation may thus be employed to determine whether the identified sequences from a second organism inhibit the proliferation of the second organism.

Antisense nucleic acids required for the proliferation of organisms other than *E. coli* or the genes corresponding thereto, may also be hybridized to a microarray containing the *E. coli* ORFs to gauge the homology between the *E. coli* sequences and the proliferation-required nucleic acids from other organisms. For example, the proliferation-required nucleic acid may be from *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni* or *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species. The proliferation-required nucleic acids from an organism other than *E. coli* may be hybridized to the array under a variety of conditions which permit hybridization to occur when the probe has different levels of homology to the sequence on the microarray. This would provide an indication of homology across the organisms as well as clues to other possible essential genes in these organisms.

In still another embodiment, the exogenous nucleic acid sequences of the present invention that are identified as required for bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. The antisense sequences can be directed against the proliferation-required genes whose sequence corresponds to the exogenous nucleic acid probes identified here (i.e. the antisense nucleic acid may hybridize to the gene or a portion thereof). Alternatively, antisense therapeutics can be directed against operons in which proliferation-required genes reside (i.e. the antisense nucleic acid may hybridize to any gene in the operon in which the proliferation-required genes reside). Further, antisense

therapeutics can be directed against a proliferation-required gene or portion thereof with or without adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a sequence spanning at least a portion of two or more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual sequence that is required for bacterial proliferation or an operon containing a proliferation-required gene.

In addition to therapeutic applications, the present invention encompasses the use of nucleic acid sequences complementary to sequences required for proliferation as diagnostic tools. For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. This utility provides a rapid and dependable method by which to identify the causative agent or agents of a bacterial infection. This utility would provide clinicians the ability to prescribe species specific antimicrobial compounds to treat such infections. In an extension of this utility, antibodies generated against proteins translated from mRNA transcribed from proliferation-required sequences can also be used to screen for specific microorganisms that produce such proteins in a species-specific manner.

The following examples teach the genes of the present invention and a subset of uses for the *E. coli* genes identified as required for proliferation. These examples are illustrative only and are not intended to limit the scope of the present invention.

EXAMPLES

The following examples are directed to the identification and exploitation of *E. coli* genes required for proliferation. Methods of gene identification are discussed as well as a variety of methods to utilize the identified sequences.

Genes Identified as Required for Proliferation of *E. coli*

Exogenous nucleic acid sequences were cloned into an inducible expression vector and assayed for growth inhibition activity. Example 1 describes the examination of a library of exogenous nucleic acid sequences cloned into IPTG-inducible expression vectors. Upon activation or induction, the expression vectors produced an RNA molecule corresponding to the subcloned exogenous nucleic acid sequences. The RNA product was in an antisense orientation with respect to the *E. coli* genes from which it was originally derived. This antisense RNA then interacted with sense mRNA produced from various *E. coli* genes and interfered with or inhibited the translation of the sense messenger RNA (mRNA) thus preventing protein production from these sense mRNA molecules. In cases where the sense mRNA encoded a protein required for the proliferation, bacterial cells containing an activated expression vector failed to grow or grew at a substantially reduced rate.

EXAMPLE 1

Inhibition of Bacterial Proliferation after IPTG induction

To study the effects of transcriptional induction in liquid medium, growth curves were carried out by back diluting cultures 1:200 into fresh media with or without 1 mM IPTG and measuring the OD₄₅₀ every 30 minutes (min). To

study the effects of transcriptional induction on solid medium, 10^2 , 10^3 , 10^4 , 10^5 , 10^6 , 10^7 and 10^8 fold dilutions of overnight cultures were prepared. Aliquots of from 0.5 to 3 μ l of these dilutions were spotted on selective agar plates with or without 1 mM IPTG. After overnight incubation, the plates were compared to assess the sensitivity of the clones to IPTG.

Of the numerous clones tested, some clones were identified as a containing sequence that inhibited *E. coli* growth after IPTG induction. Accordingly, the gene to which the inserted nucleic acid sequence corresponds, or a gene within the operon containing the inserted nucleic acid, may be required for proliferation in *E. coli*.

Characterization of Isolated Clones Negatively Affecting *E. coli* Proliferation

Following the identification of those expression vectors that, upon expression, negatively impacted *E. coli* growth or proliferation, the inserts or nucleic acid fragments contained in those expression vectors were isolated for subsequent characterization. Expression vectors of interest were subjected to nucleic acid sequence determination.

EXAMPLE 2

Nucleic Acid Sequence Determination of Identified Clones Expressing Nucleic Acid Fragments with Detrimental Effects of *E. coli* Proliferation

The nucleotide sequences for the exogenous identified sequences were determined using plasmid DNA isolated using QIAPREP (Qiagen, Valencia, CA) and methods supplied by the manufacturer. The primers used for sequencing the inserts were 5' - TGTTTATCAGACCGCTT - 3' (SEQ ID NO: 403) and 5' - ACAATTCACACAGCCTC - 3' (SEQ ID NO: 404). These sequences flank the polylinker in pLEX58A. Sequence identification numbers (SEQ ID NOs) for the identified inserts are listed in Table I and discussed below.

EXAMPLE 3

Comparison Of Isolated Sequences to Known Sequences

The nucleic acid sequences of the subcloned fragments obtained from the expression vectors discussed above were compared to known *E. coli* sequences in GenBank using BLAST version 1.4 or version 2.0.8 using the following default parameters: Filtering off, cost to open a gap=5, cost to extend a gap=2, penalty for a mismatch in the blast portion of run=-3, reward for a match in the blast portion of run=1, expectation value (e)=10.0, word size=11, number of one-line descriptions=100, number of alignments to show (B)=100. BLAST is described in Altschul, J Mol Biol. 215:403-10 (1990), the disclosure of which is incorporated herein by reference in its entirety. Expression vectors were found to contain nucleic acid sequences in both the sense and antisense orientations. The presence of known genes, open reading frames, and ribosome binding sites was determined by comparison to public databases holding genetic information and various computer programs such as the Genetics Computer Group programs FRAMES and CODONPREFERENCE. Clones were designated as "antisense" if the cloned fragment was oriented to the promoter such that the RNA transcript produced was complementary to the expressed mRNA from a chromosomal locus. Clones were designated as "sense" if they coded for an RNA fragment that was identical to a portion of a wild type mRNA from a chromosomal locus.

The sequences described in Examples 1-2 that inhibited bacterial proliferation and contained gene fragments in an antisense orientation are listed in Table I. This table lists each identified sequence by: a sequence identification number; a Molecule Number; a gene to which the identified sequence corresponds, listed according to the National Center for Biotechnology Information (NCBI), Blattner (Science 277:1453-1474(1997); also contains the *E. coli* K-12 genome sequence), or Rudd (Micro. and Mol. Rev. 62:985-1019 (1998)), (both papers are hereby incorporated by reference) nomenclatures. The CONTIG numbers for each identified sequence is shown, as well as the location of the first and last base pairs located on the *E. coli* chromosome. A Molecule Number with a "*" indicates a clone corresponding to an intergenic sequence.

The sequences of the nucleic acid inserts of SEQ ID NOs: 1-81 from U.S. Provisional Patent Application No. 60/117,405 which inhibited proliferation were further analyzed. The reanalyzed sequences corresponding to SEQ ID NOs. 1-81 of U.S. Provisional Patent Application No. 60/117,405 have SEQ ID NOs. 405-485 in the present application.

SEQ ID NOs: 82-242 in U.S. Provisional Patent Application No. 60/117,405 are identical to SEQ ID NOs: 82-242 of the present application with the following exceptions. SEQ ID NO: 148 in the present application is the complementary strand of SEQ ID NO: 148 in U.S. Provisional Patent Application No. 60/117,405. Accordingly, the protein of SEQ ID NO: 308 which is encoded by SEQ ID NO: 148 has also been revised. SEQ ID NO: 163 in the present application is the complementary strand of SEQ ID NO: 163 in U.S. Provisional Patent Application No. 60/117,405. Accordingly, the protein of SEQ ID NO: 323 which is encoded by SEQ ID NO: 163 has also been revised.

The target gene of SEQ ID NOs. 18 and 19 of U.S. Provisional Patent Application No. 60/117,405 (SEQ ID NOs. 18, 19, 422, 423 of the present application) has been revised from *dicF* to *ftsZ* to reflect the fact that these SEQ ID NOs. include natural antisense molecules which inhibit *ftsZ* expression.

The gene products of the nucleic acids of SEQ ID NOs. 198 and 239-242 in U.S. Provisional Patent Application No. 60/117,405 and in the present application (SEQ ID NOs. 358 and 399-402 of the present application) have been revised to reflect the fact that these nucleic acids encode nontranslated tRNAs and rRNAs. Tables I and II have been revised accordingly. The SEQ ID NOs. in Table II were also revised to reflect the fact that SEQ ID NOs: 89 and 402 were identical in U.S. Provisional Patent Application No. 60/117,405.

TABLE I

Identified Clones with Corresponding Genes and Operons

SEQ ID NO.	Molecule No.	Gene (NCBI)	Gene (Blattner)	Gene (Rudd)	CONTIG
1, 405	EcXA001	<i>yhhQ</i>	<i>b3471</i>	<i>yhhQ</i>	AE000423
2, 406	EcXA002	<i>lepB</i>	<i>lepB</i>	<i>lepB</i>	AE000343
3, 407	EcXA003	<i>f586</i>	<i>b0955</i>	<i>ycbZ</i>	AE000197
4, 408	EcXA004	<i>rpsG, rpsL</i>	<i>b3341</i>	<i>rpsG, rpsL</i>	AE000410
5, 409	EcXA005a	<i>rplL, rplJ</i>	<i>b3986</i>	<i>rplL, rplJ</i>	AE000472
6, 410	EcXA005b	<i>rplL</i>	<i>rplL</i>	<i>rplL</i>	AE000472
7, 411	EcXA005c	<i>rplL, rplJ</i>	<i>rplL, rplJ</i>	<i>rplL, rplJ</i>	AE000472
8, 412	EcXA005d	<i>rplL, rplJ</i>	<i>rplL, rplJ</i>	<i>rplL, rplJ</i>	AE000472
9, 413	EcXA005e	<i>rplL</i>	<i>rplL</i>	<i>rplL</i>	AE000472

SEQ ID NO.	Molecule No.	Gene (NCBI)	Gene (Blattner)	Gene (Rudd)	CONTIG
10, 414	EcXA005f	<i>rplL</i>	<i>rplL</i>	<i>rplL</i>	AE000472
11, 415	EcXA005g	<i>rplL</i>	<i>rplL</i>	<i>rplL</i>	AE000472
12, 416	EcXA006	<i>pta</i>	<i>b2297</i>	<i>pta</i>	AE000319
13, 417	EcXA007	<i>yicP</i>	<i>b3666</i>	<i>yicP</i>	AE000444
14, 418	EcXA008a	<i>yhaU</i>	<i>b3127</i>	<i>yhaU</i>	AE000394
15, 419	EcXA008b	<i>yhaU</i>	<i>yhaU</i>	<i>yhaU</i>	AE000394
16, 420	EcXA008c	<i>yhaU</i>	<i>yhaU</i>	<i>yhaU</i>	AE000394
17, 421	EcXA009	<i>ydeY</i>	<i>ydeY</i>	<i>ydeY</i>	AE000249
18, 422	EcXA010a (natural as)	<i>dicF</i>	<i>b1575</i>	<i>dicF</i>	AE000253
19, 423	EcXA010b	<i>dicF</i>	<i>dicF</i>	<i>dicF</i>	AE000253
20, 424	EcXA011	<i>fdnG</i>	<i>b1474</i>	<i>fdnG</i>	AE000244
21, 425	EcXA012a	<i>fusA</i>	<i>b3340</i>	<i>fusA</i>	AE000410
22, 426	EcXA012b	<i>fusA</i>	<i>fusA</i>	<i>fusA</i>	AE000410
23, 427	EcXA012c	<i>fusA</i>	<i>fusA</i>	<i>fusA</i>	AE000410
24, 428	EcXA013a	<i>o86</i>	<i>b2562</i>	<i>yfhL</i>	AE000342
25, 429	EcXA013b	<i>o86</i>	<i>b2562</i>	<i>yfhL</i>	AE000342
26, 430	EcXA013c	<i>o86</i>	<i>b2562</i>	<i>yfhL</i>	AE000342
27, 431	EcXA014	<i>visC</i>	<i>b2906</i>	<i>visC</i>	AE000374
28, 432	EcXA015	<i>yfdI</i>	<i>yfdI</i>	<i>yfdI</i>	AE000323
29, 433	EcXA016	<i>yeaQ</i>	<i>yeaQ</i>	<i>yeaQ</i>	AE000274
		<i>yoaG</i>	<i>yoaG</i>	<i>yoaG</i>	
30, 434	EcXA017a	<i>yggE</i>	<i>b2922</i>	<i>yggE</i>	AE000375
31, 435	EcXA017b	<i>yggE</i>	<i>yggE</i>	<i>yggE</i>	AE000375
32, 436	EcXA018a	<i>o464</i>	<i>b2074</i>	<i>yegM</i>	AE000297
33, 437	EcXA018b	<i>o464</i>	<i>b2074</i>	<i>yegM</i>	AE000297
34, 438	EcXA019a	<i>yehA</i>	<i>yehA</i>	<i>yehA</i>	AE000300
					AE000299
35, 439	EcXA019b	<i>o172, yehA</i>	<i>o172, yehA</i>	<i>o172, yehA</i>	AE000298
36, 440	EcXA020	<i>o384, f82</i>	<i>b1794, b1795</i>	<i>yeaP, yeaQ</i>	AE000274
37, 441	EcXA021a	<i>f112</i>	<i>b0218</i>	<i>yafU</i>	AE000130
38, 442	EcXA021b	<i>f112</i>	<i>b0218</i>	<i>yafU</i>	AE000130
39, 443	EcXA022	<i>o740</i>	<i>b1629</i>	<i>ydgN</i>	AE000258
40, 444	EcXA023a	<i>f176, f382</i>	<i>b1504, b1505</i>	<i>ydeS, ydeT</i>	AE000247
41, 445	EcXA023b	<i>f176, f382</i>	<i>b1504, b1505</i>	<i>ydeS, ydeT</i>	AE000247
42, 446	EcXA024	<i>ygiM, ygiN</i>	<i>b3082</i>	<i>ygiM, ygiN</i>	AE000390
43, 447	EcXA025	<i>O2383</i>	<i>b1878</i>	<i>yeaJ</i>	AE000289
44, 448	EcXA026	<i>o61</i>	<i>Unpre-dicted</i>	<i>Unpre-dicted</i>	AE000138
45, 449	EcXA027a	<i>yohH</i>	<i>yohH</i>	<i>yohH</i>	AE000303
46, 450	EcXA027b	<i>yohH</i>	<i>yohH</i>	<i>yohH</i>	AE000303
47, 451	EcXA027c	<i>yohH</i>	<i>yohH</i>	<i>yohH</i>	AE000303
		<i>yohI</i>	<i>yohI</i>	<i>yohI</i>	
48, 452	EcXA027d	<i>yohH</i>	<i>yohH</i>	<i>yohH</i>	AE000303
49, 453	EcXA028	<i>f296</i>	<i>b2305</i>	<i>yfcI</i>	AE000319
50, 454	EcXA029	<i>yjiK</i>	<i>b4391</i>	<i>yjiK</i>	AE000509
51, 455	EcXA030	<i>yi5A</i>	<i>b3557</i>	<i>yi5A</i>	AE000433
52, 456	EcXA031	<i>rplE</i>	<i>B3308</i>	<i>rplE</i>	AE000408
53, 457	EcXA032a	<i>ybgD</i>	<i>ybgD</i>	<i>ybgD</i>	AE000175
54, 458	EcXA032b**	<i>ybgD</i>	<i>ybgD</i>	<i>ybgD</i>	AE000175

SEQ ID NO.	Molecule No.	Gene (NCBI)	Gene (Blattner)	Gene (Rudd)	CONTIG
		<i>gltA</i>	<i>gltA</i>	<i>gltA</i>	
55,459	EcXA033a	<i>f477 (as)</i>	<i>b3052</i>	<i>waaE</i>	AE000387
					AE000386
56,460	EcXA033b	<i>f477</i>	<i>b3052</i>	<i>waaE</i>	AE000387
57,461	EcXA034a	<i>cspA</i>	<i>b3556</i>	<i>cspA</i>	AE000433
58,462	EcXA034b	<i>cspA</i>	<i>b3556</i>	<i>cspA</i>	AE000433
59,463	EcXA035	<i>yhjU</i>	<i>yhjU</i>	<i>yhjU</i>	AE000431
60,464	EcXA036	<i>yqiF</i>	<i>b3101</i>	<i>yqiF</i>	AE000392
		<i>o99</i>	<i>b3100</i>	<i>yqiK</i>	
61,465	EcXA037	<i>ydeH</i>	<i>b1535</i>	<i>ydeH</i>	AE000251
62,466	EcXA038	<i>sieB</i>	<i>b1353</i>	<i>sieB</i>	AE000233
63,467	EcXA039	<i>ybbD</i>		<i>ybbD</i>	AE000156
64,468	EcXA040	<i>insB 6</i>	<i>b3445</i>	<i>insB 6</i>	AE000420
65,469	EcXA041	<i>f234</i>	<i>b1138</i>	<i>ymfE</i>	AE000214
66,470	EcXA042a	<i>rplY</i>	<i>rplY</i>	<i>rplY</i>	AE000308
67,471	EcXA042b	<i>rplY</i>	<i>rplY</i>	<i>rplY</i>	AE000308
68,472	EcXA043	<i>ybgB</i>	<i>ybgB</i>	<i>ybgB</i>	AE000176
		<i>cydA</i>	<i>cydA</i>	<i>cydA</i>	
69,473	EcXA044	<i>purB</i>	<i>b1131</i>	<i>purB</i>	AE000213
70,474	EcXA045**	<i>csrA</i>	<i>csrA</i>	<i>csrA</i>	AE000353
		<i>serV</i>	<i>serV</i>	<i>serV</i>	
71,475	EcXA046**	<i>fimE, fimA</i>	<i>b4313</i>	<i>fimE, fimA</i>	AE000502
72,476	EcXA047**	<i>f96, cspB</i>	<i>f96, cspB</i>	<i>cspB, ydIS</i>	AE000252
73,477	EcXA048	<i>yefE</i>	<i>yefE</i>	<i>yefE</i>	AE000294
74,478	EcXA049	<i>yaiC</i>	<i>b0385</i>	<i>yaiC</i>	AE000145
75,479	EcXA050	<i>o467, o222</i>	<i>yaiU, yaiV</i>	<i>yaiU, yaiV</i>	AE000144
76,480	EcXA051a	<i>rplB, rplW</i>	<i>rplB, rplW</i>	<i>rplB, rplW</i>	AE000408
77,481	EcXA051b	<i>rplW</i>	<i>rplW</i>	<i>rplW</i>	AE000408
78,482	EcXA052	<i>infC</i>	<i>infC</i>	<i>infC</i>	AE000267
					AE000266
79,483	EcXA053	<i>gor</i>	<i>gor</i>	<i>gor</i>	AE000426
80,484	EcXA054	<i>rplF</i>	<i>rplF</i>	<i>rplF</i>	AE000408
81,485	EcXA055	<i>rrlG</i>	<i>rrlG</i>	<i>rrlG</i>	AE000345

EXAMPLE 4

Identification of Genes and their Corresponding Operons Affected by Antisense Inhibition

The sequencing of the entire *E. coli* genome is described in Blattner et al., Science 277:1453-1474(1997) the entirety of which is hereby incorporated by reference and the sequence of the genome is listed in GenBank Accession No.U00096, the disclosure of which is incorporated herein by reference in its entirety. The operons to which the proliferation-inhibiting nucleic acids correspond were identified using RegulonDB and information in the literature. The coordinates of the boundaries of these operons on the *E. coli* genome are listed in Table III. Table II lists the molecule numbers of the inserts containing the growth inhibiting nucleic acid fragments, the genes in the operons corresponding to the inserts, the SEQ ID NOs of the genes containing the inserts, the SEQ ID NOs of the proteins encoded by the genes, the start and stop points of the genes on the *E. coli* genome, the orientation of the genes on the genome, whether the operons

are predicted or documented, and the predicted functions of the genes. The identified operons, their putative functions, and whether or not the genes are presently thought to be required for proliferation are discussed below.

Functions for the identified genes were determined by using either Blattner functional class designations or by comparing identified sequence with known sequences in various databases. A variety of biological functions were noted for the genes to which the clones of the present invention correspond. The functions for the genes of interest appear in Table II.

The proteins that are listed in Table II are involved in a wide range of biological functions.

TABLE II
All Operon Data with Whole Chromosome Coordinates

GeneSeq ID No.	Gene Prod. Seq ID No.	Mole. No.	Genes On Operon	Left Coordinate	Right Coordinate	Predicted (P) Or Documented (D) Operon	Blattner functional class of encoded proteins	Predicted functional class of encoded proteins
82	243	EcXA001	<i>phd</i>	3606848	3607513	(P)	Hypothetical ORF, unclassified, unknown	Hypothetical outer membrane protein
83	244		<i>dcrB</i>	3607532	3608143		Hypothetical ORF, unclassified, unknown	Resistance to phage C1; periplasmic protein perhaps anchored to inner membrane
84	245	EcXA002	<i>lepB</i>	2702355	2703329	(P)	Transport and binding proteins	Secretion
85	246	EcXA003	<i>ycbZ</i>	1015762	1017522	(P)	Unknown	Protease
86	247	EcXA004	<i>tufA</i>	3467782	3468966	(D)	Translation, post-translational modification	Translation (Elongation factor Tu)
87	248		<i>fusA</i>	3469037	3471151		Translation, post-translational modification	Translation (elongation factor efp)
88	249		<i>rpsG</i>	3471179	3471718		Translation, post-translational modification	Translation
89	402	EcXA055	<i>rpsG</i>	2727636	2729178		Translation, post-translational modification	Translation (rRNA)
90	250		<i>rpsL</i>	3471815	3471815		Translation, post-translational modification	Translation
91	251	EcXA005a-g	<i>rplJ</i>	4177574	4178071	(D)	Translation, post-translational modification	Translation
92	252		<i>rplL</i>	4178138	4178503		Translation, post-translational modification	Translation
93	253	EcXA006	<i>pta</i>	2412767	2414911	(P)	Carbon compound catabolism	Carbon compound catabolism
94	254	EcXA007	<i>yicP</i>	3841591	3843357	(P)	Hypothetical ORF, unclassified, unknown	Probable adenine deaminase

GeneSeq ID No.	Gene Prod. Seq ID No.	Mole. No.	Genes On Operon	Left Coordinate	Right Coordinate	Predicted (P) Or Documented (D) Operon	Blattner functional class of encoded proteins	Predicted functional class of encoded proteins
95	255	EcXA008a-c	<i>yhaD</i>	3268266	3269492	(P)	Hypothetical ORF, unclassified, unknown	
96	256		<i>yhaE</i>	3269508	3270407		Putative enzymes	
97	257		<i>yhaF</i>	3270428	3271198		Hypothetical ORF, unclassified, unknown	
98	258		<i>yhaU</i>	3271214	3272548		Carbon compound catabolism	Probable integral membrane protein Phthalate permease family
99	259	EcXA009	<i>ydeX</i>	1599514	1601049	(P)	Putative transport proteins	
100	260		<i>ydeY</i>	1601043	1602071		Putative transport proteins	Putative ABC transporter
101	261		<i>ydeZ</i>	1602071	1603063		Hypothetical ORF, unclassified, unknown	
102	262		<i>ymeA</i>	1603075	1604097		Hypothetical ORF, unclassified, unknown	
103	263		<i>ymeB</i>	1604124	1604999		Hypothetical ORF, unclassified, unknown	
104	264		<i>ymeC</i>	1605023	1605313		Hypothetical ORF, unclassified, unknown	
105	265	EcXA010a-b	<i>fisZ</i>	105305	106456	(P)	Cell processes (incl. Adaptation, protection)	Regulator of cell division
106	266	EcXA011	<i>fahG</i>	1545425	1548472	(D)	Energy metabolism	Anaerobic respiration (formate dehydrogenase)
107	267		<i>fahH</i>	1548485	1549369		Energy metabolism	
108	268	EcXA 012a-c	<i>fahI</i>	1549362	1550015		Energy metabolism	
			Same operon as EcXA004					
109	269	EcXA013a-c	<i>yhlZ</i>	2697683	2697943	(P)	Hypothetical ORF, unclassified, unknown	No homologues, no motifs
110	270	EcXA014	<i>visC</i>	3049135	3050337	(P)	Hypothetical ORF, unclassified, unknown	Ubiquinone synthesis

GeneSeq ID No.	Gene Prod. Seq ID No.	Mole. No.	Genes On Operon	Left Coordinate	Right Coordinate	Predicted (P) Or Documented (D)	Blattner functional class of encoded proteins	Predicted functional class of encoded proteins
111	271		<i>ubtH</i>	3050360	3051538	Operon	Biosynthesis of cofactors, prosthetic groups and carriers	
112	272		<i>pepP</i>	3051535	3052860		Translation, post-translational modification	
113	273		<i>ygfB</i>	3052886	3053470		Hypothetical ORF, unclassified, unknown	
114	274	EcXA015	<i>ydgG</i>	2465875	2466237	(P)	Hypothetical ORF, unclassified, unknown	
115	275		<i>ydhH</i>	2466234	2467154		Cell structure	Putative membrane protein
116	276		<i>ydlI</i>	2467151	2468482		Hypothetical ORF, unclassified, unknown	
117	277	EcXA016	<i>yeaQ</i>	1877031	1877279	(P)	Hypothetical ORF, unclassified, unknown	Homologue to transglycosylase associated protein
118	278		<i>yeaG</i>	1877427	1877609	(P)	Hypothetical ORF, unclassified, unknown	No homologues
119	279		<i>yeaR</i>	1877613	1877972		Hypothetical ORF, unclassified, unknown	
120	280	EcXA017a-b	<i>yggE</i>	3065360	3066100	(P)	Structural proteins	Homologues in multiple bacteria, no motifs
121	281	EcXA018a-b	<i>pegM</i>	2151891	2153285	(P)	Putative transport proteins	Transport (multiple transferable resistance)
122	282		<i>yegW</i>	2153285	2156407		Hypothetical ORF, unclassified, unknown	
123	283		<i>yegO</i>	2156408	2159485		Hypothetical ORF, unclassified, unknown	
124	284		<i>yegB</i>	2159486	2160901		Putative transport proteins	
125	285	EcXA019a-b	<i>yebA</i>	2185400	2186434	(P)	Cell structure	Weak homology to pilin precursor from <i>H. Inf.</i>

GeneSeq ID No.	Gene Prod. Seq ID No.	Mole. No.	Genes On Operon	Left Coordinate	Right Coordinate	Predicted (P) Or Documented (D) Operon	Blattner functional class of encoded proteins	Predicted functional class of encoded proteins
126	286		<i>yehB</i>	2186450	2188930		Hypothetical ORF, unclassified, unknown	
127	287		<i>yehC</i>	2188946	2189665		Putative chaperones	
128	288		<i>yehD</i>	2189700	2190242		Cell structure	
		EcXA020	Same operon as EcXA018 (one of the two)					
129	289	EcXA021a-b	<i>yaU</i>	238746	239084	(P)	Hypothetical ORF, unclassified, unknown	Homologues in <i>H. Inf.</i> and <i>S. Pombe.</i> , no motifs, transmembrane region present
130	290	EcXA022	<i>ydgL</i>	1703791	1704372	(P)	Hypothetical ORF, unclassified, unknown	
131	291		<i>ydgM</i>	1704372	1704950		Hypothetical ORF, unclassified, unknown	
132	292		<i>ydgN</i>	1704943	1707165		Hypothetical ORF, unclassified, unknown	
133	293		<i>ydgO</i>	1707166	1708224		Hypothetical ORF, unclassified, unknown	
134	294		<i>ydgP</i>	1708228	1708848		Hypothetical ORF, unclassified, unknown	
135	295		<i>ydgQ</i>	1708852	1709547		Hypothetical ORF, unclassified, unknown	
136	296		<i>nth</i>	1709547	1710182		Transcription, RNA processing and degradation	
137	297	EcXA023a-b	<i>ydeR</i>	1585817	1586320	(P)	Hypothetical ORF, unclassified, unknown	
138	298		<i>ydeS</i>	1586333	1586863		Hypothetical ORF, unclassified, unknown	fim1-like

GeneSeq ID No.	Gene Prod. Seq ID No.	Mole. No.	Genes On Operon	Left Coordinate	Right Coordinate	Predicted (P) Or Documented (D) Operon	Blattner functional class of encoded proteins	Predicted functional class of encoded proteins
139	299		<i>ydeT</i>	1586877	1586025		Structural proteins	fmd-like
140	300	EcXA024	<i>ygiM</i>	3231359	3231785	(P)	Hypothetical ORF, unclassified, unknown	Weak homology to long chain fatty acid coa ligase in <i>Archaeoglobus</i>
141	301		<i>ygiW</i>	3231782	3232096		Hypothetical ORF, unclassified, unknown	Homologues in various bacteria
142	302	EcXA025	<i>yeaJ</i>	2042885	2050036	(P)	Hypothetical ORF, unclassified, unknown	Strong similarity to numerous attaching and effacing proteins and invasins
143	303	EcXA026	<i>raxA</i>	331001	331184	unpredicted		nifm like
144	304	EcXA027a-d	<i>yohG</i>	2225343	2226539	(P)	Putative transport proteins	
145	305		<i>yohH</i>	2226569	2226859		Hypothetical ORF, unclassified, unknown	Xylose binding protein-like
146	306		<i>yohI</i>	2227458	2228405	(P)	Putative regulatory protein	
147	307	EcXA028	<i>ycfI</i>	2420669	2421559	(P)	Hypothetical ORF, unclassified, unknown	Similar to <i>S. Typhi</i> histidine transport gene
148	308	EcXA029	<i>yjiK</i>	4626424	4628091	(P)	Hypothetical ORF, unclassified, unknown	Similar to ABC transporter
149	309	EcXA030	<i>yisA</i>	3718309	3718830	(P)	Hypothetical ORF, unclassified, unknown	IS150 ori A
150	310		<i>yisB</i>	3718827	3719678		Phage, transposon, or plasmid	
151	311	EcXA031	<i>rpmJ</i>	340255	3440371	(D)	Translation, post-translational modification	
152	312		<i>pilA</i>	3440403	3441734		Putative transport proteins	
153	313		<i>rpID</i>	3441742	3442176		Translation, post-translational modification	

GeneSeq ID No.	Gene Prod. Seq ID No.	Mole. No.	Genes On Operon	Left Coordinate	Right Coordinate	Predicted (P) Or Documented (D) Operon	Blattner functional class of encoded proteins	Predicted functional class of encoded proteins
154	314		<i>rpmD</i>	3442180	3442359		Translation, post-translational modification	
155	315		<i>rpsE</i>	3442363	3442866		Translation, post-translational modification	
156	316		<i>rplR</i>	3442881	3443234		Translation, post-translational modification	
157	317		<i>rplF</i>	3443244	3443777		Translation, post-translational modification	Translation
158	318		<i>rpsH</i>	3443780	3444182		Translation, post-translational modification	
159	319		<i>rpsN</i>	3444216	3444521		Translation, post-translational modification	
160	320		<i>rplE</i>	3444536	3445075		Translation, post-translational modification	Translation
161	321		<i>rplX</i>	3445090	3445404		Translation, post-translational modification	
162	322		<i>rplN</i>	3445415	3445786		Translation, post-translational modification	
163	323	EcXA032a-b	<i>yhgD</i>	751452	752018	(P)	translational modification Cell processes (incl. Adaptation, protection)	Hypothetical fibrillar protein
164	324		<i>glaA</i>	752408	753691	(D)	Energy metabolism	Glutamine biosynthesis
165	325	EcXA033a-b	<i>waaE</i>	3192961	3194394	(P)	Purative enzymes	ADP heptose synthase/ autotrophic growth protein
166	326		<i>glnE</i>	3194442	3197262		Translation, post-translational modification	
167	327		<i>yrfF</i>	3197305	3198608		Hypothetical ORF, unclassified, unknown	
168	328	EcXA034a-b	<i>cspA</i>	3717678	3717890	(P)	Cell processes (incl. Adaptation, protection)	RNA chaperonin
169	329	EcXA035	<i>yhgS</i>	3694087	3695658	(P)	Translation, post-translational modification	

GeneSeq ID No.	Gene Prod. Seq ID No.	Mole. No.	Genes On Operon	Left Coordinate	Right Coordinate	Predicted (P) Or Documented (D) Operon	Blattner functional class of encoded proteins	Predicted functional class of encoded proteins
170	330		<i>yhjT</i>	3695658	3695846		Hypothetical ORF, unclassified, unknown	
171	331		<i>yhjU</i>	3695843	3697522		Hypothetical ORF, unclassified, unknown	Regions similar to dehydrogenases, nucleases etc.
172	332	EcXA036	<i>yqjC</i>	3246594	3246977	(P)	Hypothetical ORF, unclassified, unknown	
173	333		<i>yqjD</i>	3247015	3247320		Hypothetical ORF, unclassified, unknown	
174	334		<i>yqjE</i>	3247323	3247727		Hypothetical ORF, unclassified, unknown	
175	335		<i>yqjK</i>	3247717	3248016		Similar to mukB from H. Inf.	
176	336		<i>yqjF</i>	3248112	3248594	(P)	Hypothetical ORF, unclassified, unknown	Homologues in many bacteria, blocks; secretion/ATP synthase/lfsz
177	337	EcXA037	<i>ydeH</i>	1620984	1621874	(P)	Hypothetical ORF, unclassified, unknown	Similar to carbonyl-ketoreductase, symporters
178	338	EcXA038	<i>sieB</i>	1416572	1417183	(P)	Phage, transposon, or plasmid	Super-infection exclusion factor B-like
179	339		<i>rajB (b1354)</i>	1417192	1417368		Hypothetical ORF, unclassified, unknown	
180	340	EcXA039	<i>thsD</i>	522485	526765	(P)	Hypothetical ORF, unclassified, unknown	
181	341		<i>ybbC</i>	526805	527173		Hypothetical ORF, unclassified, unknown	
182	342		<i>ybbH</i>	527173	527883		Hypothetical ORF, unclassified, unknown	Rhs-like element
183	343		<i>ybbD</i>	527864	528124		Hypothetical ORF, unclassified, unknown	ATP synthase, desaturase

GeneSeq ID No.	Gene Prod. Seq ID No.	Mole. No.	Genes On Operon	Left Coordinate	Right Coordinate	Predicted (P) Or Documented (D)	Blattner functional class of encoded proteins	Predicted functional class of encoded proteins
184	344		<i>ybl</i>	528163	528354	Operon	Hypothetical ORF, unclassified, unknown	
185	345	EcXA040	<i>insB_6</i>	351114	351389	(P)	Phage, transposon, or plasmid	
186	346		<i>insA</i>	351308	3581811		Phage, transposon, or plasmid	
187	347		<i>yrbA</i>	3580669	3581085		Hypothetical ORF, unclassified, unknown	
188	348		<i>yhbZ</i>	3579494	3580672		Hypothetical ORF, unclassified, unknown	
189	349	EcXA041	<i>ymiD</i>	1196090	1196755	(P)	Hypothetical ORF, unclassified, unknown	No assigned role
190	350		<i>ymiE</i>	1196756	1197460		Hypothetical ORF, unclassified, unknown	No assigned role
191	351	EcXA042a-b	<i>rplY</i>	2280537	2280821	(P)	Translation, post-translational modification	Translation
192	352	EcXA043	<i>hrsA</i>	765207	767183	(P)	Translation, post-translational modification	
193	353		<i>ygbB</i>	767201	769834		Carbon compound catabolism	Unknown
194	354		<i>cydA</i>	770678	772249	(D)	Energy metabolism	Cytochrome D oxidase
195	355		<i>cydB</i>	772285	773404		Energy metabolism	
196	356	EcXA044	<i>purB</i>	1189839	1191209	(D)	Nucleotide biosynthesis and metabolism	Purine biosynthesis
197	357	EcXA045	<i>csrA</i>	2816983	2817168	(P)	Regulatory function	Carbon storage regulator (mRNA decay factor)
198	358		<i>serV</i>	2816575	2816667	Unpredicted	Translation, post-translational modification	Translation (tRNA)
199	359	EcXA046	<i>fimB</i>	4538525	4539127	(D)	Cell structure	
200	360		<i>fimE</i>	4539605	4540201		Cell structure	Fimbriae
201	361		<i>fimA</i>	4540683	4541231		Cell structure	Regulator of inversion

GeneSeq ID No.	Gene Prod. Seq ID No.	Mole. No.	Genes On Operon	Left Coordinate	Right Coordinate	Predicted (P) Or Documented (D) Operon	Blattner functional class of encoded proteins	Predicted functional class of encoded proteins
202	362		<i>fimI</i>	4541188	4541835		Cell structure	
203	363		<i>fimC</i>	4541872	4542597		Cell structure	
204	364		<i>fimD</i>	4542665	4545301		Cell structure	
205	365		<i>fimF</i>	4545311	4545841		Cell structure	
206	366		<i>fimG</i>	4545854	4546357		Cell structure	
207	367		<i>fimH</i>	4546377	4547279		Cell structure	
208	368	EcXA047	<i>ydiP</i>	1637054	1638684	(P)	Hypothetical ORF, unclassified, unknown	
209	369		<i>ydiQ</i>	1637548	1638081		Hypothetical ORF, unclassified, unknown	
210	370		<i>ydiR</i>	1638078	1638389		Hypothetical ORF, unclassified, unknown	
211	371		<i>ydiS</i>	1638394	1638684		Hypothetical ORF, unclassified, unknown	Lysis protein
212	372		<i>cspB</i>	1639363	1639578	(P)	Cell processes (incl. Adaptation, protection)	
213	373	EcXA048	<i>yisZ_7</i>	2099917	2100933	(P)	Phage, transposon, or plasmid	
214	374		<i>yefJ</i>	2100938	2101411		Putative enzymes	
215	375		<i>yefI</i>	2101413	2102531		Hypothetical ORF, unclassified, unknown	
216	376		<i>yefH</i>	2102516	2103106		Putative enzymes	
217	377		<i>yefG</i>	2103087	2104079		Hypothetical ORF, unclassified, unknown	
218	378		<i>ric</i>	2104082	2105248		Cell structure	
219	379		<i>yefE</i>	2105248	2106351		Hypothetical ORF, unclassified, unknown	UDP galacto-pyranase mutase
220	380	EcXA049	<i>yaiC</i>	402927	404042	(P)	Hypothetical ORF, unclassified, unknown	Unknown
221	381	EcXA050	<i>yaiU</i>	392239	393642	(P)	Putative enzymes	Putative auto-transporter

GeneSeq ID No.	Gene Prod. Seq ID No.	Mole. No.	Genes On Operon	Left Coordinate	Right Coordinate	Predicted (P) Or Documented (D) Operon	Blattner functional class of encoded proteins	Predicted functional class of encoded proteins
222	382		<i>yanV</i>	393885	394353		Hypothetical ORF, unclassified, unknown	Hypothetical outer membrane protein
223	383	EcXA051a-b	<i>rpsQ</i>	3445951	3446205	(D)	Translation, post-translational modification	
224	384		<i>rpmC</i>	3446205	3446396		Translation, post-translational modification	
225	385		<i>rplP</i>	3446396	3446806		Translation, post-translational modification	
226	386		<i>rpsC</i>	3446819	3447520		Translation, post-translational modification	
227	387		<i>rplV</i>	3447538	3447870		Translation, post-translational modification	
228	388		<i>rpsS</i>	3447885	3448163		Translation, post-translational modification	
229	389		<i>rplB</i>	3448180	3449001		Translation, post-translational modification	Translation
230	390		<i>rplW</i>	3449019	3449321		Translation, post-translational modification	Translation
231	391		<i>rplD</i>	3449318	3449923		Translation, post-translational modification	
232	392		<i>rplC</i>	3449934	3450563		Translation, post-translational modification	
233	393		<i>rpsJ</i>	3450596	3450907		Translation, post-translational modification	
234	394	EcXA052	<i>rplT</i>	1797417	1797773	(D)	Translation, post-translational modification	
235	395		<i>rplM</i>	1797826	1798023		Translation, post-translational modification	
236	396		<i>infC</i>	1798120	1798662		Translation, post-translational modification	Translation

GeneSeq ID No.	Gene Prod. Seq ID No.	Mole. No.	Genes On Operon	Left Coordinate	Right Coordinate	Predicted (P) Or Documented (D) Operon	Blattner functional class of encoded proteins	Predicted functional class of encoded proteins
237	397		<i>thrS</i>	1798666	1800594		Translation, post-translational modification	
238	398	EcXA053	<i>gor</i>	3643929	3645281	(P)	Biosynthesis of cofactors, prosthetic groups and carriers	Glutathione oxidoreductase
		EcXA054	Same operon as EcXA031					
239	399	EcXA055	<i>mig</i>	2724301	2727204	(D)	Translation, post-translational modification	Translation (rRNA)
240	400		<i>mig</i>	2724089	2724208		Translation, post-translational modification	Translation (rRNA)
241	401		<i>glfW</i>	2727389	2727464		Translation, post-translational modification	Translation (rRNA)
242	402		<i>rrsB</i>	2727636	2729178		Translation, post-translational modification	Translation (rRNA)

5 Several of the expression vectors contain fragments that correspond to genes of unknown function or if the function is known, it is not known whether the gene is essential. For example, EcXA001, 003, 007, 008, 013, 015, 016, 017, 018, 019, 020, 021, 022, 023, 024, 025, 026, 027, 028, 029, 030, 032, 033, 034, 035, 036, 037, 038, 039, 040, 041, 047, 048, 049 and 050 are all exogenous nucleic acid sequences that correspond to *E. coli* proteins that have no known function or
10 5 where the function has not been shown to be essential or nonessential.

 The present invention reports a number of novel *E. coli* genes and operons that are required for proliferation. From the list clone sequences identified here, each was identified to be a portion of a gene in an operon required for the proliferation of *E. coli*. Cloned sequences corresponding to genes already known to be required for proliferation in *E. coli* include EcXA002, 004, 005, 010, 012, 014, 031, 02, 043, 045, 051, 052, 054, and 055. The remaining identified sequences correspond to *E. coli*
15 10 genes previously undesignated as required for proliferation in the art.

 An interesting observation of the present invention is that there are also several sequence fragments that correspond to *E. coli* genes that are not thought to be required for *E. coli* proliferation. Nevertheless, under the conditions described above, the antisense expression of these gene fragments causes a reduction in cell growth. This result implies that the genes
20 15 corresponding to the identified sequences are actually required for proliferation. Molecule Nos. corresponding to these genes are EcXA006, 044, 046, and 053.

 Following identification of the sequences of interest, these sequences were localized into operons. Since bacterial genes are expressed in a polycistronic manner, the antisense inhibition of a single gene in an operon might effect the expression of all the other genes on the operon or the genes down stream from the single gene identified. In order to determine which of the gene products in an operon are required for proliferation, each of the genes contained within an operon may be analyzed for
30 20 their effect on viability as described below.

TABLE III

Open Boundaries

Mole. No.	Left Coordinate	Right Coordinate
EcXA001	3606848	3608143
EcXA002	2702355	2703329
EcXA003	1015782	1017522
EcXA004	3467782	3472189
EcXA005	4177574	4178503
EcXA006	2412767	2414911
EcXA007	3841591	3843357
EcXA008	3268266	3272548
EcXA009	1599514	1605313
EcXA010	1647406	1647458
EcXA011	1545425	1550015
EcXA012	3467782	3472189
EcXA013	2697683	2697943
EcXA014	3049135	3053470
EcXA015	2465875	2468482
EcXA016	1877031	1877972
EcXA017	3065360	3066100
EcXA018	2151891	2160901
EcXA019	2185400	2190242
EcXA020	1877031	1877972
EcXA021	238746	239084
EcXA022	1703791	1710182
EcXA023	1585817	1588025
EcXA024	3231369	3232096
EcXA025	2042885	2050036
EcXA026	331001	331184
EcXA027c	2225343	2228405
EcXA028	2420669	2421559
EcXA029	4626424	4628091
EcXA030	3718309	3719678
EcXA031	3440255	3445786
EcXA032b	751452	753691
EcXA033	3192961	3188606
EcXA034	3717678	3717890
EcXA035	3694087	3697522
EcXA036	3246594	3248594
EcXA037	1620984	1621874
EcXA038	1416572	1417368
EcXA039	522485	528354
EcXA040	3580669	3580672
EcXA041	1196090	1197460
EcXA042	2280537	2280821

Mols. No.	Left Coordinate	Right Coordinate
EcXA043	765207	773404
EcXA044	1189839	1191209
EcXA045	2816575	2817168
EcXA046	4538525	4547279
EcXA047	1637054	1639578
EcXA048	2099917	2106351
EcXA049	402927	404042
EcXA050	392239	394353
EcXA051	3445951	3450907
EcXA052	1797417	1800594
EcXA053	3643929	3645281
EcXA054	3440255	3445786
EcXA055	2724301	2729178

EXAMPLE 5

Identification of Individual Genes within an Operon Required for Proliferation

The following example illustrates a method for determining which gene in an operon is required for proliferation. The clone insert corresponding to Molecule No. EcXA004 possesses nucleic acid sequence homology to the *E. coli* genes *rspG* and *rspL*. This molecule corresponds to an operon containing two additional genes *fusA* and *tufA*. The *rspL* gene is the first gene in the operon. To determine which gene or genes in this operon are required for proliferation, each gene is selectively inactivated using homologous recombination. Gene *rspL* is the first gene to be inactivated.

Deletion inactivation of a chromosomal copy of a gene in *E. coli* can be accomplished by integrative gene replacement. The principle of this method (Hamilton, C. M., et al 1989. *J. Bacteriol.* 171: 4617-4622) is to construct a mutant allele of the targeted gene, introduce that allele into the chromosome using a conditional suicide vector, and then force the removal of the native wild type allele and vector sequences. This will replace the native gene with a desired mutation(s) but leave promoters, operators, etc. intact. Essentiality of a gene is determined either by deduction from genetic analysis or by conditional expression of a wild type copy of the targeted gene (trans complementation).

The first step is to generate a mutant *rspL* allele using PCR amplification. Two sets of PCR primers are chosen to produce a copy of *rspL* with a large central deletion to inactivate the gene. In order to eliminate polar effects, it is desirable to construct a mutant allele comprising an in-frame deletion of most or all of the coding region of the *rspL* gene. Each set of PCR primers is chosen such that a region flanking the gene to be amplified is sufficiently long to allow recombination (typically at least 500 nucleotides on each side of the deletion). The targeted deletion or mutation will be contained within this fragment. To facilitate cloning of the PCR product, the PCR primers may also contain restriction endonuclease sites found in the cloning region of a conditional knockout vector such as pK03 (Link, et al 1997 *J. Bacteriol.* 179 (20): 6228-6237). Suitable sites include NotI, SalI, BamHI and SmaI. The *rspL* gene fragments are produced using standard PCR conditions including, but not limited to, those outlined in the manufacturers directions for the

Hot Start Taq PCR kit (Qiagen, Inc., Valencia, CA). The PCR reactions will produce two fragments that can be fused together. Alternatively, crossover PCR can be used to generate a desired deletion in one step (Ho, S. N., et al 1989. *Gene* 77: 51-59, Horton, R. M., et al 1989. *Gene* 77: 61-68). The mutant allele thus produced is called a "null" allele because it cannot produce a functional gene product.

The mutant allele obtained from PCR amplification is cloned into the multiple cloning site of pK03. Directional cloning of the *rpsL* null allele is not necessary. The pK03 vector has a temperature-sensitive origin of replication derived from pSC101. Therefore, clones are propagated at the permissive temperature of 30°C. The vector also contains two selectable marker genes: one that confers resistance to chloramphenicol and another, the *Bacillus subtilis* *sacB* gene, that allows for counter-selection on sucrose containing growth medium. Clones that contain vector DNA with the null allele inserted are confirmed by restriction endonuclease analysis and DNA sequence analysis of isolated plasmid DNA. The plasmid containing the *rpsL* null allele insert is known as a knockout plasmid.

Once the knockout plasmid has been constructed and its sequence verified, it is transformed into a Rec⁺ *E. coli* host cell. Transformation can be by any standard method such as electroporation. In some fraction of the transformed cells, plasmids will integrate into the *E. coli* chromosome by homologous recombination between the *rpsL* null allele in the plasmid and the *rpsL* gene in the chromosome. Transformant colonies in which such an event has occurred are readily selected by growth at the non-permissive temperature of 43°C and in the presence of chloramphenicol. At this temperature, the plasmid will not replicate as an episome and will be lost from cells as they grow and divide. These cells are no longer resistant to chloramphenicol and will not grow when it is present. However, cells in which the knockout plasmid has integrated into the *E. coli* chromosome remain resistant to chloramphenicol and propagate.

Cells containing integrated knock-out plasmids are usually the result of a single crossover event that creates a tandem repeat of the mutant and native wild type alleles of *rpsL* separated by the vector sequences. A consequence of this is that *rpsL* will still be expressed in these cells. In order to determine if the gene is essential for growth, the wild type copy must be removed. This is accomplished by selecting for plasmid excision, a process in which homologous recombination between the two alleles results in looping out of the plasmid sequences. Cells that have undergone such an excision event and have lost plasmid sequences including *sacB* gene are selected for by addition of sucrose to the medium. The *sacB* gene product converts sucrose to a toxic molecule. Thus counter selection with sucrose ensures that plasmid sequences are no longer present in the cell. Loss of plasmid sequences is further confirmed by testing for sensitivity to chloramphenicol (loss of the chloramphenicol resistance gene). The latter test is important because occasionally a mutation in the *sacB* gene can occur resulting in a loss of *sacB* function with no effect on plasmid replication (Link, et. al., 1997 *J. Bacteriol.* 179 (20): 6228-6237). These artifact clones retain plasmid sequences and are therefore still resistant to chloramphenicol.

In the process of plasmid excision, one of the two *rpsL* alleles is lost from the chromosome along with the plasmid DNA. In general, it is equally likely that the null allele or the wild type allele will be lost. Therefore, if the *rpsL*

5 gene is not essential, half of the clones obtained in this experiment will have the wild type allele on the chromosome and half will have the null allele. However, if the *rpsL* gene is essential, cells containing the null allele will not be obtained as a single copy of the null allele would be lethal.

10 5 To determine the essentiality of *rpsL*, a statistically significant number of the resulting clones, at least 20, are analyzed by PCR amplification of the *rpsL* gene. Since the null allele is missing a significant portion of the *rpsL* gene, its PCR product is significantly shorter than that of the wild type gene and the two are readily distinguished by gel electrophoretic analysis. The PCR products may also be subjected to sequence determination for further confirmation by methods well known to those in the art.

15 The above experiment is generally adequate for determining the essentiality of a gene such as *rpsL*. However, it may be necessary or desirable to more directly confirm the essentiality of the gene. There are several methods by which this can be accomplished. In general, these involve three steps: 1) construction of an episome containing a wild type allele, 2) isolation of clones containing a single chromosomal copy of the mutant null allele as described above but in the presence of the episomal wild type allele, and then 3) determining if the cells survive when the expression of the episomal allele is shut off. In this case, the trans copy of wild type *rpsL* is made by PCR cloning of the entire coding region of *rpsL* and inserting it in the sense orientation downstream of an inducible promoter such as the *E. coli lac* promoter. Transcription of this allele of *rpsL* will be induced in the presence of IPTG which inactivates the *lac* repressor. Under IPTG induction *rpsL* protein will be expressed as long as the recombinant gene also possesses a ribosomal binding site, also known as a "Shine-Dalgarno Sequence". The trans copy of *rpsL* is cloned on a plasmid that is compatible with pSC101. Compatible vectors include p15A, pBR322, and the pUC plasmids, among others. Replication of the compatible plasmid will not be temperature-sensitive. The entire process of integrating the null allele of *rpsL* and subsequent plasmid excision is carried out in the presence of IPTG to ensure the expression of functional *rpsL* protein is maintained throughout. After the null *rpsL* allele is confirmed as integrated on the chromosome in place of the wild type *rpsL* allele, then IPTG is withdrawn and expression of functional *rpsL* protein shut off. If the *rpsL* gene is essential, cells will cease to proliferate under these conditions. However, if the *rpsL* gene is not essential, cells will continue to proliferate under these conditions. In this experiment, essentiality is determined by conditional expression of a wild type copy of the gene rather than inability to obtain the intended chromosomal disruption.

40 An advantage of this method over some other gene disruption techniques is that the targeted gene can be deleted or mutated without the introduction of large segments of foreign DNA. Therefore, polar effects on downstream genes are eliminated or minimized. There are methods described to introduce inducible promoters upstream of potential essential bacterial genes. However in such cases, polarity from multiple transcription start points can be a problem. One way of preventing this is to insert a gene disruption cassette that contains strong transcriptional terminators upstream of the integrated inducible promoter (Zhang, Y, and Cronan, J. E. 1996 *J. Bacteriol.* 178 (12): 3614-3620). The described techniques will all be familiar to one of ordinary skill in the art.

5 Following the analysis of the *rpsL* gene, the other genes of the operon are investigated to determine if they are required for proliferation.

EXAMPLE 6

Expression of the Proteins Encoded by Genes Identified as Required for *E. coli* Proliferation

10 5 The following is provided as one exemplary method to express the proliferation-required proteins encoded by the identified sequences described above. First, the initiation and termination codons for the gene are identified. If desired, methods for improving translation or expression of the protein are well known in the art. For example, if the nucleic acid encoding the polypeptide to be expressed lacks a methionine codon to serve as the initiation site, a strong Shine-Delgarno sequence, or a stop codon, these sequences can be added. Similarly, if the identified nucleic acid sequence lacks a transcription termination signal, this sequence can be added to the construct by, for example, splicing out such a sequence from an appropriate donor sequence. In addition, the coding sequence may be operably linked to a strong promoter or an inducible promoter if desired. The identified nucleic acid sequence or portion thereof encoding the polypeptide to be expressed is obtained by PCR from the bacterial expression vector or genome using oligonucleotide primers complementary to the identified nucleic acid sequence or portion thereof and containing restriction endonuclease sequences for *NcoI* incorporated into the 5' primer and *BglII* at the 5' end of the corresponding 3'-primer, taking care to ensure that the identified nucleic acid sequence is positioned in frame with the termination signal. The purified fragment obtained from the resulting PCR reaction is digested with *NcoI* and *BglII*, purified and ligated to an expression vector.

20 15 The ligated product is transformed into DH5 α or some other *E. coli* strain suitable for the over expression of potential proteins. Transformation protocols are well known in the art. For example, transformation protocols are described in: **Current Protocols in Molecular Biology**, Vol. 1, Unit 1.8, (Ausubel, et al., Eds.) John Wiley & Sons, Inc. (1997). Positive transformants are selected after growing the transformed cells on plates containing 50-100 μ g/ml Ampicillin (Sigma, St. Louis, Missouri). In one embodiment, the expressed protein is held in the cytoplasm of the host organism. In an alternate embodiment, the expressed protein is released into the culture medium. In still another alternative, the expressed protein can be sequestered in the periplasmic space and liberated therefrom using any one of a number of cell lysis techniques known in the art. For example, the osmotic shock cell lysis method described in Chapter 16 of **Current Protocols in Molecular Biology**, Vol. 2, (Ausubel, et al., Eds.) John Wiley & Sons, Inc. (1997). Each of these procedures can be used to express a proliferation-required protein.

30 20 Expressed proteins, whether in the culture medium or liberated from the periplasmic space or the cytoplasm, are then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, standard chromatography, immunoprecipitation, immunochromatography, size exclusion chromatography, ion exchange chromatography, and HPLC. Alternatively, the secreted protein can be in a sufficiently enriched or pure state in the supernatant or growth media of the host to permit it to be used for its intended purpose without further enrichment. The purity of the protein product

5 obtained can be assessed using techniques such as Coomassie or silver staining or using antibodies against the control protein. Coomassie and silver staining techniques are familiar to those skilled in the art.

Antibodies capable of specifically recognizing the protein of interest can be generated using synthetic peptides using methods well known in the art. See, *Antibodies: A Laboratory Manual*, (Harlow and Lane, Eds.) Cold Spring Harbor Laboratory (1988). For example, 15-mer peptides having a sequence encoded by the appropriate identified gene sequence of interest or portion thereof can be chemically synthesized. The synthetic peptides are injected into mice to generate antibodies to the polypeptide encoded by the identified nucleic acid sequence of interest or portion thereof. Alternatively, samples of the protein expressed from the expression vectors discussed above can be purified and subjected to amino acid sequencing analysis to confirm the identity of the recombinantly expressed protein and subsequently used to raise antibodies. An Example describing in detail the generation of monoclonal and polyclonal antibodies appears in Example 7.

The protein encoded by the identified nucleic acid sequence of interest or portion thereof can be purified using standard immunochromatography techniques. In such procedures, a solution containing the secreted protein, such as the culture medium or a cell extract, is applied to a column having antibodies against the secreted protein attached to the chromatography matrix. The secreted protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically bound secreted protein is then released from the column and recovered using standard techniques. These procedures are well known in the art.

In an alternative protein purification scheme, the identified nucleic acid sequence of interest or portion thereof can be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies the coding sequence of the identified nucleic acid sequence of interest or portion thereof is inserted in-frame with the gene encoding the other half of the chimera. The other half of the chimera can be maltose binding protein (MBP) or a nickel binding polypeptide encoding sequence. A chromatography matrix having antibody to MBP or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites can be engineered between the MBP gene or the nickel binding polypeptide and the identified expected gene of interest, or portion thereof. Thus, the two polypeptides of the chimera can be separated from one another by protease digestion.

One useful expression vector for generating maltose binding protein fusion proteins is pMAL (New England Biolabs), which encodes the *malE* gene. In the pMal protein fusion system, the cloned gene is inserted into a pMal vector downstream from the *malE* gene. This results in the expression of an MBP-fusion protein. The fusion protein is purified by affinity chromatography. These techniques as described are well known to those skilled in the art of molecular biology.

EXAMPLE 7

Production of an Antibody to an isolated *E. coli* Protein

Substantially pure protein or polypeptide is isolated from the transformed cells as described in Example 6. The concentration of protein in the final preparation is adjusted, for example, by concentration on a 10,000 molecular weight cut off

AMICON filter device (Millipore, Bedford, MA), to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* 256:495 (1975) or any of the well-known derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as described by Engvall, E., "Enzyme immunoassay ELISA and EMIT," *Meth. Enzymol.* 70:419 (1980), and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. et al. *Basic Methods in Molecular Biology* Elsevier, New York. Section 21-2.

Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogeneous epitopes of a single protein or a peptide can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than larger molecules and can require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. et al. *J. Clin. Endocrinol. Metab.* 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. et al., Chap. 19 in: *Handbook of Experimental Immunology* D. Wier (ed) Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980).

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to

5 identify the presence of antigen in a biological sample. The antibodies can also be used in therapeutic compositions for killing bacterial cells expressing the protein.

EXAMPLE 8

Screening Chemical Libraries

A. Protein-Based Assays

10 5 Having isolated and expressed bacterial proteins shown to be required for bacterial proliferation, the present invention further contemplates the use of these expressed proteins in assays to screen libraries of compounds for potential drug candidates. The generation of chemical libraries is well known in the art. For example combinatorial chemistry can be used to generate a library of compounds to be screened in the assays described herein. A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining amino acids in every possible combination to yield peptides of a given length. Millions of chemical compounds theoretically can be synthesized through such combinatorial mixings of chemical building blocks. For example, one commentator observed that the systematic, combinatorial mixing of 100 interchangeable chemical building blocks results in the theoretical synthesis of 100 million tetrameric compounds or 10 billion pentameric compounds. (Gallop et al., "Applications of Combinatorial Technologies to Drug Discovery, Background and Peptide Combinatorial Libraries," *Journal of Medicinal Chemistry*, Vol. 37, No. 9, 1233-1250 (1994). Other chemical libraries known to those in the art may also be used, including natural product libraries.

20 20 Once generated, combinatorial libraries can be screened for compounds that possess desirable biological properties. For example, compounds which may be useful as drugs or to develop drugs would likely have the ability to bind to the target protein identified, expressed and purified as discussed above. Further, if the identified target protein is an enzyme, candidate compounds would likely interfere with the enzymatic properties of the target protein. Any enzyme can be a target protein. For example, the enzymatic function of a target protein can be to serve as a protease, nuclease, phosphatase, dehydrogenase, transporter protein, transcriptional enzyme, and any other type of enzyme known or unknown. Thus, the present invention contemplates using the protein products described above to screen combinatorial chemical libraries.

30 25 Those in the art will appreciate that a number of techniques exist for characterizing target proteins in order to identify molecules useful for the discovery and development of therapeutics. For example, some techniques involve the generation and use of small peptides to probe and analyze target proteins both biochemically and genetically in order to identify and develop drug leads. Such techniques include the methods described in PCT publications No. W09935494, W09819162, W09954728, the disclosures of which are incorporated herein by reference in their entireties.

40 30 In another example, the target protein is a serine protease and the substrate of the enzyme is known. The present example is directed towards the analysis of libraries of compounds to identify compounds that function as inhibitors of the target enzyme. First, a library of small molecules is generated using methods of combinatorial library formation well known in

5 the art. U.S. Patent NOs. 5,463,564 and 5,574, 656, to Agrafiotis, et al., entitled "System and Method of Automatically Generating Chemical Compound with Desired Properties," are two such teachings. Then the library compounds are screened to identify library compounds that possess desired structural and functional properties. U.S. Patent No. 5,684,711 also discusses a method for screening libraries.

10 5 To illustrate the screening process, the combined target and chemical compounds of the library are exposed to and permitted to interact with the purified enzyme. A labeled substrate is added to the incubation. The label on the substrate is such that a detectable signal is emitted from metabolized substrate molecules. The emission of this signal permits one to measure the effect of the combinatorial library compounds on the enzymatic activity of target enzymes. The characteristics of each library compound is encoded so that compounds demonstrating activity against the enzyme can be analyzed and features common to the various compounds identified can be isolated and combined into future iterations of libraries.

15 10 Once a library of compounds is screened, subsequent libraries are generated using those chemical building blocks that possess the features shown in the first round of screen to have activity against the target enzyme. Using this method, subsequent iterations of candidate compounds will possess more and more of those structural and functional features required to inhibit the function of the target enzyme, until a group of enzyme inhibitors with high specificity for the enzyme can be found. These compounds can then be further tested for their safety and efficacy as antibiotics for use in mammals.

20 15 It will be readily appreciated that this particular screening methodology is exemplary only. Other methods are well known to those skilled in the art. For example, a wide variety of screening techniques are known for a large number of naturally-occurring targets when the biochemical function of the target protein is known.

25 B. Cell Based Assays

30 20 Current cell-based assays used to identify or to characterize compounds for drug discovery and development frequently depend on detecting the ability of a test compound to inhibit the activity of a target molecule located within a cell or located on the surface of a cell. Most often such target molecules are proteins such as enzymes, receptors and the like. However, target molecules may also include other molecules such as DNAs, lipids, carbohydrates and RNAs including messenger RNAs, ribosomal RNAs, tRNAs and the like. A number of highly sensitive cell-based assay methods are available to those of skill in the art to detect binding and interaction of test compounds with specific target molecules. However, these methods are generally not highly effective when the test compound binds to or otherwise interacts with its target molecule with moderate or low affinity. In addition, the target molecule may not be readily accessible to a test compound in solution, such as when the target molecule is located inside the cell or within a cellular compartment such as the periplasm of a bacterial cell. Thus, current cell-based assay methods are limited in that they are not effective in identifying or characterizing compounds that interact with their targets with moderate to low affinity or compounds that interact with targets that are not readily accessible.

40 30 Cell-based assay methods of the present invention have substantial advantages over current cell-based assays practiced in the art. These advantages derive from the use of sensitized cells in which the level or activity of a

proliferation-required gene product (the target molecule) has been specifically reduced to the point where the presence or absence of its function becomes a rate-determining step for cellular proliferation. Bacterial, fungal, plant, or animal cells can all be used with the present method. Such sensitized cells become much more sensitive to compounds that are active against the affected target molecule. Thus, cell-based assays of the present invention are capable of detecting compounds exhibiting low or moderate potency against the target molecule of interest because such compounds are substantially more potent on sensitized cells than on non-sensitized cells. The affect may be such that a test compound may be two to several times more potent, at least 10 times more potent or even at least 100 times more potent when tested on the sensitized cells as compared to the non-sensitized cells.

Due in part to the increased appearance of antibiotic resistance in pathogenic microorganisms and to the significant side-effects associated with some currently used antibiotics, novel antibiotics acting at new targets are highly sought after in the art. Yet, another limitation in the current art related to cell-based assays is the problem of identifying hits against the same kinds of target molecules in the same limited set of biological pathways over and over again. This may occur when compounds acting at such new targets are discarded, ignored or fail to be detected because compounds acting at the "old" targets are encountered more frequently and are more potent than compounds acting at the new targets. As a result, the majority of antibiotics in use currently interact with a relatively small number of target molecules within an even more limited set of biological pathways.

The use of sensitized cells of the current invention provides a solution to the above problem in two ways. First, desired compounds acting at a target of interest, whether a new target or a previously known but poorly exploited target, can now be detected above the "noise" of compounds acting at the "old" targets due to the specific and substantial increase in potency of such desired compounds when tested on the sensitized cells of the current invention. Second, the methods used to sensitize cells to compounds acting at a target of interest may also sensitize these cells to compounds acting at other target molecules within the same biological pathway. For example, expression of an antisense molecule to a gene encoding a ribosomal protein is expected to sensitize the cell to compounds acting at that ribosomal protein and may also sensitize the cells to compounds acting at any of the ribosomal components (proteins or rRNA) or even to compounds acting at any target which is part of the protein synthesis pathway. Thus an important advantage of the present invention is the ability to reveal new targets and pathways that were previously not readily accessible to drug discovery methods.

Sensitized cells of the present invention are prepared by reducing the activity or level of a target molecule. The target molecule may be a gene product, such as an RNA or polypeptide produced from the proliferation-required nucleic acids described herein. Alternatively, the target may be a gene product such as an RNA or polypeptide which is produced from a sequence within the same operon as the proliferation-required nucleic acids described herein. In addition, the target may be an RNA or polypeptide in the same biological pathway as the proliferation-required nucleic acids described herein.

5 Such biological pathways include, but are not limited to, enzymatic, biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such the cell wall.

Current methods employed in the arts of medicinal and combinatorial chemistries are able to make use of structure-activity relationship information derived from testing compounds in various biological assays including direct
10 5 binding assays and cell-based assays. Occasionally compounds are directly identified in such assays that are sufficiently potent to be developed as drugs. More often, initial hit compounds exhibit moderate or low potency. Once a hit compound is identified with low or moderate potency, directed libraries of compounds are synthesized and tested in order to identify more potent leads. Generally these directed libraries are combinatorial chemical libraries consisting of compounds with
15 structures related to the hit compound but containing systematic variations including additions, subtractions and substitutions of various structural features. When tested for activity against the target molecule, structural features are identified that either alone or in combination with other features enhance or reduce activity. This information is used to design subsequent directed libraries containing compounds with enhanced activity against the target molecule. After one or several iterations of this process, compounds with substantially increased activity against the target molecule are identified and may be further developed as drugs. This process is facilitated by use of the sensitized cells of the present
20 invention since compounds acting at the selected targets exhibit increased potency in such cell-based assays, thus; more compounds can now be characterized providing more useful information than would be obtained otherwise.

Thus, it is now possible using cell-based assays of the present invention to identify or characterize compounds that previously would not have been readily identified or characterized including compounds that act at targets that previously were not readily exploited using cell-based assays. The process of evolving potent drug leads from initial hit
30 20 compounds is also substantially improved by the cell-based assays of the present invention because, for the same number of test compounds, more structure-function relationship information is likely to be revealed.

The method of sensitizing a cell entails selecting a suitable gene or operon. A suitable gene or operon is one whose expression is required for the proliferation of the cell to be sensitized. The next step is to introduce into the cells to be sensitized, an antisense RNA capable of hybridizing to the suitable gene or operon or to the RNA encoded by the suitable
35 25 gene or operon. Introduction of the antisense RNA can be in the form of an expression vector in which antisense RNA is produced under the control of an inducible promoter. The amount of antisense RNA produced is limited by varying the inducer concentration to which the cell is exposed and thereby varying the activity of the promoter driving transcription of the antisense RNA. Thus, cells are sensitized by exposing them to an inducer concentration that results in a sub-lethal level of antisense RNA expression.

30 In one embodiment of the cell-based assays, the identified exogenous *E. coli* nucleotide sequences of the present invention are used to inhibit the production of a proliferation-required protein. Expression vectors producing antisense RNA against identified genes required for proliferation are used to limit the concentration of a proliferation-required protein without severely inhibiting growth. To achieve that goal, a growth inhibition dose curve of inducer is calculated by plotting
45

5 various doses of inducer against the corresponding growth inhibition caused by the antisense expression. From this curve, various percentages of antisense induced growth inhibition, from 1 to 100% can be determined. If the promoter contained in the expression vector contains a *lac* operator the transcription is regulated by *lac* repressor and expression from the promoter is inducible with IPTG. For example, the highest concentration of the inducer IPTG that does not reduce the growth rate (0% growth inhibition) can be predicted from the curve. Cellular proliferation can be monitored by growth medium turbidity via OD measurements. In another example, the concentration of inducer that reduces growth by 25% can be predicted from the curve. In still another example, a concentration of inducer that reduces growth by 50% can be calculated. Additional parameters such as colony forming units (cfu) can be used to measure cellular viability.

10 5 Cells to be assayed are exposed to the above-determined concentrations of inducer. The presence of the inducer at this sub-lethal concentration reduces the amount of the proliferation required gene product to the lowest amount in the cell that will support growth. Cells grown in the presence of this concentration of inducer are therefore specifically more sensitive to inhibitors of the proliferation-required protein or RNA of interest or to inhibitors of proteins or RNAs in the same biological pathway as the proliferation-required protein or RNA of interest but not to inhibitors of unrelated proteins or RNAs.

15 Cells pretreated with sub-inhibitory concentrations of inducer and thus containing a reduced amount of proliferation-required target gene product are then used to screen for compounds that reduce cell growth. The sub-lethal concentration of inducer may be any concentration consistent with the intended use of the assay to identify candidate compounds to which the cells are more sensitive. For example, the sub-lethal concentration of the inducer may be such that growth inhibition is at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60% at least about 75%, or more. Cells which are pre-sensitized using the preceding method are more sensitive to inhibitors of the target protein because these cells contain less target protein to inhibit than wild-type cells.

20 20 In another embodiment of the cell based assays of the present invention, the level or activity of a proliferation required gene product is reduced using a temperature sensitive ...mutation in the proliferation-required sequence and an antisense nucleic acid against the proliferation-required sequence. Growing the cells at an intermediate temperature between the permissive and restrictive temperatures of the temperature sensitive mutant where the mutation is in a proliferation-required gene produces cells with reduced activity of the proliferation-required gene product. The antisense RNA directed against the proliferation-required sequence further reduces the activity of the proliferation required gene product. Drugs that may not have been found using either the temperature sensitive mutation or the antisense nucleic acid alone may be identified by determining whether cells in which expression of the antisense nucleic acid has been induced and which are grown at a temperature between the permissive temperature and the restrictive temperature are substantially more sensitive to a test compound than cells in which expression of the antisense nucleic acid has not been induced and which are grown at a permissive temperature. Also drugs found previously from either the antisense nucleic acid alone or the

5 temperature sensitive mutation alone may have a different sensitivity profile when used in cells combining the two approaches, and that sensitivity profile may indicate a more specific action of the drug in inhibiting one or more activities of the gene product.

10 5 Temperature sensitive mutations may be located at different sites within the gene and correspond to different domains of the protein. For example, the *dnaB* gene of *Escherichia coli* encodes the replication fork DNA helicase. DnaB has several domains, including domains for oligomerization, ATP hydrolysis, DNA binding, interaction with primase, interaction with DnaC, and interaction with DnaA [(Biswas, E.E. and Biswas, S.B. 1999. Mechanism and DnaB helicase of *Escherichia coli*: structural domains involved in ATP hydrolysis, DNA binding, and oligomerization. *Biochem.* 38:10919-10928; Hiasa, H. and Marians, K.J. 1999. Initiation of bidirectional replication at the chromosomal origin is directed by the interaction between helicase and primase. *J. Biol. Chem.* 274:27244-27248; San Martin, C., Rademacher, M., Wolpensinger, B., Engel, A., Miles, C.S., Dixon, N.E., and Carazo, J.M. 1998. Three-dimensional reconstructions from cryoelectron microscopy images reveal an intimate complex between helicase DnaB and its loading partner DnaC. *Structure* 6:501-9; Sutton, M.D., Carr, K.M., Vicente, M., and Kaguni, J.M. 1998. *Escherichia coli* DnaA protein. The N-terminal domain and loading of DnaB helicase at the *E. coli* chromosomal. *J. Biol. Chem.* 273:34255-62.), the disclosures of which are incorporated herein by reference in their entirety]. Temperature sensitive mutations in different domains of DnaB confer different phenotypes at the restrictive temperature, which include either an abrupt stop or slow stop in DNA replication with or without DNA breakdown (Wechsler, J.A. and Gross, J.D. 1971. *Escherichia coli* mutants temperature-sensitive for DNA synthesis. *Mol. Gen. Genetics* 113:273-284, the disclosure of which is incorporated herein by reference in its entirety) and termination of growth or cell death. Combining the use of temperature sensitive mutations in the *dnaB* gene that cause cell death at the restrictive temperature with an antisense to the *dnaB* gene could lead to the discovery of very specific and effective inhibitors of one or a subset of activities exhibited by DnaB.

35 25 When screening for antimicrobial agents against a gene product required for proliferation, growth inhibition of cells containing a limiting amount of that proliferation-required gene product can be assayed. Growth inhibition can be measured by directly comparing the amount of growth, measured by the optical density of the growth medium, between an experimental sample and a control sample. Alternative methods for assaying cell proliferation include measuring green fluorescent protein (GFP) reporter construct emissions, various enzymatic activity assays, and other methods well known in the art.

40 30 It will be appreciated that the above method may be performed in solid phase, liquid phase or a combination of the two. For example, cells grown on nutrient agar containing the inducer of the antisense construct may be exposed to compounds spotted onto the agar surface. A compound's effect may be judged from the diameter of the resulting killing zone, the area around the compound application point in which cells do not grow. Multiple compounds may be transferred to agar plates and simultaneously tested using automated and semi-automated equipment including but not restricted to

5 multi-channel pipettes (for example the Beckman Multimek) and multi-channel spotters (for example the Genomic Solutions Flexys). In this way multiple plates and thousands to millions of compounds may be tested per day.

10 5 The compounds may also be tested entirely in liquid phase using microtiter plates as described below. Liquid phase screening may be performed in microtiter plates containing 96, 384, 1536 or more wells per microtiter plate to screen multiple plates and thousands to millions of compounds per day. Automated and semi-automated equipment may be used for addition of reagents (for example cells and compounds) and determination of cell density.

EXAMPLE 9

15 The effectiveness of the above cell based assay was validated using constructs expressing antisense RNA to *E. coli* genes *rplL*, *rplJ*, and *rplW* encoding ribosomal proteins L7/L12, L10 and L23 respectively. These proteins are part of the protein synthesis apparatus of the cell and as such are required for proliferation. These constructs were used to test the effect of antisense expression on cell sensitivity to antibiotics known to bind to the ribosome and thereby inhibit protein synthesis. Constructs expressing antisense RNA to several other genes (*elaD*, *visC*, *yohH*, and *aptE/B*), the products of which are not involved in protein synthesis were used for comparison.

20 First expression vectors containing antisense constructs to either *rplW* or to *elaD* were introduced into separate *E. coli* cell populations. Vector introduction is a technique well known to those of ordinary skill in the art. The expression vectors of this example contain IPTG inducible promoters that drive the expression of the antisense RNA in the presence of the inducer. However, those skilled in the art will appreciate that other inducible promoters may also be used. Suitable expression vectors are also well known in the art. The *E. coli* antisense clones encoding ribosomal proteins L7/L12, L10 and L23 were used to test the effect of antisense expression on cell sensitivity to the antibiotics known to bind to these proteins. First, expression vectors containing antisense to either the genes encoding L7/L12 and L10 or L23 were introduced into separate *E. coli* cell populations.

25 The cell populations were exposed to a range of IPTG concentrations in liquid medium to obtain the growth inhibitory dose curve for each clone (Fig. 1). First, seed cultures were grown to a particular turbidity that is measured by the optical density (OD) of the growth solution. The OD of the solution is directly related to the number of bacterial cells contained therein. Subsequently, sixteen 200 μ l liquid medium cultures were grown in a 96 well microtiter plate at 37 C with a range of IPTG concentrations in duplicate two-fold serial dilutions from 1600 μ M to 12.5 μ M (final concentration). Additionally, control cells were grown in duplicate without IPTG. These cultures were started from equal amounts of cells derived from the same initial seed culture of a clone of interest. The cells were grown for up to 15 hours and the extent of growth was determined by measuring the optical density of the cultures at 600 nm. When the control culture reached mid-log phase the percent growth of the control for each of the IPTG containing cultures was plotted against the log concentrations of IPTG to produce a growth inhibitory dose response curve for the IPTG. The concentration of IPTG that inhibits cell growth to 50% (IC_{50}) as compared to the 0 mM IPTG control (0% growth inhibition) was then calculated from

the curve. Under these conditions, an amount of antisense RNA was produced that reduced the expression levels of *rplW* and *elaD* to a degree such that growth was inhibited by 50%.

Alternative methods of measuring growth are also contemplated. Examples of these methods include measurements of proteins, the expression of which is engineered into the cells being tested and can readily be measured. Examples of such proteins include green fluorescent protein (GFP) and various enzymes.

Cells were pretreated with the selected concentration of IPTG and then used to test the sensitivity of cell populations to tetracycline, erythromycin and other protein synthesis inhibitors. An example of a tetracycline dose response curve is shown in Figures 2A and 2B for the *rplW* and *elaD* genes, respectively. Cells were grown to log phase and then diluted into media alone or media containing IPTG at concentrations which give 20% and 50% growth inhibition as determined by IPTG dose response curves. After 2.5 hours, the cells were diluted to a final OD600 of 0.002 into 96 well plates containing (1) +/- IPTG at the same concentrations used for the 2.5 hour pre-incubation; and (2) serial two-fold dilutions of tetracycline such that the final concentrations of tetracycline range from 1 µg/ml to 15.6 ng/ml and 0 µg/ml. The 96 well plates were incubated at 37°C and the OD600 was read by a plate reader every 5 minutes for up to 15 hours. For each IPTG concentration and the no IPTG control, tetracycline dose response curves were determined when the control (absence of tetracycline) reached 0.1 OD600. To compare tetracycline sensitivity with and without IPTG, tetracycline IC50s were determined from the dose response curves (Figs. 2A-B). Cells with reduced levels of L23 (*rplW*) showed increased sensitivity to tetracycline (Fig. 2A) as compared to cells with reduced levels of *elaD* (Fig. 2B). Figure 3 shows a summary bar chart in which the ratios of tetracycline IC50s determined in the presence of IPTG which gives 50% growth inhibition versus tetracycline IC50s determined without IPTG (fold increase in tetracycline sensitivity) were plotted. Cells with reduced levels of either L7/L12 (genes *rplL*, *rplJ*) or L23 (*rplW*) showed increased sensitivity to tetracycline (Fig. 3). Cells expressing antisense to genes not known to be involved in protein synthesis (*atpB/E*, *visC*, *elaD*, *yohM*) did not show the same increased sensitivity to tetracycline, validating the specificity of this assay (Fig. 3).

In addition to the above, it has been observed in initial experiments that clones expressing antisense RNA to genes involved in protein synthesis (including genes encoding ribosomal proteins L7/L12 & L10, L7/L12 alone, L22, and L18, as well as genes encoding rRNA and Elongation Factor G) have increased sensitivity to the macrolide, erythromycin, whereas clones expressing antisense to the non-protein synthesis genes *elaD*, *atpB/E* and *visC* do not. Furthermore, the clone expressing antisense to *rplL* and *rplJ* does not show increased sensitivity to nalidixic acid and ofloxacin, antibiotics which do not inhibit protein synthesis.

The results with the ribosomal protein genes *rplL*, *rplJ*, and *rplW* as well as the initial results using various other antisense clones and antibiotics show that limiting the concentration of an antibiotic target makes cells more sensitive to the antimicrobial agents that specifically interact with that protein. The results also show that these cells are sensitized to antimicrobial agents that inhibit the overall function in which the protein target is involved but are not sensitized to antimicrobial agents that inhibit other functions.

5 The cell based assay described above may also be used to identify the biological pathway in which a proliferation-required nucleic acid or its gene product lies. In such methods, cells expressing a sub-lethal level of antisense to a target proliferation-required nucleic acid and control cells in which expression of the antisense has not been induced are contacted with a panel of antibiotics known to act in various pathways. If the antibiotic acts in the pathway in which the target proliferation-required nucleic acid or its gene product lies, cells in which expression of the antisense has been induced will be more sensitive to the antibiotic than cells in which expression of the antisense has not been induced.

10 5 As a control, the results of the assay may be confirmed by contacting a panel of cells expressing antisense nucleic acids to many different proliferation-required genes including the target proliferation-required gene. If the antibiotic is acting specifically, heightened sensitivity to the antibiotic will be observed only in the cells expressing antisense to a target proliferation-required gene (or cells expressing antisense to other proliferation-required genes in the same pathway as the target proliferation-required gene) but will not be observed generally in all cells expressing antisense to proliferation-required genes.

15 10 Similarly, the above method may be used to determine the pathway on which a test antibiotic acts. A panel of cells, each of which expresses antisense to a proliferation-required nucleic acid in a known pathway, is contacted with a compound for which it is desired to determine the pathway on which it acts. The sensitivity of the panel of cells to the test compound is determined in cells in which expression of the antisense has been induced and in control cells in which expression of the antisense has not been induced. If the test antibiotic acts on the pathway on which an antisense nucleic acid acts, cells in which expression of the antisense has been induced will be more sensitive to the antibiotic than cells in which expression of the antisense has not been induced. In addition, control cells in which expression of antisense to proliferation-required genes in other pathways has been induced will not exhibit heightened sensitivity to the antibiotic. In this way, the pathway on which the test antibiotic acts may be determined.

20 20 The Example below provides one method for performing such assays.

EXAMPLE 10

25 Identification of the Pathway in which a Proliferation-Required Gene Lies or the Pathway on which an Antibiotic Acts

30 A. Preparation of Bacterial Stocks for Assay

40 To provide a consistent source of cells to screen, frozen stocks of host bacteria containing the desired antisense construct are prepared using standard microbiological techniques. For example, a single clone of the organism can be isolated by streaking out a sample of the original stock onto an agar plate containing nutrients for cell growth and an antibiotic for which the antisense construct contains a gene which confers resistance. After overnight growth an isolated colony is picked from the plate with a sterile needle and transferred to an appropriate liquid growth media containing the antibiotic required for maintenance of the plasmid. The cells are incubated at 30°C to 37°C with vigorous shaking for 4 to

6 hours to yield a culture in exponential growth. Sterile glycerol is added to 15% (volume to volume) and 100 μ L to 500 μ L aliquots are distributed into sterile cryotubes, snap frozen in liquid nitrogen, and stored at -80°C for future assays.

B. Growth of Bacteria for Use in the Assay

A day prior to an assay, a stock vial is removed from the freezer, rapidly thawed (37°C water bath) and a loop of culture is streaked out on an agar plate containing nutrients for cell growth and an antibiotic to which the antisense construct confers resistance. After overnight growth at 37°C, ten randomly chosen, isolated colonies are transferred from the plate (sterile inoculum loop) to a sterile tube containing 5 mL of LB medium containing the antibiotic to which the antisense vector confers resistance. After vigorous mixing to form a homogeneous cell suspension, the optical density of the suspension is measured at 600 nm (OD600) and if necessary an aliquot of the suspension is diluted into a second tube of 5 mL, sterile, LB medium plus antibiotic to achieve an $OD_{600} \leq 0.02$ absorbance units. The culture is then incubated at 37° C for 1-2 hrs with shaking until the OD600 reaches OD 0.2 – 0.3. At this point the cells are ready to be used in the assay.

C. Selection of Media to be Used in Assay

Two fold dilution series of the inducer are generated in culture media containing the appropriate antibiotic for maintenance of the antisense construct. Several media are tested side by side and three to four wells are used to evaluate the effects of the inducer at each concentration in each media. For example, M9 minimal media, LB broth, TBD broth and Muller-Hinton media may be tested with the inducer IPTG at the following concentrations, 50 μ M, 100 μ M, 200 μ M, 400 μ M, 600 μ M, 800 μ M and 1000 μ M. Equal volumes of test media-inducer and cells are added to the wells of a 384 well microtiter plate and mixed. The cells are prepared as described above and diluted 1:100 in the appropriate media containing the test antibiotic immediately prior to addition to the microtiter plate wells. For a control, cells are also added to several wells of each media that do not contain inducer, for example 0 M IPTG. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD600 of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of inducer is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in media without inducer. The medium yielding greatest sensitivity to inducer is selected for use in the assays described below.

D. Measurement of Test Antibiotic Sensitivity in the Absence of Antisense Construct Induction

Two-fold dilution series of antibiotics of known mechanism of action are generated in the culture media selected for further assay development that has been supplemented with the antibiotic used to maintain the construct. A panel of test antibiotics known to act on different pathways is tested side by side with three to four wells being used to evaluate the effect of a test antibiotic on cell growth at each concentration. Equal volumes of test antibiotic and cells are added to the wells of a 384 well microtiter plate and mixed. Cells are prepared as described above using the media selected for assay development supplemented with the antibiotic required to maintain the antisense construct and are diluted 1:100 in identical media immediately prior to addition to the microtiter plate wells. For a control, cells are also added to several

5 wells that contain the solvent used to dissolve the antibiotics but no antibiotic. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD600 of the wells over an 18-hour period. The percent inhibition of growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in media without antibiotic. A plot of percent inhibition against
10 5 log[antibiotic concentration] allows extrapolation of an IC₅₀ value for each antibiotic.

E. Measurement of Test Antibiotic Sensitivity in the Presence of Antisense Construct Inducer

15 The culture media selected for use in the assay is supplemented with inducer at concentrations shown to inhibit cell growth by 50 and 80% as described above and the antibiotic used to maintain the construct. Two fold dilution series of the panel of test antibiotics used above are generated in each of these media. Several antibiotics are tested side by side
20 10 with three to four wells being used to evaluate the effects of an antibiotic on cell growth at each concentration, in each media. Equal volumes of test antibiotic and cells are added to the wells of a 384 well microtiter plate and mixed. Cells are prepared as described above using the media selected for use in the assay supplemented with the antibiotic required to maintain the antisense construct. The cells are diluted 1:100 into two 50 mL aliquots of identical media containing concentrations of inducer that have been shown to inhibit cell growth by 50% and 80 % respectively and incubated at
25 15 37°C with shaking for 2.5 hours. Immediately prior to addition to the microtiter plate wells, the cultures are adjusted to an appropriate OD₆₀₀ (typically 0.002) by dilution into warm (37°C) sterile media supplemented with identical concentrations of the inducer and antibiotic used to maintain the antisense construct. For a control, cells are also added to several wells that contain solvent used to dissolve test antibiotics but which contain no antibiotic. Cell growth is monitored continuously by incubation at 37°C in a microtiter plate reader monitoring the OD600 of the wells over an 18-
30 20 hour period. The percent inhibition of growth produced by each concentration of antibiotic is calculated by comparing the rates of logarithmic growth against that exhibited by cells growing in media without antibiotic. A plot of percent inhibition against log[antibiotic concentration] allows extrapolation of an IC₅₀ value for each antibiotic.

F. Determining the Specificity of the Test Antibiotics

35 A comparison of the IC₅₀s generated by antibiotics of known mechanism of action under antisense induced and non-induced conditions allows the pathway in which a proliferation-required nucleic acid lies to be identified. If cells
40 25 expressing an antisense nucleic acid against a proliferation-required gene are selectively sensitive to an antibiotic acting via a particular pathway, then the gene against which the antisense acts is involved in the pathway in which the antibiotic acts.

G. Identification of Pathway in which a Test Antibiotic Acts

30 As discussed above, the cell based assay may also be used to determine the pathway against which a test antibiotic acts. In such an analysis, the pathways against which each member of a panel of antisense nucleic acids acts are identified as described above. A panel of cells, each containing an inducible antisense vector against a gene in a known proliferation-required pathway, is contacted with a test antibiotic for which it is desired to determine the pathway
45 50

on which it acts under inducing an non-inducing conditions. If heightened sensitivity is observed in induced cells expressing antisense against a gene in a particular pathway but not in induced cells expressing antisense against genes in other pathways, then the test antibiotic acts against the pathway for which heightened sensitivity was observed.

One skilled in the art will appreciate that further optimization of the assay conditions, such as the concentration of inducer used to induce antisense expression and/or the growth conditions used for the assay (for example incubation temperature and media components) may further increase the selectivity and/or magnitude of the antibiotic sensitization exhibited.

The following example confirms the effectiveness of the methods described above.

EXAMPLE 11

Identification of the Pathway in which a Proliferation-Required Gene Lies

Antibiotics of various chemical classes and modes of action were purchased from Sigma Chemicals (St. Louis, MO). Stock solutions were prepared by dissolving each antibiotic in an appropriate aqueous solution based on information provided by the manufacturer. The final working solution of each antibiotic contained no more than 0.2% (w/v) of any organic solvent. To determine their potency against a bacterial strain engineered for expression of an antisense against a proliferation-required 50S ribosomal protein, each antibiotic was serially diluted two or three fold in growth medium supplemented with the appropriate antibiotic for maintenance of the anti-sense construct. At least ten dilutions were prepared for each antibiotic. 25 μ L aliquots of each dilution were transferred to discrete wells of a 384-well microplate (the assay plate) using a multi-channel pipette. Quadruplicate wells were used for each dilution of an antibiotic under each treatment condition (plus and minus inducer). Each assay plate contained twenty wells for cell growth controls (growth media replacing antibiotic), ten wells for each treatment (plus and minus inducer, in this example IPTG). Assay plates were usually divided into the two treatments: half the plate containing induced cells and an appropriate concentrations of inducer (in this example IPTG) to maintain the state of induction, the other half containing non-induced cells in the absence of IPTG.

Cells for the assay were prepared as follows. Bacterial cells containing a construct, from which expression of antisense nucleic acid against *rplL* and *rplJ*, which encode proliferation-required 50S ribosomal subunit proteins, is inducible in the presence of IPTG, were grown into exponential growth (OD_{600} 0.2 to 0.3) and then diluted 1:100 into fresh media containing either 400 μ M or 0 μ M inducer (IPTG). These cultures were incubated at 37° C for 2.5 hr. After a 2.5 hr incubation, induced and non-induced cells were respectively diluted into an assay medium at a final OD_{600} value of 0.0004. The medium contained an appropriate concentration of the antibiotic for the maintenance of the anti-sense construct. In addition, the medium used to dilute induced cells was supplemented with 800 μ M IPTG so that addition to the assay plate would result in a final IPTG concentration of 400 μ M. Induced and non-induced cell suspensions were dispensed (25 μ L/well) into the appropriate wells of the assay plate as discussed previously. The plate was then loaded into a plate reader, incubated at constant temperature, and cell growth was monitored in each well by the measurement of

light scattering at 595 nm. Growth was monitored every 5 minutes until the cell culture attained a stationary growth phase. For each concentration of antibiotic, a percentage inhibition of growth was calculated at the time point corresponding to mid-exponential growth for the associated control wells (no antibiotic, plus or minus IPTG). For each antibiotic and condition (plus or minus IPTG), a plot of percent inhibition versus log of antibiotic concentration was generated and the IC₅₀ determined. A comparison of the IC₅₀ for each antibiotic in the presence and absence of IPTG revealed whether induction of the antisense construct sensitized the cell to the mechanism of action exhibited by the antibiotic. Cells which exhibited a significant (standard statistical analysis) numerical decrease in the IC₅₀ value in the presence of inducer were considered to have an increased sensitivity to the test antibiotic.

The results are provided in the table below, which lists the classes and names of the antibiotics used in the analysis, the targets of the antibiotics, the IC₅₀ in the absence of IPTG, the IC₅₀ in the presence of IPTG, the concentration units for the IC₅₀s, the fold increase in IC₅₀ in the presence of IPTG, and whether increased sensitivity was observed in the presence of IPTG.

TABLE IV
Effect of Expression of Antisense RNA to rplL and rplJ on Antibiotic Sensitivity

ANTIBIOTIC CLASS / Names	TARGET	IC50 (IPTG)	IC50 (+IPTG)	Conc. Unit	Fold Increase in Sensitivity	Sensitivity Increased?
PROTEIN SYNTHESIS INHIBITOR ANTIBIOTICS						
AMINOGLYCOSIDES						
Gentamicin	30S ribosome function	2715	19.19	ng/ml	141	Yes
Streptomycin	30S ribosome function	11280	161	ng/ml	70	Yes
Spectinomycin	30S ribosome function	18050	< 156	ng/ml		Yes
Tobramycin	30S ribosome function	3594	70.58	ng/ml	51	Yes
MACROLIDES						
Erythromycin	50S ribosome function	7467	187	ng/ml	40	Yes
AROMATIC POLYKETIDES						
Tetracycline	30S ribosome function	199.7	1.83	ng/ml	109	Yes
Minocycline	30S ribosome function	668.4	3.897	ng/ml	172	Yes
Doxycycline	30S ribosome function	413.1	27.81	ng/ml	15	Yes
OTHER PROTEIN SYNTHESIS INHIBITORS						
Fusidic acid	Elongation Factor G function	59890	641	ng/ml	94	Yes
Chloramphenicol	30S ribosome function	465.4	1.516	ng/ml	307	Yes
Lincomycin	50S ribosome function	47150	324.2	ng/ml	145	Yes
OTHER ANTIBIOTIC MECHANISMS						
B-LACTAMS						
Cefoxitin	Cell wall biosynthesis	2782	2484	ng/ml	1	No
Cefotaxime	Cell wall biosynthesis	24.3	24.16	ng/ml	1	No
DNA SYNTHESIS INHIBITORS						
Nalidixic acid	DNA Gyrase activity	6973	6025	ng/ml	1	No
Ofloxacin	DNA Gyrase activity	49.61	45.89	ng/ml	1	No
OTHER						
Bacitracin	Cell membrane function	4077	4677	mg/ml	1	No
Trimethoprim	Dihydrofolate Reductase activity	128.9	181.97	ng/ml	1	No
Vancomycin	Cell wall biosynthesis	145400	72550	ng/ml	2	No

5 The above results demonstrate that induction of an antisense RNA to genes encoding 50S ribosomal subunit proteins results in a selective and highly significant sensitization of cells to antibiotics that inhibit ribosomal function and protein synthesis. The above results further demonstrate that induction of an antisense construct to an essential gene sensitizes an organism to compounds that interfere with that gene products' biological role. This sensitization is restricted to compounds that interfere with pathways associated with the targeted gene and its product.

10 Assays utilizing antisense constructs to essential genes can be used to identify compounds that specifically interfere with the activity of multiple targets in a pathway. Such constructs can be used to simultaneously screen a sample against multiple targets in one pathway in one reaction (Combinatorial HTS).

15 Furthermore, as discussed above, panels of antisense construct containing cells may be used to characterize the point of intervention of any compound affecting an essential biological pathway including antibiotics with no known mechanism of action.

20 Another embodiment of the present invention is a method for determining the pathway against which a test antibiotic compound is active in which the activity of target proteins or nucleic acids involved in proliferation-required pathways is reduced by contacting cells with a sublethal concentration of a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid is a target protein or nucleic acid corresponding to a proliferation-required nucleic acid identified using the methods described above. The method is similar to those described above for determining which pathway a test antibiotic acts against except that rather than reducing the activity or level of a proliferation-required gene product using a sublethal level of antisense to a proliferation-required nucleic acid, the activity or level of the proliferation-required gene product is reduced using sublethal level of a known antibiotic which acts against the proliferation required gene product.

25 Interactions between drugs which affect the same biological pathway has been described in the literature. For example, Mecillinam (Amdinocillin) binds to and inactivates the penicillin binding protein 2 (PBP2, product of the *mrdA* in *E. coli*). This antibiotic interacts with other antibiotics that inhibit PBP2 as well as antibiotics that inhibit other penicillin binding proteins such as PBP3 [(Gutmann, L., Vincent, S., Billot-Klein, D., Acar, J.F., Mrena, E., and Williamson, R. (1986) Involvement of penicillin-binding protein 2 with other penicillin-binding proteins in lysis of *Escherichia coli* by some beta-lactam antibiotics alone and in synergistic lytic effect of amdinocillin (mecillinam). *Antimicrobial Agents & Chemotherapy*, 30:906-912), the disclosure of which is incorporated herein by reference in its entirety]. Interactions between drugs could, therefore, involve two drugs that inhibit the same target protein or nucleic acid or inhibit different proteins or nucleic acids in the same pathway [(Fukuoka, T., Domon, H., Kakuta, M., Ishii, C., Hirasawa, A., Utsui, Y., Ohya, S., and Yasuda, H. (1997) Combination effect between panipenem and vancomycin on highly methicillin-resistant *Staphylococcus aureus*. *Japan. J. Antibio.* 50:411-419; Smith, C.E., Foleno, B.E., Barrett, J.F., and Froese, M.B. (1997) Assessment of the synergistic interactions of levofloxacin and ampicillin against *Enterococcus faecium* by the checkerboard agar dilution and time-kill methods. *Diagnos. Microbiol. Infect. Disease* 27:85-92; den Hollander, J.G., Horrevorts, A.M., van Goor, M.L.,

Verbrugh, H.A., and Mouton, J.W. (1997) Synergism between tobramycin and ceftazidime against a resistant *Pseudomonas aeruginosa* strain, tested in an in vitro pharmacokinetic model. *Antimicrobial Agents & Chemotherapy*. 41:95-110), the disclosure of all of which are incorporated herein by reference in their entireties).

Two drugs may interact even though they inhibit different targets. For example, the proton pump inhibitor, Omeprazole, and the antibiotic, Amoxycillin, two synergistic compounds acting together, can cure *Helicobacter pylori* infection ([Gabryelewicz, A., Laszewicz, W., Dzieniszewski, J., Ciok, J., Marlicz, K., Bielecki, D., Popiela, T., Legutko, J., Knapik, Z., Poniewierka, E. (1997) Multicenter evaluation of dual-therapy (omeprazole and amoxycillin) for *Helicobacter pylori*-associated duodenal and gastric ulcer (two years of the observation). *J. Physiol. Pharmacol.* 48 Suppl 4:93-105), the disclosure of which is incorporated herein by reference in its entirety].

The growth inhibition from the sublethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sublethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring growth inhibition.

Cells are contacted with a combination of each member of a panel of known antibiotics at a sublethal level and varying concentrations of the test antibiotic. As a control, the cells are contacted with varying concentrations of the test antibiotic alone. The IC_{50} of the test antibiotic in the presence and absence of the known antibiotic is determined. If the IC_{50} s in the presence and absence of the known drug are substantially similar, then the test drug and the known drug act on different pathways. If the IC_{50} s are substantially different, then the test drug and the known drug act on the same pathway.

Another embodiment of the present invention is a method for identifying a candidate compound for use as an antibiotic in which the activity of target proteins or nucleic acids involved in proliferation-required pathways is reduced by contacting cells with a sublethal concentration of a known antibiotic which acts against the target protein or nucleic acid. In one embodiment, the target protein or nucleic acid is a target protein or nucleic acid corresponding to a proliferation-required nucleic acid identified using the methods described above. The method is similar to those described above for identifying candidate compounds for use as antibiotics except that rather than reducing the activity or level of a proliferation-required gene product using a sublethal level of antisense to a proliferation-required nucleic acid, the activity or level of the proliferation-required gene product is reduced using a sublethal level of a known antibiotic which acts against the proliferation required gene product.

The growth inhibition from the sublethal concentration of the known antibiotic may be at least about 5%, at least about 8%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, or at least about 75%, or more.

Alternatively, the sublethal concentration of the known antibiotic may be determined by measuring the activity of the target proliferation-required gene product rather than by measuring growth inhibition.

In order to characterize test compounds of interest, cells are contacted with a panel of known antibiotics at a sublethal level and one or more concentrations of the test compound. As a control, the cells are contacted with the same concentrations of the test compound alone. The IC_{50} of the test compound in the presence and absence of the known antibiotic is determined. If the IC_{50} of the test compound is substantially different in the presence and absence of the known drug then the test compound is a good candidate for use as an antibiotic. As discussed above, once a candidate compound is identified using the above methods its structure may be optimized using standard techniques such as combinatorial chemistry.

Representative known antibiotics which may be used in each of the above methods are provided in the table below. However, it will be appreciated that other antibiotics may also be used.

ANTIBIOTIC	INHIBITS/TARGET	RESISTANT MUTANTS
Inhibitors of Transcription		
Rifamycin, 1959 Rifampicin	Inhibits initiation of transcription/ β -subunit RNA polymerase, <i>rpoB</i>	<i>rpoB</i> , <i>crp</i> , <i>cyaA</i>
Rifabutin Rifaximin		
Streptolydigin	Accelerates transcription chain termination/ β -subunit RNA polymerase	<i>rpoB</i>
Streptovaricin	an acyclic ansamycin, inhibits RNA polymerase	<i>rpoB</i>
Actinomycin D + EDTA	Intercalates between 2 successive G-C pairs, <i>rpoB</i> , inhibits RNA synthesis	<i>pldA</i>
Inhibitors of Nucleic Acid Metabolism		
Quinolones, 1962 Nalidixic acid	subunit gyrase and/or topoisomerase IV, <i>gyrA</i>	<i>gyrAorB</i> , <i>ica</i> , <i>sloB</i>
Oxolinic acid		
Fluoroquinolones Ciprofloxacin, 1983 Norfloxacin	subunit gyrase, <i>gyrA</i> and/or topoisomerase IV (probable target in Staph)	<i>gyrA</i> <i>norA</i> (efflux in Staph) <i>hipQ</i>
Coumerins Novobiocin	Inhibits ATPase activity of β -subunit gyrase, <i>gyrB</i>	<i>gyrB</i> , <i>cysB</i> , <i>cysE</i> , <i>nov</i> , <i>ompA</i>
Coumermycin	Inhibits ATPase activity of β -subunit gyrase, <i>gyrB</i>	<i>gyrB</i> , <i>hisW</i>
Albicidin	DNA synthesis	<i>tsx</i> (nucleoside channel)
Metronidazole	Causes single-strand breaks in DNA	<i>nar</i>
Inhibitors of Metabolic Pathways		
Sulfonamides, 1932 Sulfanilamide	blocks synthesis of dihydrofolate, dihydro- pteroate synthesis, <i>folP</i>	<i>folP</i> , <i>gpt</i> , <i>pabA</i> , <i>pabB</i> , <i>pabC</i>
Trimethoprim, 1962	Inhibits dihydrofolate reductase, <i>folA</i>	<i>folA</i> , <i>thyA</i>
Showdomycin	Nucleoside analogue capable of alkylating	<i>nupC</i> , <i>prp</i>

ANTIBIOTIC	INHIBITS/TARGET	RESISTANT MUTANTS
Thiolactomycin	sulfhydryl groups, inhibitor of thymidylate synthetase type II fatty acid synthase inhibitor	<i>emrB</i> <i>fadB</i> , <i>emrB</i> due to gene dosage
Psicofuranine	Adenosine glycoside antibiotic, target is GMP synthetase	<i>guaA,B</i>
Triclosan	Inhibits fatty acid synthesis	<i>fabI (envM)</i>
Diazaborines Isoniazid, Ethionamide	heterocyclic, contains boron, inhibit fatty acid synthesis, enoyl-ACP reductase, <i>fabI</i>	<i>fabI (envM)</i>
Inhibitors of Translation		
Phenylpropanoids Chloramphenicol, 1947	Binds to ribosomal peptidyl transfer center preventing peptide translocation/ binds to S6, L3, L6, L14, L16, L25, L26, L27, but preferentially to L16	<i>rm</i> , <i>cmlA</i> , <i>marA</i> , <i>ompF</i> , <i>ompR</i>
Tetracyclines, 1948, type II polyketides Minocycline Doxycycline	Binding to 30S ribosomal subunit, "A" site on 30S subunit, blocks peptide elongation, strongest binding to S7	<i>clmA (cmr)</i> , <i>mar</i> , <i>ompF</i>
Macrolides (type I polyketides) Erythromycin, 1950 Carbomycin, Spiramycin etc	Binding to 50 S ribosomal subunit, 23S rRNA, blocks peptide translocation, L15, L4, L12	<i>rm</i> , <i>rplC</i> , <i>rplD</i> , <i>rplV</i> , <i>mac</i>
Aminoglycosides Streptomycin, 1944 Neomycin	Irreversible binding to 30S ribosomal subunit, prevents translation or causes mistranslation of mRNA/16S rRNA	<i>rpsL</i> , <i>strC,M</i> , <i>ubiF</i> <i>atpA-E</i> , <i>ecfB</i> , <i>hemAC,D,E,G</i> , <i>topA</i> , <i>rpsC,D,E</i> , <i>rm</i> , <i>spcB</i> <i>atpA-atpE</i> , <i>cpxA</i> , <i>ecfB</i> , <i>hemA,B,L</i> , <i>topA</i> <i>ksgA,B,C,D</i> , <i>rplB,K</i> , <i>rpsL,N,M,R</i> <i>rplF</i> , <i>ubiF</i> <i>cpxA</i> <i>rpsL</i>
Spectinomycin Kanamycin		
Kasugamycin		
Gentamicin, 1963 Amikacin Paromycin		
Lincosamides Lincomycin, 1955 Clindamycin	Binding to 50 S ribosomal subunit, blocks peptide translocation	<i>linB</i> , <i>rplN,O</i> , <i>rpsG</i>
Streptogramins Virginiamycin, 1955 Pristinamycin	2 components, Streptogramins A&B, bind to the 50S ribosomal subunit blocking peptide translocation and peptide bond formation	
Synercid: quinupristin /dalfopristin		
Fusidanes Fusidic Acid	Inhibition of elongation factor G (EF-G) prevents peptide translocation	<i>fusA</i>
Kirromycin (Mocimycin)	Inhibition of elongation factor TU (EF-Tu), prevents peptide bond formation	<i>tufA,B</i>

ANTIBIOTIC	INHIBITS/TARGET	RESISTANT MUTANTS
Pulvomycin	Binds to and inhibits EF-TU	
Thiopeptin	Sulfur-containing antibiotic, inhibits protein synthesis, EF-G	<i>rplE</i>
Tiamulin	Inhibits protein synthesis	<i>rplC, rplD</i>
Negamycin	Inhibits termination process of protein synthesis	<i>prfB</i>
Oxazolidinones Linezolid	23S rRNA	
Isoniazid		<i>pdx</i>
Nitrofurantoin	Inhibits protein synthesis, nitroreductases convert nitrofurantoin to highly reactive electrophilic intermediates which attack bacterial ribosomal proteins non-specifically	<i>nfnA, B</i>
Pseudomonic Acids Mupirocin (Bactroban)	Inhibition of isoleucyl tRNA synthetase-used for Staph, topical cream, nasal spray	<i>ileS</i>
Indolmycin	Inhibits tryptophanyl-tRNA synthetase	<i>trpS</i>
Viomycin		<i>rmaA</i> (23S rRNA methyltransferase; mutant has slow growth rate, slow chain elongation rate, and viomycin resistance)
Thiopeptides	Binds to L11-23S RNA complex	
Thiostrepton	Inhibits GTP hydrolysis by EF-G	
Micrococin	Stimulates GTP hydrolysis by EF-G	
Inhibitors of Cell Walls/Membranes		
β-lactams	Inhibition of one or more cell wall transpeptidases, endopeptidases, and glycosidases (PBPs), of the 12 PBPs only 2 are essential: <i>mrdA</i> (PBP2) and <i>ftsI</i> (<i>pbpB</i> , PBP3)	
Penicillin, 1929 Ampicillin		<i>ampC, ampD, ampE, envZ, galU, hipA, hipD, ompC, ompF, ompR, ptsI, rfa, tolD, tolE</i>
Methicillin, 1960		<i>tonB</i>
Cephalosporins, 1962		<i>alaS, argS, crp, cyaA, envB, mrdA, B, mreB, C, D</i>
Mecillinam (amdinocillin)	Binds to and inactivates PBP2 (<i>mrdA</i>) Inactivates PBP3 (<i>ftsI</i>)	
Aztreonam (Furazlocillin)	Dipeptide, inhib glucosamine synthase	<i>dppA</i>
Bacilysin, Tetaine	Inhib G+ cell wall syn, binds to terminal D-alanyl-D-alanine of pentapeptide,	
Glycopeptides Vancomycin, 1955	Prevents dephosphorylation and regeneration of lipid carrier	<i>rfa</i>
Polypeptides Bacitracin	Disrupts multiple aspects of membrane	
Cyclic lipopeptide Daptomycin, 1980		

5		function, including peptidoglycan synthesis, lipoteichoic acid synthesis, and the bacterial membrane potential	
	Cyclic polypeptides Polymixin, 1939	Surfactant action disrupts cell membrane lipids, binds lipid A moiety of LPS	<i>pmrA</i>
10	Fosfomycin, 1969	Analogue of P-enolpyruvate, inhibits 1 st step in peptidoglycan synthesis - UDP-N-acetylglucosamine enolpyruvyl transferase, <i>murA</i> . Also acts as immunosuppressant	<i>murA, crp, cysA glpT, hipA, ptsI, whpT</i>
	Cycloserine	Prevents formation of D-ala dimer, inhibits D-ala ligase, <i>ddlA,B</i>	<i>hipA, cycA</i>
15	Alafosfalin	phosphonodipeptide, cell wall synthesis inhibitor, potentiator of β -lactams	<i>pepA, tpp</i>
	Inhibitors of Protein Processing/Transport		
	Globomycin	Inhibits signal peptidase II (cleaves prelipoproteins subsequent to lipid modification, <i>lspA</i>)	<i>lpp, dnaE</i>
20			

EXAMPLE 12

Transfer of Exogenous Nucleic Acid Sequences to other Bacterial Species Using the *E. coli* Expression Vectors or Expression Vectors Functional in Bacterial Species other than *E. coli*.

5 The above methods were validated using antisense nucleic acids which inhibit the growth of *E. coli* which were identified using methods similar to those described above. Expression vectors which inhibited growth of *E. coli* upon induction of antisense RNA expression with IPTG were transformed directly into *Enterobacter cloacae*, *Klebsiella pneumoniae* or *Salmonella typhimurium*. The transformed cells were then assayed for growth inhibition according to the method of Example 1. After growth in liquid culture, cells were plated at various serial dilutions and a score determined by calculating the log difference in growth for INDUCED vs. UNINDUCED antisense RNA expression as determined by the maximum 10 fold dilution at which a colony was observed. The results of these experiments are listed below in Table VI. If there was no effect of antisense RNA expression in an organism, the clone is minus in Table VI. In contrast, a positive in Table VI means that at least 10 fold more cells were required to observe a colony on the induced plate than on the non-induced plate under the conditions used and in that organism.

15 Sixteen of the constructs were found to inhibit growth in all the organisms tested upon induction of antisense RNA expression with IPTG. Those skilled in the art will appreciate that a negative result in a heterologous organism does not mean that that organism is missing that gene nor does it mean that the gene is unessential. However, a positive result means that the heterologous organism contains a homologous gene which is required for proliferation of that organism. The homologous gene may be obtained using the methods described herein. Those cells that are inhibited by antisense may be used in cell based assays as described herein for the identification and characterization of compounds in order to

develop antibiotics effective in these organisms. Those skilled in the art will appreciate that an antisense molecule which works in the organism from which it was obtained will not always work in a heterologous organism.

TABLE VI
Sensitivity of Other Microorganisms to Antisense Nucleic Acids That Inhibit Proliferation in *E. coli*

Mol. No.	<i>S. typhimurium</i>	<i>E. cloacae</i>	<i>K. pneumoniae</i>
EcXA001	+	+	-
EcXA004	-	-	-
EcXA005	+	+	+
EcXA006	-	-	-
EcXA007	-	+	-
EcXA008	+	-	+
EcXA010	+	+	+
EcXA011	-	+	-
EcXA012	-	+	-
EcXA013	+	+	+
EcXA014	+	+	-
EcXA015	-	+	+
EcXA016	+	+	+
EcXA017	+	+	+
EcXA018	+	+	+
EcXA019	+	+	+
EcXA020	+	+	+
EcXA021	+	+	+
EcXA023	+	+	+
EcXA024	+	-	+
EcXA025	-	-	-
EcXA026	+	+	-
EcXA027	+	+	+
EcXA028	+	-	-
EcXA029	-	-	-

Mol. No.	<i>S. typhimurium</i>	<i>E. cloacae</i>	<i>K. pneumoniae</i>
EcXA030	+	+	+
EcXA031	+	-	-
EcXA032	+	-	-
EcXA033	+	+	+
EcXA034	+	+	+
EcXA035	-	-	-
EcXA036	+	-	+
EcXA037	-	+	-
EcXA038	+	+	-
EcXA039	+	-	-
EcXA041	+	+	+
EcXA042	-	+	+
EcXA044	-	-	-
EcXA045	-	+	-
EcXA046	-	-	-
EcXA047	+	+	-
EcXA048	-	-	-
EcXA049	+	-	-
EcXA050	-	-	-
EcXA051	+	-	-
EcXA052	+	-	-
EcXA053	+	+	+
EcXA054	-	-	+
EcXA055	+	-	-

EXAMPLE 13

Use of Identified Exogenous Nucleic Acid Sequences as Probes

The identified sequence of the present invention can be used as probes to obtain the sequence of additional genes of interest from a second organism. For example, probes to potential bacterial target proteins may be hybridized to nucleic acids from other organisms including other bacteria and higher organisms, to identify homologous sequences. Such

5 hybridization might indicate that the protein encoded by the gene to which the probe corresponds is found in humans and therefore not necessarily a good drug target. Alternatively, the gene can be conserved only in bacteria and therefore would be a good drug target for a broad spectrum antibiotic or antimicrobial.

10 5 Probes derived from the identified nucleic acid sequences of interest or portions thereof can be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe can be single stranded or double stranded and can be made using techniques known in the art, including *in vitro* transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double stranded, it can be denatured prior to contacting the probe. In some applications, the nucleic acid sample can be immobilized on a surface such as a nitrocellulose or nylon membrane. The nucleic acid sample can comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

15 10 Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic acid capable of hybridizing to the labeled probe can be cloned into vectors such as expression vectors, sequencing vectors, or *in vitro* transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques can be used to isolate, purify and clone sequences from a genomic library, made from a variety of bacterial species, which are capable of hybridizing to probes made from the sequences identified in Examples 5 and 6.

EXAMPLE 14

Preparation of PCR Primers and Amplification of DNA

30 20 The identified *E. coli* genes corresponding directly to or located within the operon of nucleic acid sequences required for proliferation or portions thereof can be used to prepare PCR primers for a variety of applications, including the identification or isolation of homologous sequences from other species, for example *S. typhimurium*, *E. cloacae*, and *Klebsiella pneumoniae*, which contain part or all of the homologous genes. Because homologous genes are related but not identical in sequence, those skilled in the art will often employ degenerate sequence PCR primers. Such degenerate sequence primers are designed based on conserved sequence regions, either known or suspected, such as conserved coding regions. The successful production of a PCR product using degenerate probes generated from the sequences identified herein would indicate the presence of a homologous gene sequence in the species being screened. The PCR primers are at least 10 bases, and preferably at least 20 bases in length. More preferably, the PCR primers are at least 20-30 bases in length. In some embodiments, the PCR primers can be more than 30 bases in length. It is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering White, B.A. Ed. in *Methods in Molecular Biology* 67: Humana Press, Totowa 1997. When the entire coding sequence of the target gene is known, the 5' and 3' regions of the target gene

5 can be used as the sequence source for PCR probe generation. In each of these PCR procedures, PCR primers on either side of
the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a
thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is
denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The
10 5 hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles
are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

EXAMPLE 15

Inverse PCR

15 The technique of inverse polymerase chain reaction can be used to extend the known nucleic acid sequence identified
10 in Examples 5 and 6. The inverse PCR reaction is described generally by Ochman et al., in Ch. 10 of *PCR Technology:
Principles and Applications for DNA Amplification*, (Henry A. Erlich, Ed.) W.H. Freeman and Co. (1992). Traditional PCR
requires two primers that are used to prime the synthesis of complementary strands of DNA. In inverse PCR, only a core
20 sequence need be known.

Using the sequences identified as relevant from the techniques taught in Examples 5 and 6 and applied to other
15 species of bacteria, a subset of exogenous nucleic sequences are identified that correspond to genes or operons that are
required for bacterial proliferation. In species for which a genome sequence is not known, the technique of inverse PCR
provides a method for obtaining the gene in order to determine the sequence or to place the probe sequences in full context to
the target sequence to which the identified exogenous nucleic acid sequence binds.

To practice this technique, the genome of the target organism is digested with an appropriate restriction enzyme so
30 20 as to create fragments of nucleic acid that contain the identified sequence as well as unknown sequences that flank the
identified sequence. These fragments are then circularized and become the template for the PCR reaction. PCR primers are
designed in accordance with the teachings of Example 15 and directed to the ends of the identified sequence are synthesized.
The primers direct nucleic acid synthesis away from the known sequence and toward the unknown sequence contained within
35 the circularized template. After the PCR reaction is complete, the resulting PCR products can be sequenced so as to extend the
25 sequence of the identified gene past the core sequence of the identified exogenous nucleic acid sequence identified. In this
manner, the full sequence of each novel gene can be identified. Additionally the sequences of adjacent coding and noncoding
regions can be identified.

EXAMPLE 16

Identification of Genes Required for *Staphylococcus aureus* Proliferation

30 Genes required for proliferation in *Staphylococcus aureus* are identified according to the methods described above.

EXAMPLE 17

Identification of Genes Required for *Neisseria gonorrhoeae* Proliferation

Genes required for proliferation in *Neisseria gonorrhoeae* are identified according to the methods described above.

EXAMPLE 18Identification of Genes Required for *Pseudomonas aeruginosa* Proliferation

Genes required for proliferation in *Pseudomonas aeruginosa* are identified according to the methods described above.

EXAMPLE 19Identification of Genes Required for *Enterococcus faecalis* Proliferation

Genes required for proliferation in *Enterococcus faecalis* are identified according to the methods described above.

EXAMPLE 20Identification of Genes Required for *Haemophilus influenzae* Proliferation

Genes required for proliferation in *Haemophilus influenzae* are identified according to the methods described above.

EXAMPLE 21Identification of Genes Required for *Salmonella typhimurium* Proliferation

Genes required for proliferation in *Salmonella typhimurium* are identified according to the methods described above.

EXAMPLE 22Identification of Genes Required for *Helicobacter pylori* Proliferation

Genes required for proliferation in *Helicobacter pylori* are identified according to the methods described above.

EXAMPLE 23Identification of Genes Required for *Mycoplasma pneumoniae* Proliferation

Genes required for proliferation in *Mycoplasma pneumoniae* are identified according to the methods described

EXAMPLE 24Identification of Genes Required for *Plasmodium ovale* Proliferation

Genes required for proliferation in *Plasmodium ovale* are identified according to the methods described above.

EXAMPLE 25Identification of Genes Required for *Saccharomyces cerevisiae* Proliferation

Genes required for proliferation in *Saccharomyces cerevisiae* are identified according to the methods described above.

EXAMPLE 26Identification of Genes Required for *Entamoeba histolytica* Proliferation

Genes required for proliferation in *Entamoeba histolytica* are identified according to the methods described above.

EXAMPLE 27Identification of Genes Required for *Candida albicans* Proliferation

Genes required for proliferation in *Candida albicans* are identified according to the methods described above.

EXAMPLE 28Identification of Genes Required for *Klebsiella pneumoniae* Proliferation

Genes required for proliferation in *Klebsiella pneumoniae* are identified according to the methods described above.

EXAMPLE 29Identification of Genes Required for *Salmonella typhi* Proliferation

Genes required for proliferation in *Salmonella typhi* are identified according to the methods described above.

EXAMPLE 30Identification of Genes Required for *Salmonella paratyphi* Proliferation

Genes required for proliferation in *Salmonella paratyphi* are identified according to the methods described above.

EXAMPLE 31Identification of Genes Required for *Salmonella choleraesuis* Proliferation

Genes required for proliferation in *Salmonella choleraesuis* are identified according to the methods described above.

EXAMPLE 32Identification of Genes Required for *Staphylococcus epidermis* Proliferation

Genes required for proliferation in *Staphylococcus epidermis* are identified according to the methods described above.

EXAMPLE 33Identification of Genes Required for *Mycobacterium tuberculosis* Proliferation

Genes required for proliferation in *Mycobacterium tuberculosis* are identified according to the methods described above.

EXAMPLE 34Identification of Genes Required for *Mycobacterium leprae* Proliferation

Genes required for proliferation in *Mycobacterium leprae* are identified according to the methods described above.

EXAMPLE 35Identification of Genes Required for *Treponema pallidum* Proliferation

Genes required for proliferation in *Treponema pallidum* are identified according to the methods described above.

EXAMPLE 36Identification of Genes Required for *Bacillus anthracis* Proliferation

Genes required for proliferation in *Bacillus anthracis* are identified according to the methods described above.

EXAMPLE 37Identification of Genes Required for *Yersinia pestis* Proliferation

Genes required for proliferation in *Yersinia pestis* are identified according to the methods described above.

EXAMPLE 38Identification of Genes Required for *Clostridium botulinum* Proliferation

Genes required for proliferation in *Clostridium botulinum* are identified according to the methods described above.

EXAMPLE 39Identification of Genes Required for *Campylobacter jejuni* Proliferation

Genes required for proliferation in *Campylobacter jejuni* are identified according to the methods described above.

EXAMPLE 40Identification of Genes Required for *Chlamydia trachomatis* Proliferation

Genes required for proliferation in *Chlamydia trachomatis* are identified according to the methods described above.

Use of Isolated Exogenous Nucleic Acid Fragments as Antisense Antibiotics

In addition to using the identified sequences to enable screening of molecule libraries to identify compounds useful to identify antibiotics, the sequences themselves can be used as therapeutic agents. Specifically, the identified exogenous sequences in an antisense orientation can be provided to an individual to inhibit the translation of a bacterial target gene.

Generation of Antisense Therapeutics from Identified Exogenous Sequences

The sequences of the present invention can be used as antisense therapeutics for the treatment of bacterial infections or simply for inhibition of bacterial growth *in vitro* or *in vivo*. The therapy exploits the biological process in cells where genes are transcribed into messenger RNA (mRNA) that is then translated into proteins. Antisense RNA technology contemplates the use of antisense oligonucleotides directed against a target gene that will bind to its target and decrease or inhibit the translation of the target mRNA. In one embodiment, antisense oligonucleotides can be used to treat and control a bacterial infection of a cell culture containing a population of desired cells contaminated with bacteria. In another embodiment, the antisense oligonucleotides can be used to treat an organism with a bacterial infection.

Antisense oligonucleotides can be synthesized from any of the sequences of the present invention using methods well known in the art. In a preferred embodiment, antisense oligonucleotides are synthesized using artificial means. Uhlmann & Peymann, Chemical Rev. 90:543-584 (1990) review antisense oligonucleotide technology in detail. Modified or unmodified antisense oligonucleotides can be used as therapeutic agents. Modified antisense oligonucleotides are preferred since it is well known that antisense oligonucleotides are extremely unstable. Modification of the phosphate backbones of the antisense oligonucleotides can be achieved by substituting the internucleotide phosphate residues with methylphosphonates, phosphorothioates, phosphoramidates, and phosphate esters. Nonphosphate internucleotide analogs such as siloxane bridges, carbonate bridges, thioester bridges, as well as many others known in the art. The preparation of certain antisense oligonucleotides with modified internucleotide linkages is described in U.S. Patent No. 5,142,047, hereby incorporated by reference.

Modifications to the nucleoside units of the antisense oligonucleotides are also contemplated. These modifications can increase the half-life and increase cellular rates of uptake for the oligonucleotides *in vivo*. For example,

5 α -anomeric nucleotide units and modified bases such as 1,2-dideoxy-d-ribofuranose, 1,2-dideoxy-1-phenyltribofuranosa, and *N*,*N*-ethano-5-methyl-cytosine are contemplated for use in the present invention.

10 5 An additional form of modified antisense molecules is found in peptide nucleic acids. Peptide nucleic acids (PNA) have been developed to hybridize to single and double stranded nucleic acids. PNA are nucleic acid analogs in which the entire deoxyribose-phosphate backbone has been exchanged with a chemically completely different, but structurally homologous, polyamide (peptide) backbone containing 2-aminoethyl glycine units. Unlike DNA, which is highly negatively charged, the PNA backbone is neutral. Therefore, there is much less repulsive energy between complementary strands in a PNA-DNA hybrid than in the comparable DNA-DNA hybrid, and consequently they are much more stable. PNA can hybridize to DNA in either a Watson/Crick or Hoogsteen fashion (Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* 92:2637-2641, 1995; Egholm, *Nature* 365:566-568, 1993; Nielsen et al., *Science* 254:1497-1500, 1991; Dueholm et al., *New J. Chem.* 21:19-31, 1997).

15 10 Molecules called PNA "clamps" have been synthesized which have two identical PNA sequences joined by a flexible hairpin linker containing three 8-amino-3,6-dioxaoctanoic acid units. When a PNA clamp is mixed with a complementary homapurine or homopyrimidine DNA target sequence, a PNA-DNA-PNA triplex hybrid can form which has been shown to be extremely stable (Bentín et al., *Biochemistry* 35:8863-8869, 1996; Egholm et al., *Nucleic Acids Res.* 23:217-222, 1995; Griffith et al., *J. Am. Chem. Soc.* 117:831-832, 1995).

20 15 The sequence-specific and high affinity duplex and triplex binding of PNA have been extensively described (Nielsen et al., *Science* 254:1497-1500, 1991; Egholm et al., *J. Am. Chem. Soc.* 114:9677-9678, 1992; Egholm et al., *Nature* 365:566-568, 1993; Almarsson et al., *Proc. Natl. Acad. Sci. U.S.A.* 90:9542-9546, 1993; Demidov et al., *Proc. Natl. Acad. Sci. U.S.A.* 92:2637-2641, 1995). They have also been shown to be resistant to nuclease and protease digestion (Demidov et al., *Biochem. Pharm.* 48:1010-1013, 1994). PNA has been used to inhibit gene expression (Harvey et al., *Science* 258:1481-1485, 1992; Nielsen et al., *Nucl. Acids. Res.*, 21:197-200, 1993; Nielsen et al., *Gene* 149:139-145, 1994; Good & Nielsen, *Science*, 95: 2073-2076, 1998; all of which are hereby incorporated by reference), to block restriction enzyme activity (Nielsen et al., *supra.*, 1993), to act as an artificial transcription promoter (Mollegaard, *Proc. Natl. Acad. Sci. U.S.A.* 91:3892-3895, 1994) and as a pseudo restriction endonuclease (Demidov et al., *Nucl. Acids. Res.* 21:2103-2107, 1993). Recently, PNA has also been shown to have antiviral and antitumoral activity mediated through an antisense mechanism (Norton, *Nature Biotechnol.*, 14:615-619, 1996; Hirschman et al., *J. Investig. Med.* 44:347-351, 1996). PNAs have been linked to various peptides in order to promote PNA entry into cells (Basu et al., *Bioconj. Chem.* 8:481-488, 1997; Partridge et al., *Proc. Natl. Acad. Sci. U.S.A.* 92:5592-5596, 1995).

25 30 The antisense oligonucleotides contemplated by the present invention can be administered by direct application of oligonucleotides to a target using standard techniques well known in the art. The antisense oligonucleotides can be generated within the target using a plasmid, or a phage. Alternatively, the antisense nucleic acid may be expressed from a sequence in the chromosome of the target cell. It is further contemplated that contemplated that the antisense oligonucleotide contemplated are incorporated in a ribozyme sequence to enable the antisense to specifically bind and cleave its

5 target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi et al., *Pharmacol. Ther.* 50(2):245-254, (1991), which is hereby incorporated by reference. The present invention also contemplates using a retron to introduce an antisense oligonucleotide to a cell. Retron technology is exemplified by U.S. Patent No. 5,405,775, which is hereby incorporated by reference. Antisense oligonucleotides can also be delivered using liposomes or by electroporation techniques which are well known in the art.

10 5 The antisense nucleic acids of the present invention can also be used to design antibiotic compounds comprising nucleic acids which function by intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. The sequences identified as required for proliferation in the present invention, or portions thereof, can be used as templates to inhibit microorganism gene expression in individuals infected with such organisms. Traditionally, homopurine sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at homopurine:homopyrimidine sequences. Thus, both types of sequences based on the sequences of the present invention that are required for proliferation are contemplated for use as antibiotic compound templates.

15 10 The antisense oligonucleotides of this example employ the identified sequences of the present invention to induce bacterial cell death or at least bacterial stasis by inhibiting target gene translation. Antisense oligonucleotides containing from about 8 to 40 bases of the sequences of the present invention have sufficient complementarity to form a duplex with the target sequence under physiological conditions.

20 15 To kill bacterial cells or inhibit their growth, the antisense oligonucleotides are applied to the bacteria or to the target cells under conditions that facilitate their uptake. These conditions include sufficient incubation times of cells and oligonucleotides so that the antisense oligonucleotides are taken up by the cells. In one embodiment, an incubation period of 7-10 days is sufficient to kill bacteria in a sample. An optimum concentration of antisense oligonucleotides is selected for use.

25 20 The concentration of antisense oligonucleotides to be used can vary depending on the type of bacteria sought to be controlled, the nature of the antisense oligonucleotide to be used, and the relative toxicity of the antisense oligonucleotide to the desired cells in the treated culture. Antisense oligonucleotides can be introduced to cell samples at a number of different concentrations preferably between $1 \times 10^{-10} \text{M}$ to $1 \times 10^{-4} \text{M}$. Once the minimum concentration that can adequately control gene expression is identified, the optimized dose is translated into a dosage suitable for use *in vivo*. For example, an inhibiting concentration in culture of 1×10^{-7} translates into a dose of approximately 0.6 mg/kg body weight. Levels of oligonucleotide approaching 100 mg/kg body weight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the subject are removed, treated with the antisense oligonucleotide, and reintroduced into the subject. This range is merely illustrative and one of skill in the art are able to determine the optimal concentration to be used in a given case.

5 After the bacterial cells have been killed or controlled in a desired culture, the desired cell population may be used for other purposes.

EXAMPLE 41

10 5 The following example demonstrates the ability of an *E. coli* antisense oligonucleotide to act as a bactericidal or bacteriostatic agent to treat a contaminated cell culture system. The application of the antisense oligonucleotides of the present invention are thought to inhibit the translation of bacterial gene products required for proliferation.

15 10 The antisense oligonucleotide of this example corresponds to a 30 base phosphorothioate modified oligodeoxynucleotide complementary to a nucleic acid involved in proliferation, such as Molecule Number EcXA001. A sense oligodeoxynucleotide complementary to the antisense sequence is synthesized and used as a control. The oligonucleotides are synthesized and purified according to the procedures of Matsukura, et al., Gene 72:343 (1988). The test oligonucleotides are dissolved in a small volume of autoclaved water and added to culture medium to make a 100 micromolar stock solution.

20 15 Human bone marrow cells are obtained from the peripheral blood of two patients and cultured according standard procedures well known in the art. The culture is contaminated with the K-12 strain of *E. coli* and incubated at 37°C overnight to establish bacterial infection.

25 20 The control and antisense oligonucleotide containing solutions are added to the contaminated cultures and monitored for bacterial growth. After a 10 hour incubation of culture and oligonucleotides, samples from the control and experimental cultures are drawn and analyzed for the translation of the target bacterial gene using standard microbiological techniques well known in the art. The target *E. coli* gene is found to be translated in the control culture treated with the control oligonucleotide, however, translation of the target gene in the experimental culture treated with the antisense oligonucleotide of the present invention is not detected or reduced.

EXAMPLE 42

35 25 A subject suffering from an *E. coli* infection is treated with the antisense oligonucleotide preparation of Example 39. The antisense oligonucleotide is provided in a pharmaceutically acceptable carrier at a concentration effective to inhibit the translation of the target gene. The present subject is treated with a concentration of antisense oligonucleotide sufficient to achieve a blood concentration of about 100 micromolar. The patient receives daily injections of antisense oligonucleotide to maintain this concentration for a period of 1 week. At the end of the week a blood sample is drawn and analyzed for the presence or absence using standard techniques well known in the art. There is no detectable evidence of *E. coli* and the treatment is terminated.

EXAMPLE 43

Preparation and use of Triple Helix Probes

45 50 The sequences of microorganism genes required for proliferation of the present invention are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches that could be used in triple-helix based strategies for inhibiting gene

expression. Following identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into a population of bacterial cells that normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis, such as GENSET, Paris, France.

The oligonucleotides can be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

Treated cells are monitored for a reduction in proliferation using techniques such as monitoring growth levels as compared to untreated cells using optical density measurements. The oligonucleotides that are effective in inhibiting gene expression in cultured cells can then be introduced *in vivo* using the techniques well known in that art at a dosage level shown to be effective.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to stabilize the triple helix. For information on the generation of oligonucleotides suitable for triple helix formation see Griffin et al. (Science 245:967-971 (1989), which is hereby incorporated by this reference).

EXAMPLE 44

Identification of Bacterial Strains from Isolated Specimens by PCR

Classical bacteriological methods for the detection of various bacterial species are time consuming and costly. These methods include growing the bacteria isolated from a subject in specialized media, cultivation on selective agar media, followed by a set of confirmation assays that can take from 8 to 10 days or longer to complete. Use of the identified sequences of the present invention provides a method to dramatically reduce the time necessary to detect and identify specific bacterial species present in a sample.

In one exemplary method, bacteria are grown in enriched media and DNA samples are isolated from specimens of, for example, blood, urine, stool, saliva or central nervous system fluid by conventional methods. A panel of PCR primers based on identified sequences unique to various species of microorganisms are then utilized in accordance with Example 12 to amplify DNA of approximately 100-200 bases in length from the specimen. A separate PCR reaction is set up for each pair of PCR primers and after the PCR reaction is complete, the reaction mixtures are assayed for the presence of PCR product. The presence or absence of bacteria from the species to which the PCR primer pairs belong is determined by the presence or absence of a PCR product in the various test PCR reaction tubes.

Although the PCR reaction is used to assay the isolated sample for the presence of various bacterial species, other assays such as the Southern blot hybridization are also contemplated.

WHAT IS CLAIMED IS:

1. A purified or isolated nucleic acid sequence consisting essentially of one of SEQ ID NOs: 405-485, wherein said nucleic acid inhibits microorganism proliferation.

2. The nucleic acid sequence of Claim 1, wherein said nucleic acid sequence is complementary to at least a portion of a coding sequence of a gene whose expression is required for microorganism proliferation.

3. The nucleic acid sequence of Claims 1 or 2, wherein said nucleic acid comprises a fragment of one of SEQ ID NOs. 405-485, said fragment selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 405-485.

4. The nucleic acid sequence of Claim 3, wherein said nucleic acid sequence is complementary to a coding sequence of a gene whose expression is required for microorganism proliferation.

5. A vector comprising a promoter operably linked to a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 405-485.

6. The vector of Claim 5, wherein said promoter is active in an organism selected from the group consisting of *Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klasiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *campylobacter jejuni*, *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

7. A host cell containing the vector of Claim 5 or Claim 6.

8. A purified or isolated nucleic acid consisting essentially of the coding sequence of one of SEQ ID NOs: 82-88, 90-242.

9. A fragment of the nucleic acid of Claim 8, said fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 82-88, 90-242.

10. A vector comprising a promoter operably linked to the nucleic acid of Claim 8 or Claim 9.

11. A purified or isolated nucleic acid comprising a nucleic acid sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding region, or 3' noncoding region within an operon encoding a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs: 243-357, 359-398.

12. A purified or isolated nucleic acid comprising a nucleic acid having at least 70% homology to a sequence selected from the group consisting of SEQ ID NOs 405-485, 82-88, 90-242 or the sequences complementary thereto as determined using BLASTN version 2.0 with the default parameters.

13. The nucleic acid of Claim 12, wherein said nucleic acid is from an organism selected from the group consisting of *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*, *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*, *Salmonella paratyphi*, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, and *Chlamydia trachomatis*, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

14. A purified or isolated nucleic acid consisting essentially of a nucleic acid encoding a polypeptide having a sequence selected from the group consisting of SEQ ID NOs: 243-357, 359-398.

15. A vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide having a sequence selected from the group consisting of SEQ ID NOs: 243-357, 359-398.

16. A host cell containing the vector of Claim 15.

17. A purified or isolated polypeptide comprising the sequence of one of SEQ ID NOs: 243-357, 359-398.

18. A purified or isolated polypeptide comprising a fragment of one of the polypeptides of SEQ ID NOs. 243-357, 359-398, said fragment selected from the group consisting of fragments comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the polypeptides of SEQ ID NOs: 243-357, 359-398.

19. An antibody capable of specifically binding the polypeptide of Claim 17 or Claim 18.

20. A method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide having a sequence selected from the group consisting of SEQ ID NOs. 243-357, 359-398 into a cell.

21. The method of Claim 20, further comprising the step of isolating said protein.

22. A method of inhibiting proliferation comprising inhibiting the activity or reducing the amount of a polypeptide having a sequence selected from the group consisting of SEQ ID NOs. 243-357, 359-398 or inhibiting the activity or reducing the amount of a nucleic acid encoding said polypeptide.

23. A method for identifying compounds which influence the activity of a polypeptide required for proliferation comprising:

contacting a polypeptide having a sequence selected from the group consisting of 243-357, 359-398 with a candidate compound; and

determining whether said compound influences the activity of said polypeptide.

24. The method of Claim 23, wherein said activity is an enzymatic activity.

25. The method of Claim 23, wherein said activity is a carbon compound catabolism activity.

- 5 26. The method of Claim 23, wherein said activity is a biosynthetic activity.
27. The method of Claim 23, wherein said activity is a transporter activity.
28. The method of Claim 23, wherein said activity is a transcriptional activity.
29. The method of Claim 23, wherein said activity is a DNA replication activity.
- 10 5 30. The method of Claim 23, wherein said activity is a cell division activity.
31. A method for assaying compounds for the ability to reduce the activity or level of a polypeptide
required for proliferation, comprising:
- providing a target, wherein said target comprises the coding sequence of a sequence selected from the
15 group consisting of SEQ ID NOs. 82-88, 90-242;
- 10 contacting said target with a candidate compound; and
- measuring an activity of said target.
- 20 32. The method of Claim 31, wherein said target is a messenger RNA molecule transcribed from a coding
region of one of SEQ ID. NOs.: 82-88, 90-242 and said activity is translation of said messenger RNA.
33. The method of Claim 32, wherein said target is a coding region of one of SEQ ID. NOs. 82-88, 90-242
15 and said activity is transcription of said messenger RNA.
- 25 34. A compound identified using the method of Claim 31.
35. A method for identifying compounds which reduce the activity or level of a gene product required for
cell proliferation comprising the steps of:
- expressing an antisense nucleic acid against a nucleic acid encoding said gene product in a cell to
30 reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;
- 20 contacting said sensitized cell with a compound; and
- determining whether said compound inhibits the growth of said sensitized cell to a greater extent than
said compound inhibits the growth of a nonsensitized cell.
- 35 36. The method of Claim 35, wherein said cell is selected from the group consisting of bacterial cells,
25 fungal cells, plant cells, and animal cells.
37. The method of Claim 36, wherein said cell is an *E. coli* cell.
- 40 38. The method of Claim 36, wherein said cell is from an organism selected from the group consisting of
Staphylococcus aureus, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*,
Enterococcus faecalis, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces*
30 *cerevisiae*, *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*,
Salmonella paratyphi, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium*
45 *leprae*, *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *Campylobacter jejuni*, and *Chlamydia*
trachomatis, *Chlamydia pneumoniae* or any species falling within the genera of any of the above species.

- 5 39. The method of Claim 35, wherein said antisense nucleic acid is transcribed from an inducible promoter.
40. The method of Claim 39, further comprising the step of contacting said cell with a concentration of inducer which induces said antisense nucleic acid to a sublethal level.
- 10 5 41. The method of Claim 40, wherein said sub-lethal concentration of said inducer is such that growth inhibition is 8% or more.
42. The method of Claim 40, wherein said inducer is isopropyl-1-thio- β -D-galactoside.
43. The method of Claim 35, wherein growth inhibition is measured by monitoring optical density of a culture growth solution.
- 15 44. The method of Claim 35, wherein said gene product is a polypeptide.
45. The method of Claim 35, wherein said gene product is an RNA.
46. The method of Claim 44, wherein said gene product comprises a polypeptide having a sequence selected from the group consisting of SEQ ID NOs.: 243-357, 359-398.
- 20 47. A compound identified using the method of Claim 35.
48. A method for inhibiting cellular proliferation comprising introducing a compound with activity against a gene corresponding to one of SEQ ID NOs.: 82-88, 90-242 or with activity against the product of said gene into a population of cells expressing a gene.
- 25 49. The method of Claim 48, wherein said compound is an antisense oligonucleotide comprising a sequence selected from the group consisting of SEQ ID NOs.: 405-485, or a proliferation-inhibiting portion thereof.
50. The method of Claim 49, wherein said proliferation inhibiting portion of one of SEQ ID NOs. 405-485 is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 405-485.
- 30 51. The method of Claim 48, wherein said compound is a triple helix oligonucleotide.
52. A preparation comprising an effective concentration of an antisense oligonucleotide comprising a sequence selected from the group consisting of SEQ ID NOs.: 405-485, or a proliferation-inhibiting portion thereof in a pharmaceutically acceptable carrier.
- 35 53. The preparation of Claim 52, wherein said proliferation-inhibiting portion of one of SEQ ID NOs. 405-485 comprises at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 405-485.
- 40 54. A method for inhibiting the expression of a gene in an operon required for proliferation comprising contacting a cell in a cell population with an antisense nucleic acid, said cell expressing a gene corresponding to one of SEQ ID NOs.: 82-88, 90-242, wherein said antisense nucleic acid comprises at least a proliferation-inhibiting portion of said operon in an antisense orientation that is effective in inhibiting expression of said gene.
- 45
- 50
- 55

5 55. The method of Claim 54, wherein said antisense nucleic acid is complementary to a sequence of a gene comprising one or more of SEQ ID NOs.: 82-88, 90-242.

56. The method of Claim 54, wherein said antisense nucleic acid is a sequence of one of SEQ ID NOs.: 405-485, or a portion thereof.

10 5 57. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which expresses said antisense nucleic acid into said cell population.

58. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by introducing a phage which expresses said antisense nucleic acid into said cell population.

15 59. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by introducing a sequence encoding said antisense nucleic acid into the chromosome of said cell into said cell population.

20 60. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population.

61. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme is complementary to said antisense oligonucleotide.

25 62. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by introducing a liposome comprising said antisense oligonucleotide into said cell.

63. The method of Claim 54, wherein said cell is contacted with said antisense nucleic acid by electroporation.

30 20 64. The method of Claim 54, wherein said antisense nucleic acid is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive bases of one of SEQ ID NOs: 82-88, 90-242.

65. The method of Claim 54 wherein said antisense nucleic acid is an oligonucleotide.

35 66. A method for identifying bacterial strains comprising the steps of:

providing a sample containing a bacterial species; and

25 identifying a bacterial species using a species specific probe having a sequence selected from the group consisting of SEQ ID NOs. 405-485, 82-88, 90-242.

40 67. A method for identifying a gene in a microorganism required for proliferation comprising:

(a) identifying an inhibitory nucleic acid which inhibits the activity of a gene or gene product required for proliferation in a first microorganism;

30 (b) contacting a second microorganism with said inhibitory nucleic acid;

45 (c) determining whether said inhibitory nucleic acid from said first microorganism inhibits proliferation of said second microorganism; and

(d) identifying the gene in said second microorganism which is inhibited by said inhibitory nucleic acid.

68. A method for assaying a compound for the ability to inhibit proliferation of a microorganism comprising:

(a) identifying a gene or gene product required for proliferation in a first microorganism;

(b) identifying a homolog of said gene or gene product in a second microorganism;

(c) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said second microorganism;

(d) contacting said second microorganism with a proliferation-inhibiting amount of said inhibitory nucleic acid, thus sensitizing said second microorganism;

(e) contacting the sensitized microorganism of step (d) with a compound; and

(f) determining whether said compound inhibits proliferation of said sensitized microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized microorganism.

69. The method of Claim 68, wherein said step of identifying a gene involved in proliferation in a first microorganism comprises:

introducing a nucleic acid comprising a random genomic fragment from said first microorganism operably linked to a promoter wherein said random genomic fragment is in the antisense orientation; and

comparing the proliferation of said first microorganism transcribing a first level of said random genomic fragment to the proliferation of said first microorganism transcribing a lower level of said random genomic fragment, wherein a difference in proliferation indicates that said random genomic fragment comprises a gene involved in proliferation.

70. The method of Claim 69, wherein said step of identifying a homolog of said gene in a second microorganism comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a database using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default parameters.

71. The method of Claim 69, wherein said step of identifying a homolog of said gene in a second microorganism comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide by identifying nucleic acids which hybridize to said first gene.

72. The method of Claim 69, wherein the step of identifying a homolog of said gene in a second microorganism comprises expressing a nucleic acid which inhibits the proliferation of said first microorganism in said second microorganism.

73. The method of Claim 69, wherein said inhibitory nucleic acid is an antisense nucleic acid.

74. The method of Claim 69, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of said homolog.

5 75. The method of Claim 69, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding said homolog.

10 76. The method of Claim 69, wherein the step of contacting the second microorganism with a proliferation-inhibiting amount of said nucleic acid sequence comprises directly contacting said second microorganism with said nucleic acid.

15 77. The method of Claim 69, wherein the step of contacting the second microorganism with a proliferation-inhibiting amount of said nucleic acid sequence comprises expressing an antisense nucleic acid to said homolog in said second microorganism.

10 78. A compound identified using the method of Claim 68.

15 79. A method of assaying a compound for the ability to inhibit proliferation comprising:

20 (a) identifying an inhibitory nucleic acid sequence which inhibits the activity of a gene or gene product required for proliferation in a first microorganism;

 (b) contacting a second microorganism with a proliferation-inhibiting amount of said inhibitory nucleic acid, thus sensitizing said second microorganism;

15 (c) contacting the proliferation-inhibited microorganism of step (b) with a compound; and

25 (d) determining whether said compound inhibits proliferation of said sensitized second microorganism to a greater extent than said compound inhibits proliferation of a nonsensitized second microorganism.

 80. The method of Claim 79, wherein said inhibitory nucleic acid is an antisense nucleic acid which inhibits the proliferation of said first microorganism.

30 81. The method of Claim 79, wherein said inhibitory nucleic acid comprises a portion of an antisense nucleic acid which inhibits the proliferation of said first microorganism.

 82. The method of Claim 79, wherein said inhibitory nucleic acid comprises an antisense molecule against the entire coding region of the gene involved in proliferation of the first microorganism.

35 83. The method of Claim 79, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding the gene involved in proliferation of the first microorganism.

25 84. A compound identified using the method of Claim 79.

40 85. A method for assaying compounds for activity against a biological pathway required for proliferation comprising:

 sensitizing a cell by expressing an antisense nucleic acid against a nucleic acid encoding a gene product required for proliferation in a cell to reduce the activity or amount of said gene product;

30 contacting the sensitized cell with a compound; and

45 determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

5 86. The method of Claim 85, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

 87. The method of Claim 86, wherein said cell is an *E. coli* cell.

10 88. The method of Claim 85, wherein said cell is from an organism selected from the group consisting of
5 *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Helicobacter pylori*, *Neisseria gonorrhoeae*,
Enterococcus faecalis, *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Salmonella typhimurium*, *Saccharomyces cerevisiae*,
15 *Candida albicans*, *Cryptococcus neoformans*, *Aspergillus fumigatus*, *Klebsiella pneumoniae*, *Salmonella typhi*,
Salmonella paratyphi, *Salmonella choleraesuis*, *Staphylococcus epidermidis*, *Mycobacterium tuberculosis*, *Mycobacterium leprae*,
10 *Treponema pallidum*, *Bacillus anthracis*, *Yersinia pestis*, *Clostridium botulinum*, *campylobacter jejuni*, and *Chlamydia trachomatis*,
Chlamydia pneumoniae or any species falling within the genera of any of the above species.

 89. The method of Claim 85, wherein said antisense nucleic acid is transcribed from an inducible promoter.

20 90. The method of Claim 89, further comprising contacting the cell with an agent which induces expression of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is expressed at a sublethal level.

15 91. The method of Claim 90, wherein said sublethal level of said antisense nucleic acid inhibits proliferation by 8% or more.

25 92. The method of Claim 90, wherein said agent is isopropyl-1-thio- β -D-galactoside (IPTG).

 93. The method of Claim 91, wherein inhibition of proliferation is measured by monitoring the optical density of a liquid culture.

30 94. The method of Claim 85, wherein said gene product comprises a polypeptide having a sequence selected from the group consisting of SEQ ID NOs: 243-357, 359-398.

 95. A compound identified using the method of Claim 85.

35 96. A method for assaying a compound for the ability to inhibit cellular proliferation comprising:

25 contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell;

 contacting said cell with said compound; and

40 determining whether said compound reduces proliferation to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent.

30 97. The method of Claim 96, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises an antisense nucleic acid to a gene or operon required for proliferation.

45 98. The method of Claim 96, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises an antibiotic.

5 99. The method of Claim 96, wherein said cell contains a temperature sensitive mutation which reduces the activity or level of said gene product required for proliferation of said cell.

10 5 100. The method of Claim 99, wherein said antisense nucleic acid is directed against the nucleic acid encoding the same functional domain of said gene product required for proliferation of said cell to which said antisense nucleic acid is directed.

15 101. The method of Claim 99, wherein said antisense nucleic acid is directed against the nucleic acid a different functional domain of said gene product required for proliferation of said cell than the functional domain to which said antisense nucleic acid is directed.

102. A compound identified using the method of Claim 96.

10 103. A method for identifying the pathway in which a proliferation-required nucleic acid or its gene product lies comprising:

20 expressing a sublethal level of an antisense nucleic acid directed against said proliferation-required nucleic acid in a cell;

15 contacting said cell with an antibiotic, wherein the biological pathway on which said antibiotic acts is known; and

25 determining whether said cell has a substantially greater sensitivity to said antibiotic than a cell which does not express said sublethal level of said antisense nucleic acid.

104. A method for determining the pathway on which a test compound acts comprising:

30 20 (a) expressing a sublethal level of an antisense nucleic acid directed against a proliferation-required nucleic acid in a cell, wherein the biological pathway in which said proliferation-required nucleic acid lies is known,

(b) contacting said cell with said test compound; and

35 (c) determining whether said cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid.

105. The method of Claim 104, further comprising:

25 (d) expressing a sublethal level of a second antisense nucleic acid directed against a second proliferation-required nucleic acid in said cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

40 (e) determining whether said cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid.

30 106. A purified or isolated nucleic acid consisting essentially of one of SEQ ID NOs: 358, 399-402.

45 107. A compound identified using the method of Claim 23.

108. A compound which interacts with the gene or gene product of a nucleic acid comprising a sequence of one of SEQ ID NOs: 82-88, 90-242 to inhibit proliferation.

5 109. A compound which interacts with a polypeptide comprising one of SEQ ID NOs. 243-357, 359-398 to inhibit proliferation.

 110. A compound which interacts with a nucleic acid comprising one of SEQ ID NOs: 358, 399-402 to inhibit proliferation.

10 5

15

20

25

30

35

40

45

50

55

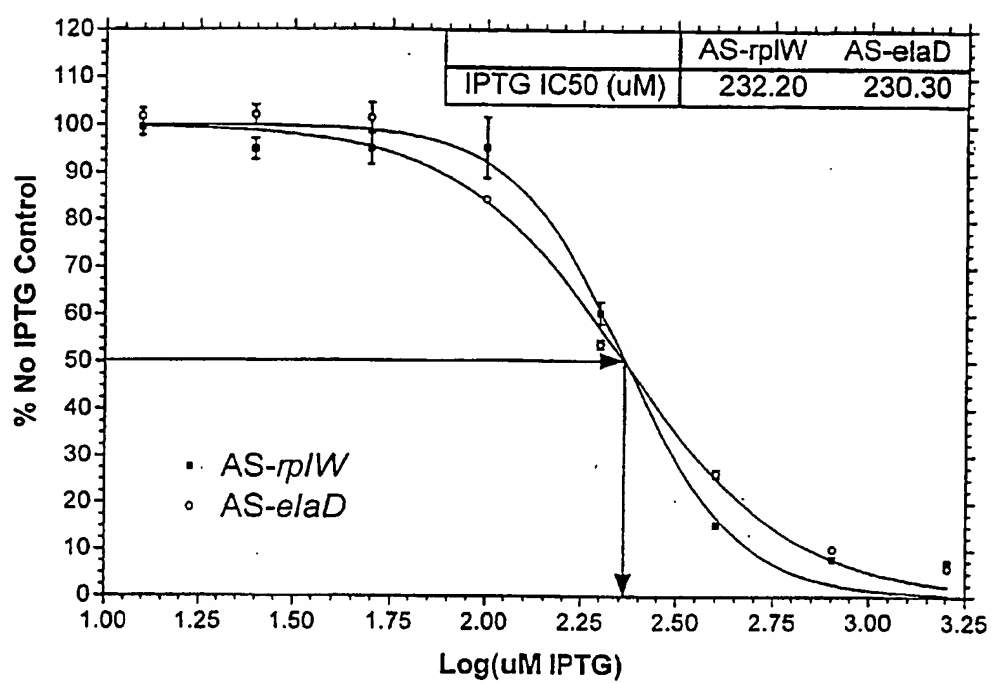
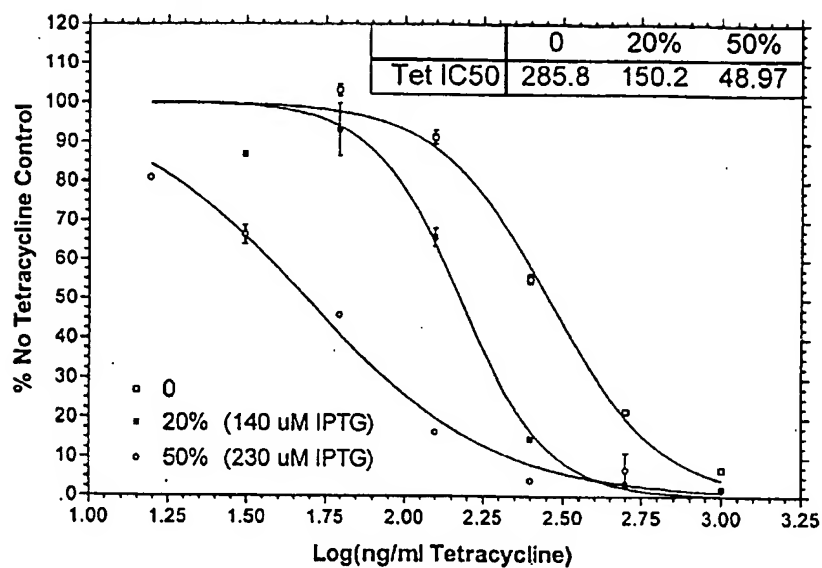
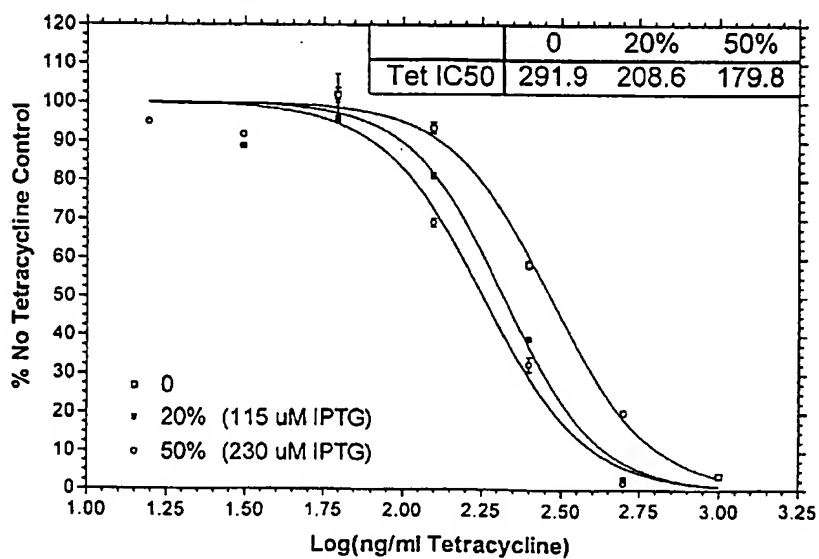


Fig. 1

AS-rplW**Fig. 2a****AS-elaD****Fig. 2b**

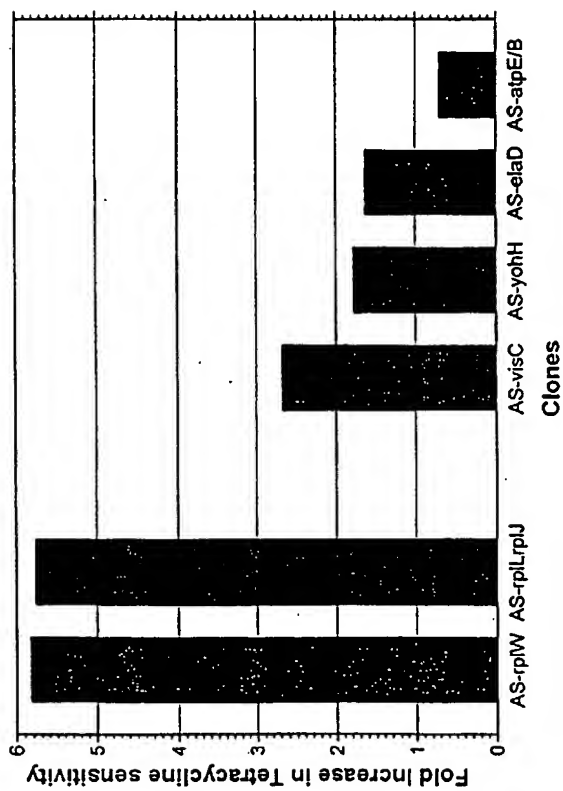


Fig. 3

SEQUENCE LISTING

<110> ELITRA PHARMACEUTICALS, INC.

Zyskind, Judith
 Ohlsen, Kari L.
 Trawick, John
 Forsyth, R. Allyn
 Froelich, Jamie M.
 Carr, Grant J.
 Yamamoto, Robert T.
 Xu, H. Howard

<120> GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
ESCHERICHIA COLI

<130> ELITRA.001VPC

<160> 485

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 159

<212> DNA

<213> E. Coli

<400> 1

caggtggtat ggaaccccaa aatggagacg ggaagctgaa ccagatagtt actggagggtg	60
atcaccagca gatgaaataa cgataaccag aacaacgcct tatagcgttg agtttgcgag	120
aaaacgttca tattgtacct ttttgattaa ccattgggg	159

<210> 2

<211> 696

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(696)

<223> n = A,T,C or G

<400> 2

gattacatca agcgcgcggt gggtttaccg ggcgataaag tcacttacga tccggtctca	60
aaagagctga cgattcaacc gggatgcagt tccggccagg cgtgtgaaaa cgcgctgccg	120
gtcacctact caaacgtgga accgagcgat ttcgttcaga ccttctcagc ccgtaatggt	180
ggggaagcga ccagcggatt ctttgaagtg ccgaaaaacg aaaccaaaga aaatggaatt	240
cgtctttccg agcgtaaaga gacactgggt gatgtgacgc accgcattct gacagtgccg	300
attgcgcagg atcaggtggg gatgtattac cagcagccag ggcaacaact ggcaacctgg	360
attgttcctc cgggacaata ctcatgatg ggcgacaacc gcgacaacag cgcggacagc	420
cgttactggg gctttgtgcc ngaagcgaat ctggtcggtc nggcaacggc tatctggatg	480
aacttcgata accaagaagg cgaatggccg aatggctctg cctaantcgc attggcgntt	540
ccnttaatan ccacttcctt cncctttgtcc ccttatggca acacttaatt tattntaaan	600
taatcncceg tggctnaca atccccgcct tttnttaaaa atttcccna anttaagggt	660
ggcctccagt tgcccgcccc aaacactttg gncccc	696

<210> 3

<211> 681

<212> DNA

<213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(681)
 <223> n = A,T,C or G

<400> 3
 ctgcagggtg atgtcgccat taaactggcg caggcagcca aagagttgct ccgcttctac 60
 ccagtcggca gcgacaactt gcgttaaagt cgcaaaatta tcatctgcac tcaactgcgtg 120
 acgtaagcgg atggagtggc cggaacotc atagtaccg cccaccagtt ggcttgcac 180
 gctttgtagc gtacgcgcgg cattggcaat aagattcaga tactcagact cttccggggc 240
 cttcgccagc ataaaagagg aggatgctcg cgtatgcagc aactgctcca gcgcaaattg 300
 cagccgcggt tgagtatcac tgaataaagg atcgttttcg tcaatcaaat gtggctgagc 360
 aaatatttcc tgatagctat cggtatcagg aaccaggtea cgccatgcaa gtttcgtaat 420
 ggtcaaagt gatgtttttt agtctgttgt caaagccgcn attataccng taaccggcac 480
 tacagcacac gtgaaagca cccgacaata ctcttgccat gggcggttaa gctcacagga 540
 tggagatcct ttcttcactg gcctaaaaag ctgatatctt gtaaagagtt acacngtaac 600
 attgagatcg ctatgaaata tcaacaactt ggaaaatctt gnaaagcngg ttggaaaatg 660
 gaaagtatct ggttaagaag c 681

<210> 4
 <211> 289
 <212> DNA
 <213> E. Coli

<400> 4
 ggcagaattt tacgctgacc aatgacgcga cgacgtggca tggaaatact ccgttggttaa 60
 ttcaggattg tccaaaactc tacgagttta gtttgacatt taagttaaaa cgtttggcct 120
 tacttaacgg agaaccatta agccttagga cgcttcacgc catacttgga acgagcctgc 180
 ttacggtcct taacgcccga gcagtcaagc gcaccacgta cgggtgtgga acgaacaccc 240
 gggaggtcct taacacgacc gtcacggatc aggatcacgg agtgctcct 289

<210> 5
 <211> 815
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(815)
 <223> n = A,T,C or G

<400> 5
 gggagcttac atcagtaagt gaccgggatg agcgagcgaa gataacgcat ctgcggcgcg 60
 aaatatgaag ggggagagcc cttatagacc aggtagtaca cgtttggtta gggggcctgc 120
 atatggcccc ctttttcaact tttatatctg tgcggtttta tgcggggcag atcacatctc 180
 cgaggatttt agaattggctg aaattaccgc atccctggta aaagagctgc gtgagcgtac 240
 tggcgacggc atgatggatt gcaaaaaagc actgactgaa gctaaccggc acatcgagct 300
 ggcaatcgaa aacatgcgta agtccggtgc tattaaagca gcgaaaaaag caggcaacgt 360
 tgctgctgac ggcgtgatca aaacaaaat cgacggcaac tacggcatca ttctggaagt 420
 taactgccag actgacttcg ttgcaaaaga cgctggtttc caggcgcttc cagacaaagt 480
 tctggacgca gctgttgcg gcaaaatcac tgacgttgaa gttctgaaag cacagttcga 540
 agaagaacgt gttgcgctgg tagcgaaaat tggtgaaaac atcaacattc gccgcgttgc 600
 tgcgctggaa ggcgacgttc tgggttctta tcagcacggt gcgcgtatcg gccgttctgg 660
 ttgctgctaa aagcgctgac gaagaactgg ttaaacacat cgttttgacc tttgttgcaa 720
 gccaaagccag aattcagaga aactttccgc ttcaccggag gtcccacca cangganccc 780
 cgattttntc agcatgggtg tcttctctnc gagtt 815

<210> 6
 <211> 403
 <212> DNA

<213> E. Coli

<400> 6

caacactatt	ttgttgaccg	gaaaatggaa	cactttccgc	aatgcctggt	gctatcacgc	60
ttaaaccatt	tcattgcgat	ttacacagaa	cggacgtect	gtcgcagtat	attaagtcgt	120
cgatagaaac	aagcattgaa	aggcacagca	gtagtcaaac	agtgtgaaac	gctactggcg	180
ccttacagcg	caaaaaggct	ggtgactaaa	aagtcaccag	ccatcagcct	gattttctcag	240
gctgcaaccg	gaagggttgg	cttatttaac	ttcaacttca	gcgccagctt	cttccagagc	300
ttttttcagt	gcttctgcgt	cgtctttgct	cagcccttct	ttcagagcag	ccgggtgcaga	360
ttctaccagc	tccttagctt	ctttcagacc	caggccagtt	gcg		403

<210> 7

<211> 149

<212> DNA

<213> E. Coli

<400> 7

gagctttttt	cagtgtctct	gcgtcgtctt	tgctcacgcc	ttctttcaga	gcagccggtg	60
cagattctac	caggtcttta	gcttctttca	gacccaggcc	agttgcgcca	cgtactgctt	120
tgataacagc	aactttgtta	gcgccagca				149

<210> 8

<211> 742

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(742)

<223> n = A,T,C or G

<400> 8

ccatctgtcc	attgagcgga	cagtttgtgc	aacactattt	tgttgaccgg	aaaatggaac	60
acttttcgca	atgcctgttg	ctatcacgct	taaaccattt	cattgcgatt	tacacagaac	120
ggacgtcctg	tcgcagtata	ttaagtcgtc	gatagaaaca	agcattgaaa	ggcacagcag	180
tagtcaaaaca	gtgtgaaacg	ctactggcgc	cttacagcgc	aaaaaggctg	gtgactaaaa	240
agtcaccagc	catcagcctg	atttctcagg	ctgcaaccgg	aagggttggc	ttatttaact	300
tcaacttcag	cgccagcttc	ttccagagct	tttttcagtg	cttctgcgtc	gtctttgctc	360
acgccttctt	tcagagcagc	cggtgcagat	tctaccaggt	ctttagcttc	tttcagaccc	420
aggccagttg	cgccacgtac	tgctttgata	acagcaactt	tgttagcgcc	agcagctttc	480
agaattacgt	cgaattcagt	tntttcttca	gcagcttcaa	ccgggccagc	agctacagct	540
acagcagcag	caagcggaaa	caccgaattt	ttcttccatt	gcagagatca	gttctacaac	600
cgtccattac	agacatagct	gcaactgctt	caatgatatt	gatctttagt	ggatagacat	660
ttaaattggt	cctgaattat	caagaaataa	gtnttatatg	taagccgaaa	tgcgttaaaa	720
aagataactg	ngattaagc	ag				742

<210> 9

<211> 421

<212> DNA

<213> E. Coli

<400> 9

agtagtcaaa	cagtgtgaaa	cgctactggc	gccttacagc	gcaaaaaggc	tggtgactaa	60
aaagtcacca	gccatcagcc	tgattttctca	ggctgcaacc	ggaagggttg	gcttattttaa	120
cttcaacttc	agcgccagct	tcttccagag	cttttttcag	tgcttctgcg	tcgtctttgc	180
tcacgccttc	tttcagagca	gccgggtcag	attctaccag	gtcttttagct	tctttcagac	240
ccaggccagt	tgcgccacgt	actgctttga	taacagcaac	tttgtttagcg	ccagcagctt	300
tcagaattac	gtcgaattca	gttttttctt	cagcagcttc	aaccgggcca	gcagctacag	360
ctacagcagc	agcagcggaa	acaccgaatt	tttcttccat	tgcaagatc	agttctacaa	420
c						421

<210> 10
 <211> 126
 <212> DNA
 <213> E. Coli

<400> 10

```
agagc:tttt tcagtgttc tgcgtcgtct ttgtcacgc cttctttcag agcagccggt    60
gcaga:ttcta ccaggtcttt agcttctttc agacccaggc cagttgcgcc acgtactgct    120
ttgata                                     126
```

<210> 11
 <211> 262
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(262)
 <223> n = A,T,C or G

<400> 11

```
ctgcaacogc aaggggtggc ttatttaact tcaacttcag cgccagcttc ttccagagct    60
tttttcagtg cttctgcgtc gtctttgctc acgccttctt tcagagcagc cgnatgcagat    120
tctaccaggt ctttagcttc ttccagaccc aggccagttg cgccacgtac tgctttgata    180
acagcaactt tgttagcgcc agcagctttc agaattacgt cgaattcagt tttttcttca    240
gcagcttcaa ccggggccagc ag                                     262
```

<210> 12
 <211> 202
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(202)
 <223> n = A,T,C or G

<400> 12

```
gogcataccc tgcagcatcg gcccgatgga gatcaggtcg gcagaacgct gtaccgcttt    60
gtagg:gggtg ttaccgggtg tcagatccgg gaagatgaac acggtagcgc gacctgcaac    120
cggagagttc ggcgctttgg attncgcaac gtcagccatt accgcagcgt cgtactgcag    180
cggaccggcg atcatcaggt ca                                     202
```

<210> 13
 <211> 261
 <212> DNA
 <213> E. Coli

<400> 13

```
tctaggagta agaatagctt caaattcagc agttgacagt ggcataaacg taactggtga    60
cttttgcccg gcatgacgcc gggctttttt tattattccg tgacttccag cgtagtgaag    120
gcaaacttct cgccatcaaa tagccctga ctgggttagtt ttagcgcggg gatcactggc    180
agagaaagaa acgcatctg aataaacggc tcatcgggta acggaccgca ttcacgggag    240
gcggc:ttca aggcgtcaat t                                     261
```

<210> 14
 <211> 224
 <212> DNA
 <213> E. Coli

<400> 14

ttcttttttt	cgtaacggt	gtccagaatc	atttttattta	cctcggggta	cttatgctga	60
tttttattat	tatggggaag	gtgtttattta	tgagtttcat	ttatgccgta	acgacaatga	120
actcgggaat	tagtataagc	agcgcgagaa	taataatcat	tgtgcaaag	ctaattta	180
taataactatt	taaatattat	tttgagcata	tgacataag	gttg		224

<210> 15
 <211> 232
 <212> DNA
 <213> E. Coli

aattcccttc	ttttttcgt	caacggtgtc	cagaatcatt	ttatttacct	cggtactta	60
tgctgatttt	tattattatg	gggaaggtgt	tatttatgag	tttcatttat	gccgtaacga	120
caatgaactc	gggaattagt	ataagcagcg	cgagaataat	aatcattgtg	caaagtctaa	180
tttaattaat	actattttaa	tattattttg	agcatatgca	cataaggttg	gg	232

<210> 16
 <211> 212
 <212> DNA
 <213> E. Coli

aatagcgggt	atgcacgcct	ttcttttttt	cgtaacggt	gtccagaatc	atttttattta	60
cctcgggtac	ttatgctgat	ttttattatt	atggggaagg	tgattttat	gagtttcatt	120
tatgccgtaa	cgacaatgaa	ctcgggaatt	agtataagca	gcgcgagaat	aataatcatt	180
gtgcaaatgc	taatttaatt	aataactattt	aa			212

<210> 17
 <211> 433
 <212> DNA
 <213> E. Coli

ccttgtaaat	tatcgccgt	ggcataaaaa	ctgcgtccaa	acgccgtctt	tgccagcagc	60
caggccataa	atgccaccag	aattatcgtc	aaccaaccaa	ttgctgaaac	gccaagcagc	120
agcggggcgg	agagctgttt	cagttcggcg	ggtaaccctt	caatccattt	gccgccagtc	180
cacagcaaca	tgatgcctct	gtacaaccct	aacgtgccaa	gggtggcaac	aatggcaggg	240
atcttttagcc	acgcgaccag	gacaccgttg	aaaaatcccc	cgagcaaaac	aagcagtaaa	300
gtcgcgacac	aagcaacag	tagtgaatat	cctgcgttca	gtaacatccc	caacagcacc	360
gcgcacattc	cggtaatcga	acccactgaa	acatcaatat	tgcgcgtaag	cattaccagc	420
gtcgcgcca	ttg					433

<210> 18
 <211> 658
 <212> DNA
 <213> E. Coli

cgtagcgttc	cggttggtgc	aaccgcgaa	atggcgcggc	ggttaagtatg	gcgggggttat	60
tccttccccg	ttgaggacac	cggttggtca	ggttgaccat	acgcttaagt	gacaacccccg	120
ctgcaacgcc	ctctgttatc	aattttcttg	tgacgttttg	cggtatcagt	tttactccgt	180
gactgctctg	ccgccctttt	taaagtgaat	tttgatgat	ggtgaatg	gctgagcgca	240
cgcggaacag	ttaaaaccaa	aaacagtgtt	atgggtggat	tctctgtatc	cggcgttaat	300
tggttaactgg	ttaacgtcac	ctggaggcac	caggcactgc	atcacaaaat	tcattgttga	360
ggacgcgata	atgaaaacgt	tattaccaaa	cgtaataacg	tctgaagggtt	gttttgaat	420
tggtgtcact	atcagtaacc	cagtattttac	tgaagatgcc	attaacaaga	gaaaacaaga	480
acgggagcta	ttaataaaaa	tatgcattgt	ttcaatgctg	gctcgtttac	gtctgatgcc	540
aaaaggatgt	gcacaatgaa	ttcagcattt	gtgcttgctc	tgacagtttt	tcttgtttcc	600
ggagagccag	ttgatattgc	agtcaagtgg	tcacaggaca	atgcaggagt	gtatgact	658

<210> 19

<211> 588
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(588)
 <223> n = A,T,C or G

<400> 19
 gtgactgctc tgcgcgccctt tttaaagtga attttgtgat gtggtgaatg cggctgagcg 60
 cacgcggaac agttaaaacc aaaaacagtg ttatgggtgg attctctgta tccggcggtta 120
 attgttaact ggtaaacgct accctggaggc accaggcact gcatcacaaa attcattgtt 180
 gaggacgcga taatgaaaac gttattacca aacgttaata cgtctgaagg ttgttttgaa 240
 attggtgtca ctatcagtaa cccagtattt actgaagatg ccattaacaa gagaaaacaa 300
 gaacgggagc tattaataaa aatatgcatt gtttcaatgc tggctcgttt acgtctgatg 360
 ccaaaaggat gtgcacaatg aattcagcat ttgtgcttgt tctgacagtt tttcttgttt 420
 cgggagagcc agttgatatt gcagtcagtg ttcacaggac aatgcangag tgtatgactg 480
 cagcaaccgc aacagaaaat tcccggtaac tgttaccgg tcgataaagt tattcaccag 540
 gataatatcg aaatcccgcc aggtctttaa aacagttccg taataaat 588

<210> 20
 <211> 101
 <212> DNA
 <213> E. Coli

<400> 20
 gatccagcaa gaagatgcgg ttgtaccgtc atcacgcaga tgcgcaaagc tactcagcaa 60
 ctgacctttc ttcgcaataa gcacgccatt agcgtcatag a 101

<210> 21
 <211> 465
 <212> DNA
 <213> E. Coli

<400> 21
 tcgcgtgttt accttcaaca tcggtaaactt tctggcggat agtttcacgg taagcaacct 60
 gcggtttacc tacgttcgct tcaacgttga attcacgctt catacgggtca acgatgatgt 120
 cgagggtcag ttcgcccata cccgcgatga tggctctggt agattcttcg tcagtcacata 180
 cacggaaaag cgggtcttct ttagccagac ggcccagagc cagaccatt tttctctggt 240
 cagcttttgt tttcggttca actgcgatgg agattaccgg ctacgggaat tccatacgtt 300
 ccagaatgat cggcgcatcc ggggtcacaca ggggtgcacc agtgggttacg tctttcagac 360
 cgatagcagc agcgatgtcg cccgcgcgaa cttctttgat ctcttcacgt ttgttagcgt 420
 gcatctgaac gatacgaccg aaacgctcac gtgcagcttt cacgg 465

<210> 22
 <211> 859
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(859)
 <223> n = A,T,C or G

<400> 22
 tgatcggctc aagcagaact ggtttcgctt tcttaaagcc ttctttaag gcgatagaag 60
 cagccagttt aaacgccagt tcagaggagt caacgtcatg gtaagaaccg aagtgcagac 120
 gaatacccat gtctactacc gggtagcctg ccagcggacc tgccttcagc tgttcctgga 180
 tacctttatc aacggccggg atgtattcgc cagggattac accaccttta atgtcgttga 240
 tgaactcgta gcctttcggg ttgaaaccg gctccagcgg gtacatgtcg ataacaacat 300

```

gaccatactg accacgacca ccagactggt tcgcgtggtt accttcaaca tcggtaactt 360
tctggcggat agtttcacgg taagcaacct gcggtttacc tacgttcgct tcaacggtga 420
attcacgctt catacgggtca acgatgatgt cgagggtgcag ttccgccata cccgcgatga 480
tggtctggtt agattcttcg tcagtcata caccgaaaga cgggtcttct ttagccagac 540
gggccanagc cagaccatt tttctctggt cagctttggt tttcgggtcaa ctgcgatgga 600
gattaccggc tcanggaatt tccatacctt ccaggaatga tcggcgcatt ccggtcaaac 660
angngntacc aggggggtac ntntttttaa nancgattgc cagcancgga tntnncccg 720
gcnaaacttc tttggaacnn ttaccgggtt ggtaaccngc cttttnaacn atccaaccga 780
aaaagngtta anngccantt ttccngnggt tnanntncgg ntcccngaa ntaaccnc 840
cggggtnaac ccnghaaaa 859

```

<210> 23
 <211> 269
 <212> DNA
 <213> E. Coli

```

<400> 23
ctttctaaa gccttcttta aaggcgatag aagcagccag tttaaacgcc agttcagagg 60
agtcaacgtc atggtaagaa ccgaagtgc gacgaatacc catgtctact accgggtagc 120
ctgccagcgg acctgtcttc agctgttctt ggataccttt atcaacggcc gggatgtatt 180
cgccagggat tacaccacct ttaatgtcgt tgatgaactc gtacgcttcc gggtttgaac 240
cgggtccag cgggtacatg tcgataaca 269

```

<210> 24
 <211> 330
 <212> DNA
 <213> E. Coli

```

<400> 24
gttttgggga gatgtaagg ctaatctgaa tggctgcatt ccttggttaa ggaaaaacga 60
atgactgatt gccgatacct gattaaacgg gtcatacaaaa tcatcattgc tgttttacag 120
ctgatccttc tgttcttata acacaaggaa acgtacttaa ggtgcgtccg gtgaaccagt 180
cggacgcacc ttttaataact ataaataagt gtctgggcag atactatata aattaactta 240
gtgaatgatt atgctaattg catcaattaa ataaatataa tggcggttaag gcttcccagt 300
aatataatta atactctact tccagagtag 330

```

<210> 25
 <211> 471
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(471)
 <223> n = A,T,C or G

```

<400> 25
gttttgggga gatgtaagg ctaatctgaa tggctgcatt ccttggttaa ggaaaaacga 60
atgactgatt gccgatacct gattaaacgg gtcatacaaaa tcatcattgc tgttttacag 120
ctgatccttc tgttcttata acacaaggaa acgtacttaa ggtgcgtccg gtgaaccagt 180
tcggacgcac ctttaataac tataaataag tgtctgggca gatactatat aaattaactt 240
agtgaatgat tatgctaatt tcatcaatta aataaatata atggcggtta ggcttcccag 300
taataataatt aatactctac ttccagagta gaataataaa ttttatccgc gtggtgcac 360
agcacaatt tatccacaaa ctgttcttct gtctcgacat gcccccgat ctttnacaaa 420
tantattggg ggattnggcc cncctttttg ncagggttgg gtcntctnat g 471

```

<210> 26
 <211> 379
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(379)
 <223> n = A,T,C or G

<400> 26

natctgantg gctgcattcc ttgtttaagg aaacccgaat gactgattgc cgatacctga	60
ttaaacgggt catcaaaatc atcattgctg ttttacagct gatccttctg ttcttataac	120
acaagaaaac gtacttaagg tgcgtccggt gaaccagtcg gacgcacctt taataactat	180
aaataagtgt ctgggcagat actatataaa ttaacttagt gaatgattat gctaattgtca	240
tcaattaaat aaatataatg gcgttaaggc ttcccaqtaa tataattaat actctacttc	300
cagagttagaa tattaattt tatccgcgtg gtgcatcagc acaaatttat cccacaactg	360
ttcttctgtc tcgacatgc	379

<210> 27
 <211> 799
 <212> DNA
 <213> E. Coli

<400> 27

aaagatgatg tgatgagaaa gtcaatttga ataagacaat attaagagct aaaaaaatgt	60
caaaaaacac taaatcaaaa aataatggca tttagaaaata taatgcgaaa acggagggtga	120
aattagttta ttccaatga ggaaaatctc ccggcgaaaa aaccgggaga tgaaagtgtg	180
atgggratca aataaacaac agaggagaaa tttttaacgc agccattcag gcaaatcgtt	240
taatcccatt gcctggcgga taagtgtcgg cttaacgcca ggaagcgtgt cggccagttt	300
caaaccaata tcacgcagca gttttttcgc cggattggta ccggaataca gatcgcggaa	360
tccctgcata ccagccagca tcaacgccgc actgtgcttg cggctacgct catagcgacg	420
cagataaatg tactgcccga tgtctgggat ccgtcgacct gcagccaaagc ttgggctttt	480
cagcctgata cagattaaat cagaacgcag aagcggctctg ataaaacaga atttgcttgg	540
cggcagtagc gcggtggtcc caccgtgaccc catgccgaac tcagaagtga aacgcccgtg	600
gcgcccagatg gtagtgtggg gtctcccat gcgagagtag ggaactgccca ggcatacaat	660
aaaacgaaag gctcagtcga aagactgggc ctttcggttt atctggtggt tgcggtgaa	720
cgctctctga gtaggacaaa tccgcgcggga gcggattttg aacgttgcca aacaaccggc	780
ccggaagggg gtggggggt	799

<210> 28
 <211> 636
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(636)
 <223> n = A,T,C or G

<400> 28

aggggggttg ttgtgggcaa tgatgcattt aagttatcgt ctgcagatag aggagatatt	60
acaataaaca acgaatcagg gcatttgata gtcaataccg caattctatc aggagatata	120
gtcactctta gaggagggaga aattaggttg gtattatagc ttgtgcgcgc catgattggc	180
gcgcaattta aacttagtgc ttacatcgc tattgtcttg atttctttga attattttat	240
aaattaaaaa aacgactggt atgtataagc aaagggtcgaa cgaaaaatac attccaaata	300
aatgcttgct taaatctcta tatccttccc cgaaaaatga cacataaaat tgagatattc	360
caaaaagaga tactacaaat aaagatgcct ttattttatt atttctaata aaaaatagaag	420
caataaaaaa taataacaat gatataaatc taatgttttt aaatatattg tcttttatgt	480
tagtaatagt cgtagtatg ttgattctc catatattac gtgtagtttt ttatatacat	540
ggaaataatt ntctttatac tgagacatca caccatcatc aaatggaagt ttgaagatgg	600
tgcttggttt gctaaccaat aaaaagagtg cattcg	636

<210> 29
 <211> 757
 <212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(757)

<223> n = A,T,C or G

<400> 29

cagcggctcg	atttttagca	tggtttttta	ttggcggcta	tgctgccccg	ggagcataaa	60
gatgaaaaaa	acaacgatta	ttatgatggg	tggtggcgatt	attgtcgtac	tcggcactga	120
gctgggatgg	tggtaacgtc	acctctaaaa	aatagcaaag	gctgcctgtg	tgacgccttt	180
gtgcaattta	agcgttaact	tttaattctt	ctgtagataa	atagcacgac	aatcgcacca	240
ataacggcaa	ccacgaagct	gccaaaattg	aagccatcga	ctttaccaa	gccaaacagc	300
gtgctgatcc	atccgcccgc	tacggcaccg	actatcccca	gcaggatagt	cataaagaat	360
ccacctccat	ctttacctgg	catgatccac	ttcgccagaa	taccggcaat	aagcccaaaa	420
ataatccatg	acagaatgcc	cattgtttcc	tcacttatct	gttttgcat	agcgggtag	480
tcgctgataa	aaagcatagc	acaacatcgg	gagggaaga	tttgtgacga	gcacacgga	540
ggtttttttt	gcgatggcgc	agaaattgcg	ccatcaacga	tcagtataa	ttaccaacca	600
caaacatcat	gttcgttttc	cgtgtcataa	gaaccgtacg	ggattcacca	gatcttttat	660
cacttcaagc	cggcactttc	ggcaccagca	aagtcacgga	cgtctctggt	tcataatcga	720
ccggaacgc	cattgctggt	attggtgaen	gtcacgg			757

<210> 30

<211> 392

<212> DNA

<213> E. Coli

<400> 30

aattacagaa	aaaggaggca	ataticggga	aaggcattag	cccagcgaat	acgtcgggct	60
acaaaatta	ttgtgctgca	ggtgttttag	cgggtgtgtg	atccacaggt	tctaactgga	120
agaccacatc	gacctgatca	tcaaaactgaa	tagcggcctg	ctcgtaaagt	tcctgggcgg	180
acaccggcgc	ggcatcggct	ttcatcatcc	gcaccattgg	gctgggctga	tagttggaaa	240
catggtagcg	cacgttatat	accggcccca	gtttacgatg	aaagccgttc	gccagttcct	300
gcgcctgatg	aatcgcggtt	tcaatcgctg	ccttacgcgc	tttgtcttta	taggcatccg	360
gctgcgccac	gcccagcgac	acagaacgaa	tt			392

<210> 31

<211> 351

<212> DNA

<213> E. Coli

<400> 31

ctatccttga	tgaaccgcgc	agcaaagata	ggtgattacg	tcattggttt	acagaaaatt	60
acagaaaaag	gaggcaatat	cgggttaaagg	cattagcccc	acgaatacgt	cgggctacaa	120
atattattgt	gctgcaggtg	ttttagcggg	ttgttgatcc	acaggttcta	actggaagac	180
cacatcgacc	tgatcatcaa	actgaatagc	ggcctgctcg	taagtttcct	ggcgggacac	240
cggcgcggca	tcggctttca	tcacccgcac	cattgggctg	ggctgatagt	tggaacatg	300
gtagcgcacg	ctatataccg	gccccagttt	acgatgaaag	ccgttcgcca	g	351

<210> 32

<211> 762

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(762)

<223> n = A,T,C or G

<400> 32

aattatgaaa	cactgtcttg	aatcgtctga	atgacgggca	catttgcgag	cacgcatcca	60
------------	------------	------------	------------	------------	------------	----

```

gtaataaacac aggaaactat tttatctacg cgtagcgat agactgcttg catggcgaaa 120
ggaggtaagc cgacgatttc agcgggacgc tgaaacggga aagcccctcc cgagggaagg 180
gccataaata aggaaagggt catgatgaag ctactcatca tcgtgggtgct cttagtcata 240
agcttccccg cttactaaga ctaccagggc gggggaaaacc ccgctctacc ctactcctg 300
aaagtatgcc ttcacgataa gattgtcaat ccgcaggctt tgtagtctgc gatcctgcca 360
gcaaataattc tttgcgagtc gttacgcaat aatcacagag gaaactatct tattcacgcg 420
ttagcgatag actgcattca gggcgaaaagg aggtaaagccg atgatttcag cgggacgctg 480
aaacgggaaa gcctctcccc gagaagaggg cttttaataa ggaaagggtt atgatgaagc 540
acgtcatcat actggtgata ctcttagtga tttagctcca ggcttactaa gaacaccagg 600
gggaggggga aacctcttcc taacctcac ttctgaaatt ggggtgctatg acgctggcgt 660
tactgcttan cgctaccagt ttgtctgccc tggcggttgt aacgccagat cggtagccgt 720
ttggatatatt taatgaaagc cgacaaatca atcancgtga cg 762

```

<210> 33
 <211> 293
 <212> DNA
 <213> E. Coli

```

<400> 33
gcacatttgc gagcacgcat ccagtaataa cacaggaaac tattttatct acgcgttagc 60
gatagactgc ttgcattggc aaaggaggta agccgacgat ttcagcggga cgctgaaacg 120
ggaaaagcccc tcccaggaa ggggccataa ataaggaaag ggtcatgatg aagctactca 180
tcatcggtgt gctcttagtc ataagcttcc ccgcttacta agactaccag ggcgggggaa 240
accccgctct accctcactc ctgaaagtat gccttcacga taagattgtc aat 293

```

<210> 34
 <211> 633
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(633)
 <223> n = A,T,C or G

```

<400> 34
atttacactt ttacgaaat catgggatca ctaacaaaa atcgcttgtc agttatattg 60
tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 120
ttaaaaaata gatgttgctg ggtgcgcttt tgctgggtac cagtgcgcgc tgggccgcac 180
cagccaccgc gggttcgacc aatacctcgg gaattttctaa gtatgagtta agtagtttca 240
ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 300
agtacaacat taagcagtg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 360
ggacctatat ggggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 420
cctacgacgg tgagattttt tatcatcgct aaaaaaagcc ccctcatcat gagggggaaa 480
tgcagacacc ttgntatttt ttattattag ccacttgcgc gtcttgcttg gtattaaatc 540
gtatttcacg ttgattaatg cnggtggctc cagtgcgcca gattaacttt gtttgatcg 600
aagacgtagt aactggctgg ttatcggaat tgg 633

```

<210> 35
 <211> 569
 <212> DNA
 <213> E. Coli

```

<400> 35
tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 60
ttaaaaaata gatgttgctg ggtgcgcttt tgctgggtac cagtgcgcgc tgggccgcac 120
cagccaccgc gggttcgacc aatacctcgg gaattttctaa gtatgagtta agtagtttca 180
ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 240
agtacaacat taagcagtg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 300
ggacctatat ggggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 360
cctacgacgg tgagattttt tatcatcgct aaaaaaagcc ccctcatcat gagggggaaa 420

```

tgcagacacc	ttgttatttt	ttattattag	ccacttgctc	gtcttgcttg	ttattagtgc	480
tatttcacgt	tgattaatgc	ggttgcctcc	agtgcgccag	atttaacttt	gtttgtatcg	540
tagacgtagt	aactggctgg	tatcggaat				569

<210> 36
 <211> 338
 <212> DNA
 <213> E. Coli

<400> 36						
cgtattcaca	tccttttgat	tggtgataac	atgcgaatcg	gtattatttt	tcgggttgta	60
atcttcatta	cagcggtcgt	atttttagca	tggtttttta	ttggcggcta	tgctgccccg	120
ggagcataaa	gatgaaaaaa	acaacgatta	ttatgatggg	tggtggcgatt	attgtcgtac	180
tcggcactgc	ctgggatggg	ggtaacgtca	cctctaaaaa	atagcaaaag	ctgcctgtgt	240
gcagcctttg	tgcaatttaa	gcgttaactt	ttaatcttcc	tgtagataaa	tagcacgaca	300
atgcgaccaa	taacggcaac	cacgaagctg	ccaaaatt			338

<210> 37
 <211> 375
 <212> DNA
 <213> E. Coli

<400> 37							
ctgaatat	ttt	aaaaaggaaa	acgacatgaa	accgaagcac	agaatcaaca	ttctccaatc	60
ataaaaat	tatt	tcogtgagc	attttattat	tgaatataga	ggtttaactc	cggtaaaaaa	120
caaagaagca	ttgaatycag	ggaaaaataa	tatggccata	aaaaacatcg	aaagaaactc		180
ttttaattta	acatgtaaac	gcatgggttaa	tcctcatatc	acgggtggag	tggttaagaac		240
atacataaat	ggagtcaggt	tttccctttt	ccatttatca	agttcctgtt	gccgttttag		300
tcctatctcta	attgcataatt	ttaatttttc	tgataaatgg	cattgagcat	cgatttcatt		360
taaaacaact	gtaca						375

<210> 38
 <211> 446
 <212> DNA
 <213> E. Coli

<400> 38						
ttacgatagc	tattagtaaa	aatataagag	ttagctgtat	tggtatgtct	gtggcgaaat	60
tgactacctt	cgtttttttg	attaagaatg	attttattat	cgtaagtaaa	attacatgaa	120
tatttaaaaa	ggaaaacgac	atgaaaaccga	agcacagaat	caacattctc	caatcataaa	180
atatttcctg	ggagcatttt	attattgaat	atagagggtt	aactccggtg	aaaaacaaaag	240
aagcattgaa	tgacgggaaa	aataaatatgg	ccataaaaaa	catcgaaaag	aactctttta	300
atttaacatg	taaacgcatg	gttaatcctc	atatcacggg	tgagagtgtta	agaacataca	360
taaatggagt	catgttttcc	ctttccatt	tatcaagttc	ctgttgccgt	tttagtccat	420
ctctaattgc	atattttaat	ttttct				446

<210> 39
 <211> 392
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(392)
 <223> n = A,T,C or G

<400> 39						
tcaccccggt	gccgattttc	aggcatcctg	atttaactta	gcacccgcaa	cttaactaca	60
ggaaaaacaaa	gagataaatg	tctaactcctg	atgcaaatcg	agccgatttt	ttaatcttta	120
cggactttta	ccgcctgggt	ttattaattg	cactgtnatc	cgggcgttcg	cccgttttaa	180
tcacaatagg	ctgtgtagcc	tgggcctggt	tccttttcac	ccgcgccaga	gcggcagcaa	240

tcgcacatctt atctttggct gcaggttgaa cggttcgct cttatgtcgt tcaaggcgag 300
 ccgctttttc gcgctccaga cgagcctggc gcgcttcgaa acgcgctttg gcttctgcgg 360
 cncgcttttc ttcttgacga atagccgcaa tt 392

<210> 40
 <211> 208
 <212> DNA
 <213> E. Coli

<400> 40
 taataacgct atctgcggat aaagcagaat aggtgggttaa cccagacat aaaccgagga 60
 aaataatggt attgtatttc ataacttatt gtcccttagc gacagattgc tgtctgctgg 120
 ttcagtaagg taccaggaga aacttcagga agcttggtact cgacaatata gtttgagttt 180
 ttatctttgc cccatgaaac ctgtaatt 208

<210> 41
 <211> 342
 <212> DNA
 <213> E. Coli

<400> 41
 catcttcaat accgttaaat gcaaccgaa ccccggtgt ccttttgcgt cattcactta 60
 acgtaactctg aaaaggagcg gctggacttg tgctaccggt cgttggaat tgtctggcac 120
 tgtttttttg gagatctacg gtaaaattaa gcgaatccga tgagactgtg cagccataat 180
 cgaggacgcg cccgctaatt ttaataacgc tatctgcgga taaagcagaa taggtgggtta 240
 accccagaca taaaccgagg aaaaataagt tattgtattt cataatctat tgttccttag 300
 cgacagattg ctgtctgctg gttcagtaag gtaccaggag aa 342

<210> 42
 <211> 841
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(841)
 <223> n = A,T,C or G

<400> 42
 agatttactg ccaatttccg gcagatcgga aagggttaaa ccatattgat ccataagggt 60
 acgaatcacg gctataccgc caggcatggc ttgagccatg gcattaaatt ccgcaaattc 120
 gggcgctgat tcttcccacg cggttatttt ggcacacacc agatccagca aggggttntc 180
 aggatcgttg agcagcagat gatctaccag ttncagcgcc tgggtgtatt gntccttgtt 240
 ctgaataccc gnnagaaaaa gtgccacagc anttagcttn tctcctgctt gcaagatgtc 300
 tggcaatngc aatcattttt tgcacttant acgatgnaca ncngtaaaaga aatcgnattt 360
 ttntatgccg tcataacttt acgtatgtan cactttttgc nattcnaaaa aagaccattn 420
 gctncaacac gtaaattna ttgncccnna catttanaac ataaatgntt aaaattttcc 480
 ccccnncnnan ttttaagntn ttanagaat ngggaattac ctgcttttna atgnactcan 540
 anttttttng naatpattcc tntatcnaa ctnnttttcn cccaanagnc nnccaaattn 600
 cggtttnttn ntnnncnng onttttttta cccnanaann tttattcaan nccttttttg 660
 tagntctatt naagngnct tntttnnatt aactttccnn ttggncaaat tttggcnnat 720
 ttttatatan aattntctta tntcntaatt tnggnanccc cngatgnaan tttatggngg 780
 gantcccnnt ccctntttta tnnatgntct gggntatttt taaancctnn attaanann 840
 c 841

<210> 43
 <211> 215
 <212> DNA
 <213> E. Coli

<400> 43

```

aataactttt cgtaggcag ttttgggtgt gagttgcaag aggggagact actgaataac    60
tcaagtttta taatcgaggg gaaaatggtg atggcggtta tagcaaaacg ccctcaacca    120
taaagggtcga gggcgcttaa gatgttaaaa acccgctatc cggttaaaaaa caatgttcaa    180
ctaagggtcag tgacattgctg ctaaaaaaagc gaatt                                215

```

```

<210> 44
<211> 395
<212> DNA
<213> E. Coli

```

```

<220>
<221> misc_feature
<222> (1)...(395)
<223> n = A,T,C or G

```

```

<400> 44
gcattattca tgagaaatgt gtatcgtaaa tcaactgaaa ttaacgcaac catttggtat    60
ttaagggtta attatctgtg tgtgatattt tattgaatgt tttaaatatt gtttttattg    120
gcattgctat aatattgggt atcatttgct gaatggattc agtcttaatg agtggggttt    180
taagggacag gcatagagta atgatacgtg tgcataacca acatctttac tcattatgtc    240
attgaatgtt gaccctatgt gtttatgaag gagaggtatt ttcagttgat ctggattgnt    300
aaattcatat aatgcgcctt tgctcatgaa tggatgccag tatgtagtgg gaaattataa    360
atattgaaat agtccaacta cttctttatt accaa                                395

```

```

<210> 45
<211> 883
<212> DNA
<213> E. Coli

```

```

<220>
<221> misc_feature
<222> (1)...(883)
<223> n = A,T,C or G

```

```

<400> 45
ataatcaggt aagaaaaaggt gcgcggagat taccgtgtgt tgcgatatat ttttagttt    60
cgcgtggcaa tacatcagtg gcaataaaac gacatatcca gaaaaatata cactaagtga    120
atgatatctt ccgattttatc ttaatcgttt atggataacg gcaaaaggct tcgttttttc    180
ctatacttat tcagcactca caaataaagg aacgccaatg aaaattatac tctgggctgt    240
attgattatt ttcctgattg ggctactggt ggtgactggc gtatttaaga tgatatttta    300
aaattaatta atgcatcag gtccgaaaat aacgagaata tttcagtctc tcatcctggt    360
gcgctcctgt catgtgcatt gcttcataata atcactggcg caaggagcgc cgcaggcgna    420
gnntgcncgn cgncccacct naccccatgc cgaacttcag aantgaaaac nccntaacnc    480
cgarngtcgg cggnggcctc cccatgcnan agtangggaa ntgccangcg ncnntataaa    540
cgaaaggctn attncaaaga ctgggccttn cntttatctg atgtttgtcg gagaacgctc    600
tcctgagnan gacaaatncc gccgggagcg gatttgaacn ttgcgaagca accgncctcna    660
aggngnngt cntgaenccc nctctanct nnngccttc ttttgcctna angncctcct    720
ancngatggc ctttttngcc ntctacccaa cnntttggtt aatgcttnta aaancctttc    780
canntncaaa tccngtnntn cccatccnnn tnntgaaagn ntncctnccn tgnctantnt    840
anntnngggg gnnngngngcc ggcggnccccc cccccccccc ccc                                883

```

```

<210> 46
<211> 1024
<212> DNA
<213> E. Coli

```

```

<220>
<221> misc_feature
<222> (1)...(1024)
<223> n = A,T,C or G

```

<400> 46
 gtttatggat aacggcaaag ggcttcggtt tttcctatac ttattcagca ctcacaaata 60
 aagggaacgcc aatgaaaatt atactctggg ctgtattgat tattttcctg attgggctac 120
 tgggtggtgac tggcgatttt aagatgatat tttaaaatta attaatgtca tcagggtccga 180
 aaataacgag aatatctcag tctctcatcc tgttgcgctc ctgtcatgtg cattgcttca 240
 tataatcact ggcgcaagga gcgcgcagag tntcccnant nnnntnnnt nntnnctnn 300
 nccttcacna tncnnccn nantnnatag nncaccnntn tntntcnntn gncncctcc 360
 nnnnnnnnn ncatnnnnt ccactnnnt tntccannn nnnnnnnntn canccnacia 420
 antncnaccn annnacctt atacnnann nancnnnnnn nncactctn nctcgnnctc 480
 cccnttcnac nncannnnnn cancnntcn ctnnnnccct nncntaattt tctnnctan 540
 ntccatncn cnnacnnncc cancnatccn nnnatacant cnattnnntn cnntcnntn 600
 cncnnttc nntnnnnnc tncncatnc ccnnnnnnn canntncccc nctnccctna 660
 cncncncnc cncncatccc nnnccnnt ccnntntga caannnnaat cncnnnnncn 720
 nnnnnnnnn tnnncnccn gcnncnccnt nccntcanc tnnncncta nannnnntac 780
 nntnacnnt cctnnacnc tncctnnng antccnana ntannnnanc nanaacnctn 840
 tnnnnccata atccacacc acnccnctc anctntntt ncntntccc ttcntatcnc 900
 agctnnnnnt nctntnnnn tncnccnnt cnnactnntn nncnccnnt cccantcagt 960
 ccacntccn cnnnnnnnt nnnnnancn ctnncacnc cnantaacct nntnnacct 1020
 tccc 1024

<210> 47

<211> 236

<212> DNA

<213> E. Coli

<400> 47
 atatacacta agtgaatgat atcttccgat ttatcttaat cgtttatgga taacggcaaa 60
 gggcttcgtt ttttctata cttattcagc actcacaat aaaggaaagc caatgaaaat 120
 tatactctgg gctgtattga ttattttcct gattgggcta ctgggtggtg ctggcgatt 180
 taagatgata ttttaaaatt aattaatgtc atcagggtccg aaaataacga gaatat 236

<210> 48

<211> 418

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(418)

<223> n = A, T, C or G

<400> 48
 cggagattac cgtgtgtgac gatataat ttagtttcgc gtggcaatac atcagtggca 60
 ataaaacgac atatccagaa aaatatacac taagtgaatg atatcttccg attnatctta 120
 ntogtttatg gataacggca aagggttcg ttttttcta tacttattca gcaactcaca 180
 ataaaggaa gcaatgaaa attatactct gggctgtatt gattatttcc ctgattgggc 240
 tactgtggt gactggcgta ttttaagatga ttttttaaaa ttaattaatg tcatcaggtc 300
 cgaaaataac gagaatattt cagtctctca tctgtgtgcg ctctgtcat gtgcattgct 360
 tcatataatc actggcgcaa ggagcgcgca nggggcgcc aatcgccgcc ggcccctg 418

<210> 49

<211> 550

<212> DNA

<213> E. Coli

<400> 49
 ctgctagtta cagggaacac taatgacaga cagctaaaag ccctgtttta ttacgtatta 60
 caaacagggg atgccagcg ttttcgtgca tttattggtg agatagcgga acgcgcacca 120
 caagaaaagg agaaactgat gaccattgct gacagattac gtgaagaagg cgcaatgcag 180
 ggcaaacacg aagaagccct gcgtattgct caggagatgc tggatagagg ttagacaga 240
 gagttagtta tgatggtgac ccgacttica ccagacgac ttatcgcgca aagccactaa 300

tcctgtaaca	ccgggagtta	actggcggat	gtttgctgta	aaccacatca	gcgaacgaca	360
tccgccagcg	cctcttctaa	atcgtagcag	cgaaacgcaa	aaccgccttc	ttccagccgt	420
ttaggcagcg	cgcggttgcc	acctaatacc	agtactgaag	attcgcccat	taacagtcga	480
atggcggtcg	cggggacgcg	caaaatgccc	gggcgatgca	gcgcgatgacc	gagcgcatgg	540
gcaaattgtt						550

<210> 50
 <211> 99
 <212> DNA
 <213> E. Coli

ttggcatctc	ggtgttgccg	atcttcatga	tatccagccc	gccggaaaact	tcttcccaaa	60
cggttttgct	gttatccatt	gagtcacgga	actgccct			99

<210> 51
 <211> 259
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(259)
 <223> n = A,T,C or G

ccgtgcccag	atgatctctg	naccatcatc	cggtgtgaag	tagtgattca	cgacttcaag	60
gcgcttttca	aaagggtatt	ttggctttga	catattaggg	gctattccat	ttcatcgnc	120
aacaaaaatg	gtgcagtaca	tactcnttgg	aatcaacac	aggaggctgg	gaatgccgca	180
gaaatataga	ttactttctt	taatagtgat	ntgtttcacg	cttttatttt	tnaaanaagt	240
tnggcttact	tcgccgggn					259

<210> 52
 <211> 877
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(877)
 <223> n = A,T,C or G

cagcagagcg	cgcccttctt	cgtagatatt	cgtagtagtg	gtaatggtaa	tatccaaacc	60
acgaacgcgg	tcgactttat	cgtagtcgat	ttctgggaag	atgatctgct	cacggacacc	120
catgctgtag	ttaccacgac	cgtagcgaag	cttagcggac	aggccacgga	agtcacggat	180
acgaggtaca	gcaatagtga	tcaggcgctc	aaagaactcc	cacatgcgtt	cgccacgcag	240
agttacttta	cagccgatcg	gatagccctg	acggattttg	aagcctgcaa	cagatttgcg	300
tgctttgggt	atcagcggtt	tttgaccgga	gattgctgcc	aggtctgctg	ctgcgttatc	360
cagcagtttt	ttgtcagcga	tcgcttcacc	aacacccatg	ttcagggtga	tcttctcgac	420
ccgagggact	tgcatgacag	aattgtagtt	aaactcagtc	atgagttttt	taactaettc	480
gtctttgtag	taatcatgca	gtttcgccat	cgtactactc	catgtcggtg	aacgctctcc	540
tgagtaggac	aaatccgccg	ggagcggatt	tgaacgttgc	gaagcaacgg	cccggagggt	600
ggcgggcagg	acgcccgcga	taaaactgcca	ggcatcaa	taagcagaag	gccatcctga	660
cggtatggcct	ttttgcgttt	ctacaaactc	ttttggttat	ttttctaaat	cattcaata	720
tgtatccgnt	catcccatcc	tatcgatgat	aagctgtcaa	acatgagaat	ttaatcaatc	780
taaaagttta	tggnngttaa	cttgggctgg	cagnttncca	atggctta	cagtngaggg	840
ccctatntta	acgaactnng	ctantttngg	tcaatcn			877

<210> 53
 <211> 291

<212> DNA
<213> E. Coli

<400> 53

tgaacagcag	agatacggcc	agtgcggcca	atgttttttg	tcctttaaac	ataacagagt	60
cctttaagg	tatagaatag	gggtatagct	acgccagaat	atcgtatttg	attattgcta	120
gttttagtt	ttgcttaaaa	atattgttag	ttttattaaa	tgcaaaacta	aattattggt	180
atcatgaatt	tgttgtaga	tgaataaaat	ataggggggt	atagatagac	gtcattttca	240
taggctata	aatgcgacta	ccatgaagtt	tttaattgaa	agtattgggt	t	291

<210> 54
<211> 282
<212> DNA
<213> E. Coli

<400> 54

ttattaaatg	caaaactaaa	ttattggtat	catgaatttg	ttgtatgatg	aataaaatat	60
aggggggtat	agatagacgt	cattttcata	gggttataaa	tgcgactacc	atgaagtgtt	120
taattgaaag	tattgggttg	ctgataattt	gagctgttct	attcttttta	aatatctata	180
taggtctgtt	aatggatttt	atttttacaa	ttttttgtgt	ttaggcataat	aaaaatcaac	240
ccgccatatg	aacggcggggt	taaaatat	acaacttagc	aa		282

<210> 55
<211> 293
<212> DNA
<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(293)

<223> n = A,T,C or G

<400> 55

cggggtccgg	cgctcatcaa	caatcggggg	gcagcaaggg	gctgaaacgg	gaaagcccct	60
cccgaagaay	gggcttgta	taaggaaagg	gttatgatga	agctcgctcat	catactgggt	120
gtgtngttac	tgtaagtgtt	cccgaacttac	taacaactca	tcagaggggg	gagaaatcct	180
cccttaccct	tggtccttta	ctctaggttg	aaaaaacaac	agcgtcaata	ggcctgccat	240
gtacgaagcg	agatctgtga	accgctttcc	ggttagcctt	ttttatcctg	ttg	293

<210> 56
<211> 300
<212> DNA
<213> E. Coli

<400> 56

tctgcgttcc	gctaaaagg	gcaaatgctc	aggacgttgc	agcgttttgc	gtgaaccgctc	60
ggggaaggca	aaattgcctc	tgggaaaagca	ttgcgcgggg	tccggcgctc	atcaacaatc	120
ggggggcagc	aaggggctga	aacgggaaag	cccctcccga	agaagggggc	ttgtataagg	180
aaagggttat	gatgaagctc	gtcatcatac	tggttgtgtt	gttactgtta	agtttcccga	240
cttactaaca	actcatcaga	ggggggagaa	atcctcccct	acccttgctc	ctttactcta	300

<210> 57
<211> 359
<212> DNA
<213> E. Coli

<400> 57

caacacagga	ggctgggaat	gccgcagaaa	tatagattac	tttctttaat	agtgatttgt	60
ttcacgcttt	tattttttcac	ctggatgata	agagattcac	tgtgtgaatt	gcatattaaa	120
caggagagtt	atgagctggc	ggcgttttta	gcctgcaaat	tgaaagagta	agagctctcg	180
gcgggaaatt	attcccgcct	tacttacggc	gttgcgcatt	ctcattgcac	ccaaatttat	240

tcttcacaaa aataataata gattttatta cgcgatcgtat tatttatttc ctgaaaacaa 300
ataaaaaaat ccccgcaaaa tggcagggat cttagattct gtgcttttaa gcagagatt 359

<210> 58
<211> 700
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(700)
<223> n = A,T,C or G

<400> 58
aaaccttttt ctctgtttt tcatagaggg caacccatgt cctgacctgg gttcggggga 60
caccaaaaacg tgccgagatg atcctgtaac catcatcagt tgtgaagtag tgattcacga 120
cttcaaggcg cttttcaaaa ggggtattttg gctttgacat attaggggct attccatttc 180
atcgtccaac aaaatgggtg cagtacatac tcgttggaat tcaacacagg aggctgggaa 240
tgccgcagaa atatagatta ctttctttaa tagtgatttg ttccacgctt ttatttttca 300
cctggatgat aagagattca ctgtgtgaat tgcatattaa acaggagagt tatgagctgg 360
cgcggttttt agcctgcaaa ttgaaagagt aagagtcttc ggcgggaaat tattcccgcc 420
ttacttacgg cggttgccat tctcattgca cccaaattta ttcttcacaa aaataataat 480
agattttatt acgcgatcga ttattttatt cctgaaaaca aataanaaaa tccccgccaa 540
atggcagggga tcttagattc tgtgctttta agcagagatt acaggctggt tacgttacca 600
gctgccgggc ctttaacgcc gctttcgatg gtgaaggaca ctttctgacc ttcgtccaga 660
gattgtaacc atcgggtcgg atagccnaga aatgtccaac 700

<210> 59
<211> 631
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(631)
<223> n = A,T,C or G

<400> 59
tggtggcatt ggttgctgga gagagaaaac ccccgcacgt tgcaggatg cacctgacaa 60
caccacgggg gctaattctg actctagacc actcaagaat agccgcgaaa cggtgtcatt 120
acaacacagg cggtctatat acgttcgcag agctgggcat ggccttctgg catgatttag 180
cggctccggg cattgctggc attcttgcca gtatgatcgt gaactggctg aacaagcgga 240
agtaacgtgt catgcggggc tcaggctgcc gtaatggcaa ttgctgccc gaccaggccg 300
caggggggaa actctgcggc ctttttcgtt ctactgcgg gtaaggcacc cagtgcggc 360
cgttcaggcg aacgtacggg ttatcctggg attgaataac tactgcattt gagttctcgg 420
agaccggtgc tgtttgtggc aaccactggg tgagtttttt ccagtcaaca ttgtcttcgg 480
tgaaaatctt gccatcgaga acgcgaacca ccagatcgga gatagccagg aagctgctcg 540
gttggttcgat gacaatcggg gccccctgat gcggtgcctt catgccgaag aatttcaccc 600
caacggggac gtcngtgata gaccgggcta g 631

<210> 60
<211> 648
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(648)
<223> n = A,T,C or G

<400> 60

```

ggctcaggcn tgctgattgt ttttttgtgc aatggccngc tattagcgtc gttgctgtcg      60
atggagagaa tcataaacgt ggtgaatgat gattgttagc aaggaaaact gtcaaaaatc      120
ttcaaaaaat ttgagggata aggccggaat ggctccggcc agaggggaagt taaccgcgaa      180
gctgttgctg cttgagggtc gttttaacca gacgccaggc gctccatacg ccaaaaccgc      240
gtctggccca gcggaccagc atattaggat ggcgaaatcg ccagatcgcc atcacgctac      300
tgccaaccag cgcccaggag cgcagactta gcagcatatt ccancgacga tcgtaagcgc      360
ctgttgtctc cagccattca cgcagactgg cggaaaggng cgcgnetgac caacttgnet      420
tttagtctga tncanattan atnataaac gcagnanncn ggtntgatta atcntatttn      480
gctctngtct ggtagttagc nncggnnngt ctctntntna cccnnttcnn tttannttac      540
natnngtaan ttatntttnt nngtctnant tntantngng tactntaagt ntatncgnnn      600
atnntnnnan nnnncagnc ntntttttta aatntttnt nanncnnc      648

```

```

<210> 61
<211> 737
<212> DNA
<213> E. Coli

```

```

<220>
<221> misc_feature
<222> (1)...(737)
<223> n = A,T,C or G

```

```

<400> 61
tgctaataatc tttctcattg agatgaaaat taaggtaagc gaggaacac accacaccat      60
aaacggaggc aaataatgct ggtgaatgat aatgttttta tggccgtact gggaataatt      120
ttattttctg gtttctggc cgcgtatttc agccacaaat gggatgacta atgaacggag      180
ataatccctc acctaacggc ccccttgtaa cagtttgtta caaggggcct gatttttatg      240
acggcgaaaa aaaaccgcca gtaaaccggc ggtgaatgct tgcattgata gatttgtgtt      300
ttgcttttac gctaaccaggc attttctgac actgataaac aatcggtgac acagtagcat      360
cagttttctc aatgaatggt aaacggagct taaactcggg taatcacatt ttgttcgtca      420
ataaacatgc agcgatttct tccggtttgc ttaccctcat acattgcccc gtccgctctt      480
ccaatgacca catccaggag ctcttcagga aatgcgcgac tcacacctgc tgtcacggta      540
atgttgatat gcccttcaga atgtgtgatg gcatgggtat cgactaactg gcaaattctg      600
acacctgcac gacatgcttc ttcattcatc gccgctttga caataatgat aaattcttcg      660
cccccgtagc gataaacctg ttcgtaatna cgcgtccaac tgggntaagt aaagtgcga      720
gggtgccgta atcttac      737

```

```

<210> 62
<211> 648
<212> DNA
<213> E. Coli

```

```

<220>
<221> misc_feature
<222> (1)...(648)
<223> n = A,T,C or G

```

```

<400> 62
tgcttttgaa tatgtgctcg caatcttgag aaggaaatgg cgaccacgaa agaaaaggca      60
aaaaccgata atctgaaaga acccaagtat ttcagtataa gcattgaatg ccgaccagta      120
aactctttcg gattcaccca gaaagtgaan ccaaaatgat aatcgatac ataagtcttt      180
cgagtggctc gttagcaaaa agtttcaaca atggagtaaa tacatccaac atatcaataa      240
ctctcaactg taaggggatt gaaatggtaa cccagctctc tcgcttgagg ggtatagccg      300
agaccaccga agccccggag gtggtgaaat aaaaccgggc acaacacgaa agggcgcatc      360
tccgatatcc ataaaagaag tcgggtcttt gtcrggtaaa attaaatttg tgggaagtgc      420
gcctccgggt tgtaaatacc gactttgctg ggtgtagcct ggcggcatca agtttttttc      480
tggaagtctg ctgatgtccg ccctttttta agggaatttt ggtgatgccg gtgaatgccg      540
cttaaccccc cgtgggcca gttaaaagtc atggtgaagc ctaatnggtt tggggtggga      600
aaagccnact gnaaattggt tacctggttt gcaagtancc ctggaagg      648

```

```

<210> 63

```

<211> 237
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(237)
 <223> n = A,T,C or G

<400> 63
 ggtgtttant tacaagagat tcattctttgt ntaaaanccn gataagtaat tacgcataaa 60
 acaacaatga ttataatagc aaaaataaat attatcatct ttgatagatt acttgagata 120
 gccagcatct tgtaaaacct ttatcggttt tttatgctct ggattaatat aatcactaca 180
 tctatctgag caatctgttg ttgatggaca tgtcaaccca tggtcattta cagccaa 237

<210> 64
 <211> 427
 <212> DNA
 <213> E. Coli

<400> 64
 gataattaga gtttgtcgtc agaaaattga cgttacccat aacaaatgaa aggccaggta 60
 aatcatgcca ttagtcattg ttgctatcgg tgtaatcttg ttgttgctcc tgatgatccg 120
 cttcaaaatg aacggcttca tcgctctcgt cctcgtggcg cttgctgttg gattaatgca 180
 aggaatgccg ctggataaag ttattggctc catcaaagcc ggtgtcggcg ggacgctcgg 240
 tagccttgcc ctgatcatgg gttttggcgc aatgctggcg aaaatgctgg cagactgcgg 300
 tggcgacaaa cgtatcgcca ccacgctgat tgccaaattt ggtaaaaaac acatccagtg 360
 ggcgggtgga ctgacgggtt ttaccgttgg ttttgccctg ttctatgaag tgggctttgt 420
 gctgatg 427

<210> 65
 <211> 261
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(261)
 <223> n = A,T,C or G

<400> 65
 caaagaacct tcaacatgaa aaatatccat ttgtttgcaa aaaaagatta ttaggaagga 60
 aattaatgca attatcgaaa attcaaaaaa tatccaaaaa tngtatactt tattccagaa 120
 gagttcaata taatgtttgt cttcaatttt tcttacttca gggtaatata gattgctcat 180
 tacattgtga gcttcatctt tatttaattt tctgttgact ccagctctcc gtgataacgg 240
 tttataatt agatgcttat c 261

<210> 66
 <211> 98
 <212> DNA
 <213> E. Coli

<400> 66
 agatgattgc cgggaacttg ttacggcac gcaggcggcg gctcgcaccc ttaccctgct 60
 ctttacgtac ttctgcgttg atagtaaaca tttctttc 98

<210> 67
 <211> 260
 <212> DNA
 <213> E. Coli

<400> 67
 aagcgcgaac gaagtcgatg tgctgcagct tcggtttgta cgggtgacgc tgtacgtcct 60
 gagctttaac ttgtatttct ttaccgtcaa caacgatggg cagaacttcg ctgtagaatt 120
 cagcttttagc ttgcatgttc atgactttgt cgtgatccag ctcgatagcc agcggcgctt 180
 ctttgcacc gtagatgatt gccgggaact tgttagcggc acgcaggcgg cggctcgcac 240
 cttaccctg ctctttacgt 260

<210> 68
 <211> 95
 <212> DNA
 <213> E. Coli

<400> 68
 aaaaacggcg taaagaaagg ttgcaaacat gttaataaaa actcaaattg atccccagta 60
 tatattacgc cgcaaatcc ttacaataaa caggg 95

<210> 69
 <211> 174
 <212> DNA
 <213> E. Coli

<400> 69
 ttaattatta aaatagtgtg acgcgattat gtggttatgg gggtaaacad taaataaacc 60
 agcggggagg ggaggtaaag tgaaaaata aaaagcggat aatcttaata agcaggccgg 120
 acagcatcgc catccggcac tgatacaggg tttatttcag ctcatcaacc atcg 174

<210> 70
 <211> 138
 <212> DNA
 <213> E. Coli

<400> 70
 agtctgtaaa aacgtcaaaa agagtgtttt atcaacagaa gaatggaggt ctgacagata 60
 gtatgaatgc aaaaaaatgg agacttaagt tgaatgaacg ggagttaaagc gaaaagacta 120
 tagagtgaag gagaaatt 138

<210> 71
 <211> 191
 <212> DNA
 <213> E. Coli

<400> 71
 tttgttggtc taatattcta ttgttatctt tatttataga tgtttatatt gcatgaggtg 60
 gtttttgagg agaagaatga ggaagatgcg tcgagccaca gaaacgtag cttracatat 120
 agcggaggtg atgtgaattt aatttacaat agaaataatt tacatatcaa acagtttagat 180
 gctttttgtc g 191

<210> 72
 <211> 244
 <212> DNA
 <213> E. Coli

<400> 72
 ggccatttat acaggaaaag cctatgtcag aacgtaaaaa ctcaaaatca cgccgtaatt 60
 atctcgttaa atgttcctgc ccaaaactgca cccaagagtc agaacacagt ttttcaagag 120
 tacaataaag tgcccttttg atctgccctc attgcaacaa agtatccag acaaatctta 180
 aagctgtagc ctgattgatt ttattagtaa caagtatttt ttatatatta ataatatatt 240
 taaa 244

<210> 73
 <211> 327

<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(327)
<223> n = A,T,C or G

<400> 73

aaattttcag gtacctgtgc accatacttt tttttctgag cattaatgat attttgagct	60
tcttgaggat ctttaactcc ccacatttgg tggaaagtat tcatattaaa aggaaggntg	120
aataatttgn ctttataaat cgccagtggg gaattagtaa aacgattaaa ttctactaaa	180
tnattaaccg naaaaaaatt cccatatata tttatcattg gtatgaaaaa tatgtgcacc	240
atatttatga atntggatgc cctnacagtc ctctgtgtac gcatttccac cgatatgatt	300
tcttttctna atcactaaaa ctttttt	327

<210> 74
<211> 150
<212> DNA
<213> E. Coli

<400> 74

gcagtgatcg aagcgatgac gaagtgtatg gaaaaatcag aaaaactcag caaatcctga	60
tgactttcgc cggacgtcag gccgccactt cgggtgcggtt acgtccggct ttctttgctt	120
tgtaagcgc caaatctgcc gatttcaacc	150

<210> 75
<211> 330
<212> DNA
<213> E. Coli

<400> 75

gaaagtattct tcgttattga catcactgga aaatataact tgcttttcat tattaaactc	60
gaagcgcgtg cgttatctgg acaaacattt atcgagctta ccaaattcct gaagagggtt	120
aactacagat aacatttgcg cgtcctttgc agtaatgccc gtcaaatcct tgacgggcat	180
tatttagatt aaattaccag tttttcttcg gagtgaagaa tattaccagg tatatttaac	240
acccacgttc gccgaccagt cttgatctac gtcaccacca ccgaggtagt tagcatcggt	300
ataggcgtcg aagttcctgg tgaagctaaa	330

<210> 76
<211> 194
<212> DNA
<213> E. Coli

<400> 76

tgtttttttc cagcaacgga gcaaaagggt tgccttcttg cagctcaggg ttaaccactt	60
taactacgtg gcgacgacc ggagatgtcg gtttacattt aacaactgcc attgtattac	120
tcctccgact tactcagcgc cgccaacgaa gtccagattc tggccttctt tcagggtgac	180
gtaagctttt ttcc	194

<210> 77
<211> 188
<212> DNA
<213> E. Coli

<400> 77

tcccttttaac taccagggtg ttaacgactt cgacttcgac ttcaaacagt ttctgcacag	60
cagctttgat ttctgctttg gtcgcgtctt tagcaacttt gagtactatg gtgttggtt	120
tttccatcgc agtagacgtc ttttcagaaa cgtgcggtgc acgcagcacc ttcagcagac	180
gttcttca	188

<210> 78
 <211> 173
 <212> DNA
 <213> E. Coli

<400> 78
 acaaaggcga acaaagcctg tgaagcccga aggcctccaca gacagtgccta cttgaaggcc 60
 ttactgtttc ttcttaggag cgagcaccat gatcatctgg cggccttcga tcttggttg 120
 gaaggattcg accactgccca gttcttgcaa atcgtctttc acgcgattaa gca 173

<210> 79
 <211> 272
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(272)
 <223> n = A,T,C or G

<400> 79
 tggagaaaac ggggtgattga taaagcaatc atcgttctag gggcgtaaat tgcgctgctg 60
 gaactgatcc cgctttctgc ttcaagcttc tgaactggat acggaacgt aatnagggt 120
 aaagaagaca ctactcttag ccctttaaca tttaacgcat tgtcacgaac tcttctgccg 180
 ccgttggtg aatggcgacg ggtattggtc gaaatctttt ttgggtggcc ccatctttaa 240
 cgccaccccg cgaaacctcg caacatttcg tc 272

<210> 80
 <211> 259
 <212> DNA
 <213> E. Coli

<400> 80
 cgcaggcagc tgatggtcaa caggatgaga gaaaccaga gacagggttaa tcacattgcc 60
 tttaaccgct gcacggtaac ctacaccaac cagctgcagc ttcttagtga agccttcggt 120
 aacaccgata accattgagt tcagcagggc acgcgcggtta ccagcctgtg cccaaccgtc 180
 tgcgtaacca tcacgcggac cgaaggctcag ggtattatct gcatgtttaa cttcaacagc 240
 atcgttgaga gtacgagtc 259

<210> 81
 <211> 73
 <212> DNA
 <213> E. Coli

<400> 81
 caggtcggaa cttacccgac aaggaatttc gctaccttag gaccgttata gttacggccg 60
 ccgtttaccg ggg 73

<210> 82
 <211> 666
 <212> DNA
 <213> E. Coli

<400> 82
 atgaacgttt tctcgcaaac tcaacgctat aaggcgttgt tctggttato gttatttcat 60
 ctgctggtga tcacctccag taactatctg gttcagcttc ccgtctccat tttgggttc 120
 cataccacct ggggcgcgtt tagctttccg tttatttttc ttgctaccga cctgaccgtg 180
 cgtatttttg gcgcaccgct ggcccgcgc attatcttcg cggtaatgat ccctgcgtta 240
 ttaatctcct acgtcatctc gtcgctattc tatatgggtt cctggcaggg attcggcgca 300
 ttcgcccact tcaacctgtt tgcgcccgt atcgccaccg ccagtttcat ggcctacgcg 360
 ctggggcaaa tctcgcagct gcacgttttt aaccgcctgc gtcagagtcg ccgctggtgg 420

ctggcaccga	cagcgctccac	actgttcggt	aacgtcagcg	acacgctggc	ctttttcttc	480
attgccttct	ggcgtagccc	ggatgccttt	atggctgaac	actggatgga	aatcgcgctg	540
gtcgattact	gtttcaaat	gttaatcagt	atcgtttct	tcccgccaat	gtatggcgta	600
ttactcaata	tgctgttgaa	aagactggca	gataaatccg	aaatcaacgc	tttgacggcg	660
agtttaa						666

<210> 83
 <211> 612
 <212> DNA
 <213> E. Coli

<400> 83						
gtgataagat	ggatgaatga	gccgttatgg	ccgtttatcg	aaaggaagaa	gtcaatgctg	60
aatctgggta	aatatgtcgg	aattggcctg	ctgggttatg	ggcttgccgc	ctgtgatgat	120
aaagacacta	acgctacggc	gcagggttcg	gtcgcggaaa	gtaacgctac	cggaatccc	180
gtcaacctgc	ttgatggcaa	gttaagtttc	tcgctgccag	cggatatgac	cgaccagagc	240
ggtaagctgg	gaacgcaggc	caataacatg	catgtctggt	ccgacgccac	cgggcagaaa	300
gcagtcacgc	tcatcatggg	cgatgatccg	aaagaagatc	tgccgggtgct	ggcgaagcgt	360
ctggaagatc	agcaacgtag	ccgcgatccg	cagctgcaag	tggttaacaa	taaagccatt	420
gagctgaaag	gtcacaaaat	gcagcagtta	gacagtatta	tctccgcgaa	agggcagacg	480
gcgtactctt	ccgttattct	gggtaacgtg	ggtaatcaac	tgctgaccat	gcaaattacg	540
ctgcccgctg	acgatcagca	aaaagcgcg	accaccgcag	aaaacatcat	taatacgcgtg	600
gttattcagt	aa					612

<210> 84
 <211> 975
 <212> DNA
 <213> E. Coli

<400> 84						
atggcggaata	tggttgcctt	gattctgggt	attgccacac	tggtgacggg	cattttatgg	60
tgctgtgata	aattcttttt	cgcacctaaa	cggcggaagc	gtcaggcagc	ggcgaggcg	120
gctgcggggg	actcactgga	ttaaagcaacg	ttgaaaaag	ttgcgccgaa	gcctggctgg	180
ctggaaacgg	gtgcttctgt	ttttccggta	ctggctatcg	tattgattgt	gcgttcgttt	240
atttatgaac	cggtccagat	cccgtcaggt	tcgatgatgc	cgactctggt	aattgggtgat	300
tttattctgg	tagagaagtt	tgcttatggc	attaaagatc	ctatctacca	gaaaacgcgt	360
atcgaaacgg	gtcatccgaa	acgcggcgat	atcggtggtc	ttaaatatcc	ggaagatcca	420
aagcttgatt	acatcaagcg	cgcgggtggg	ttaccggggc	ataaagtcac	ttacgatccg	480
gtctcaaaag	agctgacgat	tcaaccggga	tgcagttccg	gccaggcggt	tgaaaacgcg	540
ctgccgggtc	cctactcaaa	cgtggaaccg	agcgatttcg	ttcagacctt	ctcacgcggt	600
aatggtgggg	aagcgaccag	cggattcttt	gaagtgccga	aaaacgaaac	caaagaaaat	660
ggaattcgtc	tttccgagcg	taaagagaca	ctgggtgatg	tgacgcaccg	cattctgaca	720
gtgcggattg	cgcaggatca	ggtgggggatg	tattaccagc	agccagggca	acaactggca	780
acctggattg	ttcctccggg	acaatacttc	atgatggggc	acaaccgcga	caacagcgcg	840
gacagccgtt	actggggctt	tgtgccggaa	gcgaatctgg	tcgggtcggc	aacggctatc	900
tggtatgagc	tcgataagca	agaaggcgaa	tgcccgactg	gtctgcgctt	aagtcgcatt	960
ggcgcatcc	attaa					975

<210> 85
 <211> 1761
 <212> DNA
 <213> E. Coli

<400> 85						
ttgaccatta	cgaaacttgc	atggcgtgac	ctggttcctg	ataccgatag	ctatcaggaa	60
atatttgcct	agccacattt	gattgacgaa	aacgatccct	tattcagtga	tactcaaccg	120
cggtgcaat	ttgcgctgga	gcagtgtgct	catacgcgag	catactcctc	ttttatgctg	180
gcgaaggccc	cggaagagtc	tgagtatctg	aatcttattg	ccaatgccgc	gcgtacgcta	240
caaagcgatg	caggccaact	ggtggggcgt	cactatgagg	tttccggcca	ctccatccgc	300
ttacgtcacg	cagtgaagtgc	agatgataat	tttgcgactt	taacgcaagt	tgctcgctgcc	360
gactgggtag	aagcgagca	actccttggc	tgccctgcgc	agtttaattg	cgacattacc	420

ctgcagcctg	gtctggtgca	tcaggcaaat	ggcgggtattc	tcattatctc	tttgcgtaca	480
ctgctggcgc	aacctctgct	gtggatgcgg	ctgaaaaata	tcgttaaccg	cgagcgtttt	540
gactgggttg	cgtttgatga	gtcgcgccct	ctccccgtct	ctgtgccttc	gatgccattg	600
aagctgaaag	tcattctggt	aggcgaacgc	gaatcattgg	ctgatttcca	ggagatggag	660
ccagagcttt	cagagcaggc	tatttatagc	gaatttgaag	atactctgca	gattgtcgat	720
gcggagtcag	taaccacgtg	gtgtcgtctg	gtgacattta	ccgccagaca	taatcaacta	780
cctgcaccgg	gagcggatgc	ctggccgata	cttatccgcg	aagcagcacg	ctacaccggt	840
gaacaagaaa	cacttccgct	tagcccgca	tggatccctc	gccagtgtaa	agaggtcgcc	900
tcctctgttg	atggcgacac	cttctccggc	gagcagctaa	acttaatgct	gcagcagcgt	960
gaatggcgcg	aagggttcct	cgctgaacgt	atgcaggatg	agatccttca	ggagcaaatc	1020
ctgattgaaa	ccgaaggcga	acgcacgtgg	caaatatacg	ccctttcggg	cattgaattt	1080
ccgggtcatc	cacgcgcttt	tggcgaacct	tctcgatta	gctgcgttgt	gcatattggc	1140
gatggtgaat	tcaccgacat	cgaacgcaaa	gcggagcttg	gcggcaatat	ccatgcgaaa	1200
gggatgatga	tcattcgaagc	gttcctgatg	tcggaactac	agcttgagca	acagatcccc	1260
ttctcagcat	cgctgacatt	tgagcagtca	tacagtgaag	ttgatggaga	tagtgcctcg	1320
atggctgaac	tctgcgccct	gataagcgcc	ctcgccgatg	tgccggtgaa	tcagagtatc	1380
gctatcacag	gttcagtcga	tcagttcggg	cgccgccagc	cggtcgggtg	tttaaatgag	1440
aaaatcgaag	gcttctttgc	tatttgccag	caacgtgagt	taaccgggaa	acaaggtgtc	1500
attatcccca	cagctaacgt	tcgccattta	agtcctcaca	gtgaactggg	gaaagcggtc	1560
gaagaaggca	aattcaccat	ctgggcagta	gacgatgtga	ctgacgcact	gccgttatta	1620
ttaaatctgg	tgtgggatgg	cgaaggccaa	acgacgtctg	tgcaaaccat	ccaggaacgt	1680
atcgcgcaag	catcgcaaca	ggaaggacgt	caccgttttc	catggccatt	acgttggctg	1740
aactggttta	ttccgaactg	a				1761

<210> 86

<211> 1185

<212> DNA

<213> E. Coli

<400> 86

gtgtctaaag	aaaaatttga	acgtacaaaa	ccgcacgtta	acgttggtac	tatcggccac	60
gttgaccacg	gtaaaaactac	tctgaccgct	gcaatcacca	ccgtactggc	taaaacctac	120
ggcgggtgtg	ctcgtgcatt	cgaccagatc	gataacgcgc	cggaagaaaa	agctcgtggt	180
atcaccatca	acacttctca	cgttgaatac	gacaccccca	cccgtcacta	cgcacacgta	240
gactgcccg	ggcaccgcga	ctatgttaaa	aacatgatca	ccggtgctgc	tcagatggac	300
ggcgcgatcc	tggtagttag	tgccagctac	ggcccgatgc	cgccagactc	tgagcacatc	360
ctgctgggtc	gtcaggtagg	cgttccgtac	atcatcgtgt	tcctgaacaa	atgcgacatg	420
gttgatgacg	aagagctgct	ggaactgggt	gaaatggaag	ttcgtgaact	tctgtctcag	480
tacgacttcc	cgggcgacga	cactccgata	gttcgtgggt	ctgctctgaa	agcgtctgga	540
ggcgacgcag	agtgggaagc	gaaaatccct	gaactggctg	gcttccctgga	ttcttatatt	600
ccggaaccag	agcgtgcgat	tgacaaagcc	ttcctgctgc	cgatcgaaga	cgtattctcc	660
atctccggtc	gtggtaccgt	tggtaccggt	cggttagaac	gcggatcatc	caaaagtggg	720
gaagaagtgt	aaatcggttg	tatcaaaag	actcagaagt	ctacctgtac	tgccgttgaa	780
atgttccgca	aactgctgga	cgaaggccgt	gctggtgaga	acgtaggtgt	tctgctgcgt	840
ggatataaac	gtgaagaaat	cgaacgtggt	caggtagctg	ctaagccggg	caccatcaag	900
ccgcacacca	agttcgaatc	tgaagtgtac	attctgtcca	aagatgaagg	cgcccgctcat	960
actccgttct	tcaaaggcta	ccgtccgcag	ttctacttcc	gtactactga	cgtgactggt	1020
accatcgaac	tgcgggaagg	cgtagagatg	gtaatgccgg	gcgacaacat	caaaatgggt	1080
gttaccctga	tccacccgat	cgcgatggac	gacggtctgc	gttctcgaat	ccgtgaaggc	1140
ggccgtaccg	ttggcgcggg	cggtgtgtgt	aaagtctctg	gctaa		1185

<210> 87 ~

<211> 2115

<212> DNA

<213> E. Coli

<400> 87

atggctcgta	caacacccat	cgcacgctac	cgtaacatcg	gtatcagtgc	gcacatcgac	60
gccggtaaaa	ccactactac	cgaacgtatt	ctgttctaca	ccgggtgtaa	ccataaaatc	120
gggtgaagtc	atgacggcgc	tgcaaacatg	gactggatgg	agcaggagca	ggaacgtggg	180
attaccatca	cttcgcgtgc	gactactgca	ttctggtctg	gtatggctaa	gcagtatgag	240

ccgcacatcgca	tcaacatcat	cgacacccccg	gggcacggtg	acttcacaaat	cgaagtagaa	300
cgttccatgc	gtgttctcga	tgggtgcggta	atgggtttact	gcgcaggttg	tgggtgttcag	360
ccgcagctcg	aaaccgtag	gcgtcaggca	aacaaatata	aagttccgcg	cattgctgttc	420
gttaacaaaa	tggaccgcat	gggtgcgaac	ttcctgaaag	ttgttaacca	gatcaaaacc	480
cgctcggcg	cgaacccggt	tccgctgcag	ctggcgattg	gtgctgaaga	acatttcacc	540
gggtgtgttg	acctggtgaa	aatgaaagct	atcaactgga	acgacgctga	ccagggcgta	600
accttcgaat	acgaagatat	cccggcagac	atggttgaa	tggctaaccga	atggcaccag	660
aaactgatcg	aatccgcagc	tgaagcttct	gaagagctga	tggaaaaata	cctgggtggt	720
gaagaactga	ctgaagcaga	aatcaaaagg	gctctgcgtc	agcgcgttct	gaacaacgaa	780
atcatcctgg	taacctgtgg	ttctgcgttc	aagaacaaag	gtgttcaggc	gatgctggat	840
gcggtaattg	attacctgcc	atccccggtt	gacgtacctg	cgatcaacgg	tatcctggac	900
gacggtaaa	acactccggc	tgaacgtcac	gcaagtgatg	acgagccgtt	ctctgcaactg	960
gcgttcaaaa	tcgtaccga	cccgtttgtt	ggtaacctga	ccttcttccg	tgtttactcc	1020
gggtgtgtta	actctggtga	taccgtactg	aactccgtga	aagctgcacg	tgagcgtttc	1080
ggtcgtatcg	ttcagatgca	cgctaacaaa	cgtgaagaga	tcaaagaagt	tcgcgcgggc	1140
gacatcgtcg	ctgctatcgg	tctgaaagac	gtaaccactg	gtgacaccct	gtgtgacccg	1200
gatgcgcgca	tcattctgga	acgtatggaa	ttccctgagc	cggtaatctc	catcgcaagt	1260
gaaccgaaaa	ccaaagctga	ccaggaaaaa	atgggtctgg	ctctggggccg	tctggctaaa	1320
gaagaccctg	ctttccgtgt	atggactgac	gaagaatcta	accagaccat	catcgccgggt	1380
atgggcgaac	tgacacctga	catcatcggt	gaccgtatga	agcgtgaatt	caacgttgaa	1440
gcgaacgtag	gtaaacgcga	ggttgcttac	cgtgaaacta	tccgccagaa	agttaccgat	1500
gttgaaagga	aacacgcgaa	acagtctggt	ggctgtggtc	agtatggtca	tggtgttatc	1560
gacatgtacc	cgctggagcc	gggttcaaac	ccgaaaggtc	acgagttcat	caacgacatt	1620
aaaggtggtg	taatccctgg	cgaatacatc	ccggccggtg	ataaaggtat	ccaggaaacag	1680
ctgaaaacgag	gtccgctggc	aggctaccgg	gtagtagaca	tgggtattcg	tctgcacttc	1740
ggttcttacc	atgacgttga	ctcctctgaa	ctggcgttta	aactggctgc	ttctatcgcc	1800
tttaaaagag	gctttaagaa	agcgaaccca	gttctgcttg	agccgatcat	gaaggttgaa	1860
gtagaaactc	cggaaagaga	caccggtgac	gttatcggtg	acttgagccg	tcgtcgtggt	1920
atgctcaaa	gtcaggaaac	tgaagttact	ggcgttaaga	tccacgctga	agtaccgctg	1980
tctgaaatgt	tcggatacgc	aactcagctg	cggttctctga	ccaaaggtcg	tgcatcatac	2040
actatgggaat	tcctgaaagta	tgatgaaagc	ccgagtaacg	ttgctcaggc	cgtaattgaa	2100
gcccgtggtta	ataaa					2115

<210> 88
 <211> 540
 <212> DNA
 <213> E. Coli

atgccacgctc	gtcgcgtcat	tggtcagcgt	aaaattctgc	cggatccgaa	gttcggatca	60
gaactgctgg	ctaaatttgt	aaatatcctg	atggtagatg	gtaaaaaatc	tactgctgaa	120
tctatcgtat	acagcgcgct	ggagaccctg	gctcagcgtc	ctggtaaatc	tgaactggaa	180
gcattcgaag	tagctctcga	aaacgtgcgc	ccgactgtag	aagttaaatc	tcgccgcgtt	240
gggtggttcta	cttatcaggt	accagttgaa	gtccgtccgg	ttcgtcgtaa	tgctctggca	300
atgctgttga	tcgttgaagc	tgctcgtaaa	cgcggtgata	aatccatggc	tctgcgcctg	360
gcgaacgaac	tttctgatgc	tgagaaaaac	aaaggtactg	cagttaaagaa	acgtgaagac	420
gttcaccgta	tggccgaagc	caacaaggcg	ttcgcacact	accgttggtt	atcccttcgg	480
agttttatgc	accaggcggt	cgcttccagt	aagcagcccg	ctttgggcta	cttaaatgaa	540

<210> 89
 <211> 1549
 <212> DNA
 <213> E. Coli

aaattgaaga	gtttgatcat	ggctcagatt	gaacgctggc	ggcaggccta	acacatgcaa	60
gtcgaacggt	aacaggaagc	agcttgctgc	ttcgtcgacg	agtggcggac	gggtgagtaa	120
tgtctgggaa	gctgcctgat	ggagggggat	aactactgga	aacggtagct	aataccgcat	180
aatgtcgcaa	gaccaaagag	ggggaccttc	gggcctcttg	ccatcggtatg	tgcccgatg	240
ggattagctt	gttgggtggg	taacggctca	ccaaggcgac	gatccctagc	tggtctgaga	300
ggatgaccag	ccacactgga	actgagacac	ggteccagact	cctacgggag	gcagcagtgg	360

ggaatattgc	acaatgggag	caagcctgat	gcagccatgc	cgcgtgtatg	aagaagggcct	420
tcgggttgta	aagtactttc	agcgggggag	aagggagtaa	agttaatacc	tttgctcatt	480
gacgttacc	gcagaagaag	caccggccta	ctcgtgcc	gcagccgagg	taatacggag	540
ggtgcaagcg	ttaatcgga	ttactgggag	ttaagcgcac	gcaggggggt	tggttaagtc	600
agatgtgaaa	tccccgggct	caacctggga	actgcactcg	atactggcaa	gcttgagtct	660
cgtagagggg	ggtagaattc	cagggtgtagc	ggtgaaatgc	gtagagatct	ggaggaatac	720
cgggtggcga	ggcggcccc	tgagcgaaga	ctgacgtc	ggtgcgaaag	cgtggggagc	780
aaacaggatt	agataccctg	gtagtccacg	ccgtaaacga	tgtcgacttg	gaggttgtgc	840
ccttgaggcg	tggtctccg	agctaacgcg	ttaagtcgac	cgcctgggga	gtacggccgc	900
aagggtaaaa	ctcaaatgaa	ttgacggggg	cccgacaaag	cgggtggaga	tgtggtttaa	960
ttcgtatgcaa	cgcgaagaac	cttacctggt	cttgacatcc	acggaagttt	tcagagatga	1020
gaatgtgcct	tcgggaaccg	tgagacaggt	gctgcattgc	tgtcgctcagc	tcgtgttg	1080
aaatgttggg	ttaatcccc	caacgagcgc	aacctttatc	ctttgttgcc	agcgggtccg	1140
ccgggaactc	aaaggagact	gccagtata	aactggagga	aggtggggat	gacgtcaagt	1200
catcatggcc	cttacgacca	gggtctacaca	cgtgctacaa	tgccgcatac	aaagagaagc	1260
gacctcgcca	gagcaagcgg	acctcataaa	gtgcgtcgta	gtccggattg	gagtcgtcaa	1320
ctcgactcca	tgaagtcgga	atcgctagta	atcggtgac	agaatgccac	ggtgaatacg	1380
ttcccgggcc	ttgtacacac	cgcccgtcac	accatgggag	tggtgtgcaa	aagaagtagg	1440
tagcttaacc	ttcgggaggg	cgttaccac	tttgtgatc	atgactgggg	tgaagtcgta	1500
acaaggtaac	cgtaggggaa	cctgcggttg	gatcacctcc	ttaccttaa		1549

<210> 90

<211> 375

<212> DNA

<213> E. Coli

<400> 90

atggcaacag	ttaaccagct	ggtacgcaaa	ccacgtgctc	gcaaagtgc	gaaaagcaac	60
gtgcctgcgc	tggaagcatg	cccgcaaaaa	cgtggcgat	gtactcgtgt	ataactacc	120
actcctaaaa	aaaccgaactc	cgcgctgcgt	aaagtatgcc	gtgttcgtct	gactaacggt	180
ttcgaagtga	cttcctacat	cgggtgtgaa	ggtcacaacc	tgccaggagca	ctccgtgac	240
ctgatccgtg	gcggtcgtgt	ttaaagacctc	ccgggtgttc	gttaccacac	cgtacgtggt	300
gcgcttgact	gctccggcgt	ttaaagacctc	aagcaggctc	gttccaagta	tgccgtgaa	360
cgtcctaagg	cttaa					375

<210> 91

<211> 366

<212> DNA

<213> E. Coli

<400> 91

atgtctatca	ctaaagatca	aatcattgaa	gcagttgcag	ctatgtctgt	aatggacgtt	60
gtagaactga	tctctgcaat	ggaagaaaa	ttcgggtgtt	ccgctgctgc	tgctgtagct	120
gtagctgctg	gcccgggtga	agctgctgaa	gaaaaaactg	aattcgacgt	aattctgaaa	180
gctgctggcg	ctaaacaaagt	tgctgtttatc	aaagcagtac	gtggcgcaac	tgccctgggt	240
ctgaaagaag	ctaaagacct	ggtagaatct	gcaccggctg	ctctgaaaga	aggcgtgagc	300
aaagacgacg	cagaagcact	gaaaaaagct	ctggaagaag	ctggcgctga	agttgaagtt	360
aaataa						366

<210> 92

<211> 498

<212> DNA

<213> E. Coli

<400> 92

atggctttta	atcttcaaga	caaacaaagc	attgttgctg	aagtcagcga	agtagccaaa	60
ggcgcgctgt	ctgcagtagt	tgccgattcc	cgtggcgtaa	ctgtagataa	aatgactgaa	120
ctgcgtaaa	caggtcgcca	agctggcgta	tacatgcgtg	ttgttcgtaa	caccctgctg	180
cgcgctgctg	ttgaaggtac	tccgttcgag	tgccgtgaa	acgcgtttgt	tggtccgacc	240
ctgattgcac	actctatgga	acaccggg	gctgctgctc	gtctgttcaa	agagttcgcg	300
aaagcgaatg	caaaatttga	ggtcaaaagc	gctgcctttg	aaggtgagct	gatcccgccg	360

tctcagatcg	accgcctggc	aactctgccg	acctacgaag	aagcaattgc	acgcctgatg	420
gcaacctatg	aagaagcttc	ggctggcaaa	ctgggttcgta	ctctggctgc	tgtacgcgat	480
gcgaaagaag	ctgcttaa					498

<210> 93
 <211> 2145
 <212> DNA
 <213> E. Coli

<400> 93						
gtgtcccgtg	ttattatgct	gatccctacc	ggaaccagcg	tcgggtctgac	cagcgtcagc	60
cttggcgtga	tccgtgcaat	ggaacgcaaa	ggcgttcgtc	tgagcgtttt	caaacctatc	120
gctcagccgc	gtaccggtgg	cgatgcgccc	gatcagacta	cgactatcgt	gcgtgcgaac	180
tcttccacca	cgacggccgc	tgaaccgctg	aaaatgagct	acgttgaagg	tctgctttcc	240
agcaatcaga	aagatgtgct	gatggaagag	atcgtcgcaa	actaccacgc	taacaccaaa	300
gacgctgaag	tcgttctggt	tgaaggctctg	gtcccgcacac	gtaagcacca	gtttgccag	360
tctctgaact	acgaaatcgc	taaaacgctg	aatgcggaaa	tcgtcttcgt	tatgtctcag	420
ggcactgaca	ccccggaaca	gctgaaagag	cgatcgaac	tgaccgcgaa	cagcttcggc	480
ggtgccaaaa	acaccaacat	caccggcgct	atcgtaaca	aactgaacgc	accggttgat	540
gaacagggtc	gtactcgccc	ggatctgtcc	gagattttcg	acgactcttc	caaagctaaa	600
gtaaacaatg	ttgatccggc	gaagctgcaa	gaatccagcc	cgctgcgggt	tctcggcgct	660
gtgccgtgga	gctttgacct	gacgcgact	cgctgcgatcg	atatggctcg	ccacctgaat	720
gcgacctca	tcaacgaagg	cgacatcaat	actcgcgcgc	ttaaatccgt	cactttctgc	780
gcacgcagca	ttccgcacat	gctggagcac	ttccgtgccg	gttctctgct	ggtgacttcc	840
gcagaccgtc	ctgacgtgct	ggtagccgct	tgctggcgag	ccatgaacgc	cgtagaaatc	900
ggtgcccctg	tgctgactgg	cggttacgaa	atggacgcgc	gcatttctaa	actgtgcgaa	960
cgtagctttc	ctaccggcct	gccgggtattt	atggtgaaca	ccaacacctg	gcagacctct	1020
ctgagcctgc	agagcttcaa	cctggaagtt	ccggttgacg	atcacgaacg	tatcgagaaa	1080
gttcaggaat	acgttgctaa	ctacatcaac	gctgactgga	tcgaatctct	gactgccact	1140
tctgagcgca	gccgtcgtct	gtctccgcct	gcgttccggt	atcagctgac	tgaacttgcg	1200
cgcaaaagcg	gcaaacgtat	cgtagctccg	gaaggtgacg	aaccgcgtac	cgtaaagca	1260
gccgctatct	gtgctgaacg	tggtagcga	acttgcgtac	tgctgggtaa	tccggcagag	1320
atcaaccgtg	ttgcagcgct	tcaggggtga	gaactgggtg	cagggattga	aatcgttgat	1380
ccagaagtgg	ttcgcgaaag	ctatgttgggt	cgctctggtcg	aactgcgtaa	gaacaaagcg	1440
atgaccgaaa	ccgttgcccgc	cgaacagctg	gaagacaacg	tgggtgctcg	tacgctgatg	1500
ctggaacagc	atgaagttga	tgggtctggt	tcgggtgctg	ttcacactac	cgcaaacacc	1560
atccgtccgc	cgctgcagct	gatcaaaact	gcacggggca	gctccctggt	atcttccgtg	1620
ttcttcatgc	tgctgcggga	acaggtttac	gtttacggtg	actgtgcgat	caaccggat	1680
ccgacgcgtg	aacagctggc	agaaatcgcg	attcagtcgc	ctgattccgc	tgccgccttc	1740
ggtatcgaa	cgcgcttgc	tatgctctcc	tactccaccg	gtacttctg	tgacggtagc	1800
gacgtagaaa	aagttccgga	agcaactcgt	ctggcgaggg	aaaaacgtcc	tgacctgatg	1860
atcgacggtc	cgctgcagta	cgacgctgcg	gtaatggctg	acgttgcgaa	atccaaagcg	1920
ccgaactctc	cggttgccag	tcgcgctacc	gtgttcattc	tcccggtatc	gaacaccggt	1980
aaacaccact	acaaagcggt	acagcgttct	gccgacctga	tctccatcgg	gccgatgctg	2040
cagggtatgc	gcaagccggt	taacgacctg	tcccgtggcg	cactgggtga	cgatatcgct	2100
tacaccatcg	cgctgactgc	gattcagctc	gcacagcagc	agtaa		2145

<210> 94
 <211> 1767
 <212> DNA
 <213> E. Coli

<400> 94						
atgaataatt	ctattaacca	taaatttcat	cacattagcc	gggctgaata	ccaggaattg	60
ttagccgttt	cccgtggcga	cgctggtgcc	gattatatta	ttgataatgt	ctctattctc	120
gacctgatca	atggcggaga	aatttccggc	ccaattgtga	ttaaaggacg	ttacattgcc	180
ggtgttgccg	cagaatacac	tgatgctccg	gctttgcagc	ggattgatgc	tcgcggcgca	240
acggcgggtg	caggggtttat	tgatgctcac	ctgcatattg	aatccagcat	gatgacgccc	300
gtcacttttg	aaaccgctac	cctgcgcgcg	ggcctgacga	ccgttatattg	cgacctcat	360
gaaatcgta	acgtgatggg	cgaagccgga	ttcgcctggt	ttgcccgcgtg	tgccgaacag	420
gcaaggcaaa	accagtactt	acaggtcagc	tcttgctgac	ccgcctcgga	aggctgcgat	480

gtaaacggtg	ccagttttac	ccttgaacag	atgctcgcct	ggcgggacca	tccgcaggtt	540
accggccttg	cagaaatgat	ggactaccct	ggcgtaatta	gcgggcagaa	tgcgctgctc	600
gataaactgg	atgcatttcg	ccacctgacg	ctggacggtc	actgcccggg	tttgggtggg	660
aaagaactta	acgcctatat	tactgcgggt	attgaaaact	gccacgaaag	ttatcagctg	720
gaagaaggac	gccggaaatt	acaactcggc	atgtcgttga	tgatccgcga	aggggtccgt	780
gcccgcgaatc	tcaacgcgct	ggcaccgttg	atcaacgaat	ttaacagccc	gcaatgcatg	840
ctctgtaccg	atgaccgtaa	cccgtgggag	atcgcccatg	aaggacacat	cgatgcctta	900
attcgccggc	tgatcgaaac	acacaatgtg	ccgctgcacg	tgcatatcgc	cgctgccagc	960
tggtcgacgg	cgcgccactt	tggtctgaat	cacctcggct	tactggcacc	cggaagcag	1020
gccgatatcg	tcctgttgag	cgatgcgcgt	aaggtcacgg	tgacgcaggt	actggtgaaa	1080
ggcgagccga	ttgatgcgca	aaccttacag	gcggaagagt	cggcgagact	ggcacaatcc	1140
gctcccctat	atggcaacac	cattgcccgc	cagccagttt	ccgccagcga	ctttgccctg	1200
caatttacgc	ccggaaaacg	ctatcggttc	attgacgtca	tccataacga	attgattacg	1260
cactcccact	ccagcgtcta	cagcgaaaaa	ggttttgatc	gcgatgatgt	gagctttatt	1320
gccgtacttg	agcgttacgg	gcaacggctg	gctccggctt	gtggtttgct	tgccggcctt	1380
ggactgaatg	aaggtgcgct	ggctgcgacg	gtcagccatg	acagccataa	tattgtggtg	1440
atcggtcgca	gtgccgaaga	gatggcgctg	gcggtcaatc	aggtgattca	ggatggcgcg	1500
gggctgtgcg	tggtacgtaa	cgccaggtta	caaaagtcac	tgccgttacc	cattgccggg	1560
ctgatgagca	ccgacacggc	gcagtcgctg	gcggaacaaa	ttgacgcctt	gaaagccgcc	1620
gcccggtgaat	cggttccggt	acccgatgag	ccgtttattc	agatggcggt	tctttctctg	1680
ccagtgatcc	ccgcgctaaa	actaaccagt	caggggctat	ttgatggcga	gaagtttgcc	1740
ttcactacgc	tggaagtcac	ggaataaa				1767

<210> 95
 <211> 1227
 <212> DNA
 <213> E. Coli

<400> 95						
atggcggtatt	gcaatccggg	cctggaatcc	aggccgaata	agagaaacgc	cctccggcgt	60
catgtgtgtaa	caggcatagg	tatgaaaatc	gtaatcgccc	cagactctta	taaagaaagt	120
ttatctgccca	gcgaggttgc	gcaggcgata	gaaaaaggat	ttcgggaaat	ttttcctgat	180
gcacagtacg	tttctgttcc	gggtgccgac	gggtggcgaag	gaacgggtga	agcgatgatt	240
gcagccaccc	agggggctga	acgtcacgcc	tggtttacag	ggccgctggg	cgagaaagtg	300
aatgcsagtt	gggggatctc	cgcgcatggc	aaaaccgcgt	ttattgaaat	ggcgcgcgcc	360
agtgggtctg	agctggtacc	tgcggaaaaa	cgcgatccac	tcgtgaccac	ttcacgcggc	420
acaggcgagt	taactctgca	ggcgctggag	agcggtgcga	caaacattat	tatcggcatt	480
ggcggcagcg	ctacaaatga	tgccggcgca	ggcatggtac	aggcgctggg	ggcgaaatta	540
tgccgacgcca	acggcaatga	aattggtttt	ggcgcgcgta	gtcttaatac	tctgaatgat	600
attgatattt	ccggcctcga	tccgcgctta	aaagattgcg	tcattcgcgt	cgcttgtgat	660
gtcaccaatc	cgctggtggg	cgataacggc	gcatacgcca	tctttggccc	acaaaaggga	720
gccagtgaag	cgatgattgt	tgagctggac	aataacctct	ctcactatgc	cgaggtcatt	780
aaaaaagcgc	tgcatgttga	tgtgaaagat	gtccccgggt	caggagctgc	gggtggtatg	840
ggcgcgggcg	taatggcggt	tcttggtgcg	gaactgaaaa	gtggtattga	aatcgtcact	900
acggcgctga	atctggagga	acatattcac	gattgtacgc	tggtgatcac	cggtgaaggg	960
cgtattgaca	gccagagtat	tcacgggaag	gtaccgattg	gtgctgcaaa	cgtggcgaa	1020
aagtaccata	aaccggtgat	tgccattgcg	ggtagcctga	ccgatgatgt	tgccgtttga	1080
catcagcatg	gcattgatgc	ggtcttcagc	gtattgacca	gcataggtag	gttggacgaa	1140
gcattccgcg	gggttattga	caatatctgc	cgtgcttcac	gtaatatcgc	cgcgacactg	1200
gcgattggaa	tgccgaacgc	gggtgtga				1227

<210> 96
 <211> 900
 <212> DNA
 <213> E. Coli

<400> 96						
atgattgata	tgactatgaa	agttggtttt	attggcctgg	ggattatggg	taaaccaatg	60
agtaaaaaacc	ttctgaaagc	aggttactcg	ctggtggttg	ctgaccgtaa	cccagaagct	120
attgctgacg	tgattgctgc	aggtgcagaa	acagcgtcta	cggtctaaagc	gatcgctgaa	180
cagtgcgacg	tcatacataac	catgctgccca	aactccccct	atgtgaaaga	gggtggcgctg	240

gggtgagaatg	gcattattga	aggcgcggaag	ccaggtacgg	tattgatcga	tatgagttct	300
atcgccaccgc	tggcaagccg	tgaatcagc	gaagcgctga	aagcgaaagg	cattgatatg	360
ctggatgctc	cggtgagcgg	cggtgaaccg	aaagccatcg	acggtagcgt	gtcagtgatg	420
gtgggcgggc	acaaggctat	tttcgacaaa	tactatgatt	tgatgaaagc	gatggcgggt	480
tccgtgggtgc	ataccgggga	aatcggtgca	ggtaacgtca	ccaaactggc	aaatcaggtc	540
attgtggcgc	tgaatattgc	cgcgatgtca	gaagcggtta	cgctggcaac	taaagcgggc	600
gttaaccggg	acctgggtta	tcaggcaatt	cgcggtggac	tggcgggcag	taccgtgctg	660
gatgccaaaag	cgcgatggg	gatggaccgc	aacttcaagc	cgggcttccg	tattgatctg	720
catattaagg	atctggcgaa	tgcgtggat	acttctcacg	gcgtcggcgc	acaactgccg	780
ctcacagctg	cggttatgga	gatgatgcag	gcactgcgag	cagatggttt	aggaacggcg	840
gatcatagcg	ccctggcggtg	ctactacgaa	aaactggcga	aagtcgaagt	tactcgtaa	900

<210> 97
 <211> 771
 <212> DNA
 <213> E. Coli

<400> 97						
atgaataacg	atgttttccc	gaataaatcc	aaagccgcac	tggctgcgaa	acaggtacaa	60
attgggttgc	ggtcagcact	ctctaaccgc	attagcactg	aagttcttgg	tttggtcggg	120
tttgactggc	tgggtctgga	tggcgaaacat	gcgccaaacg	atatctccac	gtttattccg	180
cagttaatgg	ccttgaaagg	cagcgccagc	gcgccagtag	tgcgagtgcc	gaccaacgag	240
ccggttaatta	ttaaagcgtct	tctggatata	ggtttctata	acttctctgat	tccttttcta	300
gaaacaaaag	aggaagcaga	gctggcggtg	gcatcaaccc	gttaccaccc	ggaaggcatt	360
cgcgcgctct	ccgttttctca	ccgcgccaat	atgtttggca	ccgtggcgga	ttatttcgct	420
cagtcgaaaca	agaacatcac	tattctggtc	cagatagaaa	gtcagcaggg	cgtagataac	480
gtcgatgccca	ttgccgctac	cgaaggcgta	gacggcatct	tcgtcggccc	cagcgatctg	540
gccgcggcat	tagggcatct	cgccaatgca	tcacaccggg	atgtacaaaa	agcaattcag	600
cacattttta	accgtgccag	cgcgcacggc	aaacccagcg	gtatcctcgc	gccggtcgaa	660
gccgatgcgc	gtcgttatct	ggaatggggc	gcgacgtttg	tggctgtcgg	cagcgatctc	720
ggcgctcttc	gctctgccac	tcagaaactg	gctgatacct	ttaaaaaata	a	771

<210> 98
 <211> 1335
 <212> DNA
 <213> E. Coli

<400> 98						
atgattctcg	acaccgttga	cgaaaaaaag	aaaggcggtgc	ataccgcgta	tttaatatatta	60
ctgattattt	ttattgttac	cgccgttaac	tacgcccagc	gtgcaacgct	gtctattgct	120
ggtaaccgaag	tggcaaaaga	gttgcagtta	agtgcggttt	cgatgggtta	catcttctcc	180
gcttttggtc	gggcctactt	gctgatgcaa	atccccggcg	gctggctgct	tgataagttt	240
ggctcgaaaa	aagtttacac	ctacagcctc	tttttctggt	cgctattcac	cttccgtcaa	300
ggctttgttg	atatgttccc	gctggcctgg	gcagggatct	ccatgttctt	tatgcgcttt	360
atgctcggct	tctcggaagc	gccatcattc	ccggcgaaac	cccgaattgt	cgccgcctgg	420
ttcccagcga	aagaacgtgg	tactgcctcc	gccatcttta	actcggcgca	atatcttctcg	480
ctggcgctct	tttcgcccgt	gcttggctgg	ctgaatttgc	cctggggcgtg	ggagcacgtc	540
tttaccgtta	tgggggtgat	tgggtttgtg	ctgacggcgc	tgtggatcaa	gttgattcat	600
aacccgacag	atcaccacag	tatgtctgcg	gaagagctga	agtttatctc	tgaaaatggc	660
gcgggtggtc	atatggacca	caaaaagccg	ggcagtgccg	cagcaagcgg	accctaaactg	720
cattacatca	agcaattgct	ctctaaccgc	atgatgctgg	gcgtattttt	cggacaatat	780
tttatcaaca	ccatcacctg	gttcttcctc	acctgggtcc	cgatttatct	ggtgcaggaa	840
aaaggcatgt	cgattctgaa	agtgggtctg	gtcgcctcga	ttccagcact	gtgtggtttt	900
gcggggcgcc	tgtctgggag	tgtcttctcg	gatttatctga	tcaaacgcgg	tttatccctg	960
accctggcac	gtaagctacc	gatttgtctg	ggaatgttgc	tggcttccac	catcatctta	1020
tgtaactaca	ccaacaacac	cacgctgggtg	gtcatgctga	tggcgctggc	tttctttggc	1080
aaaggatttg	gtgcgctggg	ctggccgggtg	atttctgaca	ccgcgccgaa	agagattgtt	1140
ggcctctgcg	gcggcgctct	taacgtcttt	ggcaatgttg	cctccattgt	cactccactg	1200
gtgattggct	acctggtaag	tgaactgcac	tccttcaatg	cagcactggt	tttcgtggga	1260
tgttcagcgc	tgatggcgat	ggtctgctac	ctcttcgtag	ttggcgacat	taaacgtatg	1320
gaattgcaga	aataaa					1335

<210> 99
 <211> 1536
 <212> DNA
 <213> E. Coli

<400> 99

```

atgcaaacga gtgatacccg cgcgttacgg ctactttgcg cccgctcggg ttataaacag 60
tattcagggg tcaatgtcct gaaaggcatc gattttacgt tgcatacagg ggaggtccac 120
gcctctgctg cgcgcaatgg tgccggtaaa tcgacgttaa tgaagattat tgccggtatt 180
acccctgctg atagcgggtac gctggagatt gagggcaaca actacgtcag attaacgccca 240
gttcatgctc atcagctggg tatttatctc gttccccagg aaccgctgct ttcccaagc 300
ctgtcgataa aagaaaacat cctgtttggg ctggcaaaaa aacagctctc catgcagaaa 360
atgaagaact tgcggggcgc gctgggctgc cagtttgatc tgcatagtct ggcaggatcg 420
ctggatgctg ccgatcgcca aatggtggaa atcctccgcg ggctgatgcg cgactcgcgg 480
attctgatcc tcgatgaacc taccgcctcg cttaccctcg cggaaaccga acgcttggtt 540
agtcgcttgc aagagctgct tgctactggc gtgggtattg tttttatctc gcataagctg 600
ccggaaattc gccagattgc cgatcgaatt agcgtgatgc gcgacggaaac catcgcttca 660
agcggcaaaa ccagcgaact gtctaccgac gacattatcc aggccatcac cccagcggta 720
cgggaaaaat cgtctctctg cagccaaaaa ttatggctgg agttacctgg taaccgccca 780
caacatgccg ccggaacgcc ggtgctgaca ctggaaaatc tgaccggcga aggtttcagg 840
aatgtcagcc tgacgctcaa tgccggagaa attctgggcc tggctgggct ggtgggggcc 900
ggacgcacag aactggcoga gacgctctat ggtctgcgta ctttgctggg cggacgcatt 960
atgctgaatg gtaaaagagt caataaatta tccactggag aacgtttact gcgcggtctg 1020
gtttatctgc cgggaagatc ccagtcattc ggactgaatc tcgatgcttc gctggcctgg 1080
aacgtctgcg cccttactca taacctctgt ggattctggg cgaaaaccgc gaaagataat 1140
gccaccctgg aacgttatcg tcgggctgct aatattaaat tcaaccaacc ggaacaagct 1200
gcacggacat tatccggtgg caaccagcaa aaaatcctca ttgccaatg cttggaagct 1260
tcgcgcgaag tattgattgt cgatgagccg acgcgcggcg tggatgtctc ggcccgtaat 1320
gatactaccc agctgttgcg cagcatcgcc gcacaaaatg tggctgtgct gcttatctcc 1380
tccgacctgt aagagatcga actgatggca gatcgtgtgt atgtgatgca tcagggcgaa 1440
attaccactg ctgcactgac cgaagcgcgt attaatgtcg agactattat cgcgcttgcc 1500
ttcggcgata gtcagcgta gagggcgtca tgctga 1536

```

<210> 100
 <211> 1029
 <212> DNA
 <213> E. Coli

<400> 100

```

atgctgaagt ttattcagaa caaccgtgaa atcacggcac tgctggcggg ggtgctgctg 60
tttgtattac ccggttttct cgaccgccag tatttaagtg tgcaaacgct gaccatgggt 120
tatagcagcg cgcaaatcct gatcctgctg gcaatgggag cgacgctggt aatgcttacg 180
cgcaatattg atgtttcagt gggttcgatt accggaatgt gcgcggtgct gttggggatg 240
ttactgaacg caggatatcc actacctggt gcttgtgtcg cgactttact gcttgggttg 300
ctcgcgggat ttttcaacgg tgctctggtc gcgtggctaa agatccctgc cattgttgcc 360
acccttgcca cgttaggggt gtacagaggg atcatgttgc tgtggactgg cggcaaatgg 420
attgaagggt tacccgccga actgaaacag ctctccgccc cgctgctgct tggcgtttca 480
gcaattgggt ggttgacgat aattctgggt gcatttatgg cctggctgct ggcaaagacg 540
gcgtttggac gcagttttta tgccacgggc gataatttac agggcgctcg tcaactgggc 600
gttcgtactg aagccattcg cattgtggca ttttcgttga acggctgcat ggcggcactg 660
gcgggaattg tgtttgcttc gcagattggt ttatcccca accagaccgg tacccggctg 720
gagatgaaag caattgcagc ctgctgctg ggcggcatta gtttgctcgg tggttccggt 780
gcgatcattg gtgcgggtact cggcgcatgg ttcttgacgc agatcgatag cgtactgggt 840
ctggtgcgca ttccggcatg gtggaatgat ttatcgcgg gtctggttct gctggcgggt 900
ctgggtgttg atggacgcct gcgttgtgcg ctggaacgta atctacggcg gcaaaaatat 960
gcccgcctta tgacgccacc gccatccggt aaaccgcgtt cgtcaggtaa aaaacgggag 1020
gccgcataa 1029

```

<210> 101
 <211> 993

<212> DNA

<213> E. Coli

<400> 101

atgcgctattc	gctacgggtg	ggaactggct	cttgccgcac	tgctcgttat	tgagattgtc	60
gcatttgggtg	caattaaccc	gcgaatgtta	gatctcaata	tggtgctgtt	cagcaccagt	120
gactttatct	gcattggcat	tgctgcctta	ccgctaacga	tggtgattgt	cagtggcggg	180
atcgatattt	cgtttggttc	gaccatcggc	ctctgcgcca	ttgcattggg	cgtactgttt	240
caaagtgggtg	tgccgatgcc	gctggcgata	ctcctgacct	tactgctcgg	cgcatgtgtc	300
gggctgatca	acgccggatt	aattatctat	accaaagtta	acccgctggg	gattacgctt	360
ggcacgctgt	atctgtttgc	cggaagcgct	ctgctgcttt	ccggtatggc	cggagcgacg	420
gggtacgaag	gtattgggtg	attcccgatg	gcgtttacag	atttcgctaa	cctggatgtg	480
ctgggactcc	ccgttcgcgt	gattatcttc	ctgatatgtc	tccctgcttt	ctggctctgg	540
ctgcataaaa	cccatgccc	acgtaatgtg	tttttgattg	ggcaaagccc	gcgcgtggcg	600
ctttatagcg	cgattccagt	taaccgtacc	ttatgtgcgc	tctatgccat	gacggggctg	660
gcgtctgcgg	tcgccgctgt	gctgctggta	tcgtattttg	gttcagcacg	ttccgatctc	720
ggtgcgtcgt	ttctgatgcc	cgccatcacc	gccgtggtgc	ttggcggggc	caatatttat	780
gggtggtccg	gttccattat	cgccaccgcc	attgcggttt	tattagtggg	atatttgcaa	840
caaggtttgc	aaatggcagg	agtgcctaat	caggtgtcca	gcgccctttc	cggtgcgcta	900
cttatcgctg	ttgtcgtagg	tcgttccgtt	agcctgcatc	gccagcaaat	taaagagtgg	960
ctggcgcgtc	gggccaataa	ccattgcca	tta			993

<210> 102

<211> 1023

<212> DNA

<213> E. Coli

<400> 102

atgacacttc	atcgctttaa	gaaaatcgcc	ttacttagcg	ctcttggcat	tgccgcaatc	60
tctatgaatg	tcgagggcgc	agagcgattt	gcattttattc	ccaaactggt	tgccgtggga	120
ttttttacca	cggtggcnaa	cgccgcacaa	caagcgggta	aagagctggg	cggtgatgtg	180
acctacgacg	ggccgacaga	acccagtggt	tctgggtcagg	tacagttgat	taataacttc	240
gtcaatcaag	gttataacgc	cattatcggt	tctgcgggtt	cgctgatgg	cttgtgtccg	300
gcaactgaaac	gcgccatgca	acgtggtgtg	agagtgtga	cctgggactc	tgataactaa	360
ccggagtggc	gctcttacta	cattaatcag	ggaacgccc	cccagttagg	aggtatgttg	420
gtggatattg	cgccgcgtca	ggtgaataaa	gacaaagcca	aagtcgcgtt	tttctactca	480
agcccccacc	ttacggacca	aaaccagtgg	gtgaaagaag	cgaaagcgaa	aatcgccaaa	540
gagcatccag	gctgggaaat	tgctactacg	cagtttggtt	ataacgatgc	cactaaatcg	600
ttacaaaccg	cagaaggaaat	attaaaagcg	tatagcgatc	tcgacgccat	tatcgccccc	660
gatgccaaac	ccctgcccgc	tgccgcacaa	gccgcagaaa	acttgaaaaa	tgacaaagta	720
gcgattgtcg	gattcagtag	gccaaatgtg	atgcgcccg	atgtagagcg	cgccacgggtg	780
aaagaatttg	gcctgtggga	tgtggttcag	caaggcaaaa	tttcagtgta	tgtcgcggtg	840
gcattattga	aaaaaggatc	aatgaaaacg	ggcgacaagc	tggtatataa	ggcggtagg	900
caggttgaa	tctcgccaaa	cagcggttcag	ggctatgact	acgaagcgga	tggtaatggc	960
atcgtagctg	taccggagcg	cgtagatattc	aacaaagaga	atatcgcgaa	atacgatttc	1020
tga						1023

<210> 103

<211> 876

<212> DNA

<213> E. Coli

<400> 103

atggcagatt	tagacgatat	taaagatggt	aaagattttc	gtaccgatca	accgcaaaaa	60
aatatccctt	ttaccctgaa	agggttgcgt	gcgctggatt	ggggaatgca	gtcacgctta	120
tcgcggatat	ttaatccgaa	aacgggtaaa	accgtgatgc	tggtttttga	ccatgggttat	180
tttcagggac	cgactaccgg	acttgaacgc	attgatataa	atatcgcccc	gctgtttgaa	240
catgccgatg	tattaatgtg	tacgcgcggc	attttgcgca	gcgtagtctc	ccctgcgacc	300
aataggccgg	tggtactcgg	ggcgtcaggt	gcgaactcta	ttctggcgga	attaagtaat	360
gaagccgtgg	cgttatcgat	ggatgacgcc	gtgcgcctga	acagttgcgc	ggtggcggcg	420
caggtttata	tcggcagcga	atatgaacat	cagtcgatca	aaaatattat	tcagctggtt	480

gatgccggaa	tgaagtggg	aatgccgacc	atggccgtga	ctggcggtgg	caaagatatg	540
gtgcgcgac	agcggtattt	ctcgctcgcg	actcgaatcg	ccgctgaaat	ggggcgcaa	600
attatcaaaa	cctattatgt	cgaaaaaggt	tttgaacgga	ttgttgccgg	atgtccggta	660
cccattgtta	ttgctggcgg	taaaaaatta	ccggagcgcg	aggcgctgga	aatgtgctgg	720
caggctatcg	atcagggcgc	ttctgggttg	gatatggggc	gtaatatatt	ccagtctgac	780
catccgggtg	cgatgatgaa	agccgtacag	gcgggtggtc	accataacga	aacggctgat	840
cgggcatatg	aactctatct	gagtgaaaaa	cagtaa			876

<210> 104
 <211> 291
 <212> DNA
 <213> E. Coli

<400> 104

atgcacgtca	cactggttga	aattaacgtt	catgaagaca	aggttgacga	gtttatcgaa	60
gtttttcgcc	agaaccacct	gggctctgta	caggaagaag	gcaatttgcg	cttcgatgtc	120
ttacaggacc	cggaagtga	ttcgcgcttt	tatatctacg	aagcctataa	agatgaagac	180
gcagtggcgt	tccataaaac	cacgccccac	tacaaaaacct	gtgtcgcgaa	actggaatct	240
ttaatgaccg	ggccgcgtaa	aaaacgtctg	ttcaatgggt	tgatgccgtg	a	291

<210> 105
 <211> 1152
 <212> DNA
 <213> E. Coli

<400> 105

atgtttgaac	caatggaact	taccaatgac	gcgggtgatta	aagtcacgg	cgtcggcggc	60
ggcgccggta	atgctgttga	acacatgggt	cgcgagcgca	ttgaaggtgt	tgaattcttc	120
gcggtaataa	ccgatgcaca	agcgctcggt	aaaacagcgg	ttggacagac	gattcaaatac	180
ggtagcggtta	tcaccaaagg	actgggcgct	ggcgctaatc	cagaagttgg	ccgcaatcg	240
gctgatgagg	atcgcgatgc	attgctgctg	gcgctggaag	gtgcagacat	ggtctttatt	300
gctgcgggta	tgggtggttg	taccggtaca	ggtgcagcac	cagtcgtcgc	tgaagtggca	360
aaagatttgg	gtatcctgac	cgttgcctgc	gtcactaagc	ctttcaactt	tgaaggcaag	420
aagcgtatgg	cattcgcgga	gcaggggatc	actgaaactgt	ccaagcatgt	ggactctctg	480
atcactatcc	cgaacgacaa	actgctgaaa	gttctggggc	gcggatatctc	cctgctggat	540
gcgtttggcg	cagcgaacga	tgtactgaaa	ggcgctgtgc	aaggtatcgc	tgaactgatt	600
actcgtccgg	gtttgatgaa	cgtggacttt	gcagacgtac	gcaccgtaat	gtctgagatg	660
ggctacgcaa	tgatgggttc	tggcgtggcg	agcgggtgaag	accgtgcgga	agaagctgct	720
gaaatggcta	tctcttctcc	gctgctggaa	gatatcgacc	tgtctggcgc	gcgcggcggtg	780
ctgggttaaca	tcacggcggg	cttcgacctg	cgtctggatg	agttcgaaac	ggtaggtaac	840
accatccgtg	catttgcttc	cgacaacgcg	actgtggtta	tcggtaacttc	tcttgaccgg	900
gatatgaatg	acgagctgcg	cgtaaccggt	gttgcgacag	gtatcggcat	ggacaaaacgt	960
cctgaaatca	ctctggtgac	caataagcag	gttcagcagc	cagtgtatga	tcgctaccag	1020
cagcatggga	tggctccgct	gacccaggag	cagaagccgg	ttgctaaagt	cgtgaatgac	1080
aatgcgccgc	aaactgcgaa	agagccggat	tatctggata	tcccagcatt	cctgcgtaaag	1140
caagctgatt	aa					1152

<210> 106
 <211> 3048
 <212> DNA
 <213> E. Coli

<400> 106

atggacgtca	gtcgcagaca	atTTTTTaaa	atctgcgcgg	gcggtatggc	tggaacaaca	60
gtagcggcat	tgggctttgc	cccgaagcaa	gcaactggctc	aggcgcgaaa	ctacaaatta	120
ttacgcgcta	aagagatccg	taacacctgc	acatactggt	ccgtagggtg	cggtctattg	180
atgtatagcc	tgggtgatgg	cgcaaaaaac	gccagagaag	cgatttatca	cattgaaggt	240
gacccggatc	atccggtaa	ccgtggtgcg	ctgtgcccca	aaggggccgg	ttgtctggat	300
tacgtcaaca	gtgaaaaccg	tctgcgttac	ccggaatatc	gtgcgccagg	ttctgacaaa	360
tggcagcgca	ttagctggga	agaagcatte	tccggtattg	cgaagctgat	gaaagctgac	420
cgtgacgcta	actttattga	aaagaacgag	cagggcgtaa	cggtaaaccg	ttggtcttct	480

accggatg	tgtgtg	cggcgcc	aacgaa	ggatgct	ccagaa	540
gcccgtccc	tcgggatg	ggcggtag	aaccagg	gcgtctg	cggacca	600
gtagcaag	ttgtcca	atttgg	gggtcgat	ccaacc	ggtggat	660
aaaaacg	acgtcgt	ggtgatg	ggtaac	ctgaag	tcccgtc	720
ttccgct	cgatgga	gaaaaa	aacgacg	ccttgat	tgctgat	780
cgttttac	gtaccg	tgtggcg	atttacg	ctattcg	cggtagc	840
attacgtt	tgtctgg	tttgcg	ctgatcg	acaacaa	caacgcc	900
tacgtta	attacac	cgccagc	ctggtgc	atgattt	tttcga	960
ggtctgtt	gcgggtac	cgctgaaa	cgtaata	ataaatc	ctggaac	1020
cagctcga	aaaacgg	tgcaaac	gatgaa	tgactca	gcgctgt	1080
tggaacct	tgaaaga	cgtttcc	tacacgc	acgtcgt	aaacatc	1140
ggtagcc	aaagccg	cctgaa	tgtgaag	tgccctc	cagcgac	1200
gatcgaca	ccacctt	gtacgcg	ggctgga	agcacac	gggtgcg	1260
aaactcga	ctatggc	gatccag	ctgctcg	acatggg	ggcgggt	1320
ggcgtga	catg	tcactca	attcagg	tgactga	aggcctg	1380
tctaccag	tgccaggt	tctgacg	ccgtcag	aacagg	tttgca	1440
tatctgga	cgaaacg	gaaagcg	ctggctg	aggtgaa	ctggagc	1500
tatccga	tcttcgt	cctgatg	tctttct	gcgatgc	gcagaa	1560
aaacaact	gctatga	gctgccg	tgggacc	cctacga	catcaag	1620
ttcaacat	tgatga	caaagtc	ggttatt	gccagg	taaccgg	1680
gcgtcctt	cggacaaa	caaagtg	agctgct	gcaagct	gtacatg	1740
gttatcg	cgctgtg	tgaaacct	accttct	agaacc	tgagtcg	1800
gatgtcg	cgcgctc	tcagact	gtattcc	tgcttcg	ctgcttt	1860
gaagaaga	gttctat	taactcc	cgctggt	agtgga	gaaaggt	1920
gaacgcg	gcgaagc	taacgac	gaaattc	cggtatc	ccatcat	1980
cgcgagct	accagtc	aggtggt	ggcgtag	cgctgat	gatgagc	2040
aactcaag	agccgcg	accgcat	gacgaag	ctaaaga	caacggc	2100
gcgctgga	atctctat	cgctaag	gtgctta	cgaaaga	tcagttg	2160
agtagctt	cgcatct	tgatgac	acaaccg	cttcttg	gatctac	2220
ggtagctg	caagcag	caaccag	gctaacc	ataactc	ccgtccg	2280
ctgggga	cgctggg	ggcctgg	tgcccg	accgtcg	gctgtac	2340
cgctgctc	cggtata	cggtaaa	tggtatc	aacggat	gatccag	2400
aacgcgag	agtggac	taacgat	cctgact	gcaatgc	accgggt	2460
ccaaccgg	cgtttat	gcagccg	gggatgg	gcctgtt	catcaac	2520
atggcgga	gtccgtt	ggaacac	gagccga	aaacgcg	gggcact	2580
ccgctgca	cgaacgt	gtctaac	gttgtc	tgatgaa	agacgcg	2640
cggtagg	aaaaag	gttcccg	gtgggac	cctatcg	gaccgag	2700
ttccacac	ggacca	cgcatg	aacgca	ctcagcc	acagttt	2760
gaaatcag	aaacgct	ggcggcg	ggcatta	atggcg	tgctact	2820
tccagcaa	gtggctt	ccgcgcg	gctgtgt	cgctcgt	gaaaccg	2880
aatgtaaa	gtcagc	tgaaacg	ggtattc	tccactg	ctttgag	2940
gtcgcgcg	aaggttat	cgctaac	ctgacgc	atgtcgt	tgcaaac	3000
caaacgcg	aatataa	gttcttag	aacatcg	agcgtaa		3048

<210> 107

<211> 885

<212> DNA

<213> E. Coli

<400> 107

atggctatg	aaacgcag	cattatcaa	aggtccg	ctaactcc	cacgccgc	60
tctcaggtg	gtgattaca	agcagaag	gcaaaact	tcgacgtt	cacctgtat	120
ggctgtaaa	cctgtcag	ggcgtgtt	gagtgga	acatccgt	tgaggtggg	180
cactgcgtc	gggtttac	taacccgc	gatctgag	ccaagtc	gacgggtg	240
cgctttagc	aaaccga	gaacggca	ctggagtg	tgatccgt	agacggct	300
atgcactgt	aagatccc	ctgcctga	gcgtgccc	ctgctggt	aatcattc	360
tacgcta	ggattgtc	tttccag	gaaaactg	tcggctgt	ttactgc	420
gccgggtgt	cgtttaata	tccgcg	aacaaag	ataaccgg	atataaat	480
acgctctgc	tcgatcgc	cagcgtcg	caggaa	cttgtgtg	aacctgtc	540
accggggta	tccacttc	caccaaga	gagatg	agctggcg	acagcgct	600
gcgaaactg	aagcgcgt	ttacgaac	gctggcgt	acaaccgg	aggggtcgt	660

ggtagcgcacg	ttatgtacgt	gctgcacac	gccgatcagc	cggagctgta	tcacggctctg	720
ccgaagatc	cgaagatcga	cacctcggta	agcctgtgga	aaggcgctt	gaaaccgctg	780
gcagcggctg	gctttattgc	cacttttgcc	gggttgattt	tcactacat	cggattggc	840
ccgaataagg	aagtggacga	tgacgaggag	gatcatcatg	agtaa		885

<210> 108
 <211> 654
 <212> DNA
 <213> E. Coli

<400> 108						
atgagtaagt	cgaaaaatgat	tgtgcgcacc	aaattttattg	atcgcgcctg	tcactggacc	60
gtgggtgattt	gcttcttcct	ggtagcgctg	tccgggattt	cgttcttcct	cccgcgcctg	120
caatggctga	cgcaaacctt	cgttacgccc	cagatgggac	gcattttgca	cccgttcttc	180
ggcattgcga	ttttcgtcgc	actgatgttt	atgtttgtgc	gtttttgtgca	tcacaacatc	240
ccgataaga	aagatattcc	gtggctgttg	aacattgtcg	aagtattgaa	aggcaatgag	300
cataaagtgg	cggatgtcgg	taagtacaac	gccgggcaaa	agatgatgtt	ctggtcgac	360
atgagcatga	ttttcgtgct	gctggtgacc	gggggtgatta	tctggcgtcc	gtactttgctg	420
cagtacttcc	cgatgcagg	tgctcgtac	agcctgtctg	tccacgcggc	tgccgggtatc	480
atcctgatcc	acgccatcct	gatccatag	tatatggcat	tttgggtgaa	aggatcgatt	540
aaagggatga	tcgaagggaa	ggtaagtcgt	cgtgggcca	agaaacacca	tccgcgctgg	600
tatcgtgaaa	tcgagaaggc	agaagcga	aaagagagt	aagaaggat	ataa	654

<210> 109
 <211> 261
 <212> DNA
 <213> E. Coli

<400> 109						
atggcgctgt	taataactaa	aaaatgcac	aattgtgata	tgtgtgaacc	cgaatgcccg	60
aatgaggcga	tttcaatggg	agatcatatc	tacgagatta	acagcgataa	gtgtaccgaa	120
tgctagaggc	actacgagac	accaacctgc	cagaaggtgt	gcccgatccc	caatactatt	180
gtgaaagatc	cggcgcatgt	cgagacagaa	gaacagttgt	gggataaatt	tgtgctgatg	240
caccacgcgg	ataaaattta	a				261

<210> 110
 <211> 1203
 <212> DNA
 <213> E. Coli

<400> 110						
atgcaaatgt	ttgatgtagc	cattgttggc	ggcgccatgg	tggggctggc	ggttgcctgt	60
ggcttacagg	ggagcggctt	acgcgttgcc	gtactggagc	agcgcgtaca	ggaacctctg	120
gcggcgaatg	caccaccaca	actgcgcgtt	tccgctatca	atgccgccag	cgaaaaatta	180
ctcaccgcgc	ttggcgtctg	gcaggacatt	ctctctcgta	gggccagctg	ttatcacggg	240
atggaagtgt	gggacaaaaga	cagctttggg	cacatttcgt	ttgacgatca	aagcatgggc	300
tatagccatc	ttgggcatat	cggtgaaaat	tcagtgtatc	actacgcgct	gtggaacaaa	360
gcgcacatgt	cgatcagatat	cactctgtta	gccccgcgag	aattacagca	ggtcgcctgg	420
ggagaaaaatg	aaaccttcct	gacgctgaaa	gatggcagca	tgtaaaccgc	gcgtctggtg	480
attggcgcg	acggcgctaa	ttcctgggtg	cgcaacaaa	ccgatattcc	gctgactttc	540
tgggattatc	agcatcacgc	gctggtagcg	accattcgca	cggaaagaacc	gcatgatgcg	600
gtggcgcgcc	agggtttcca	tggcggaagg	attctggcct	ttttaccgct	tagcgatccg	660
catctttgct	cgattgtctg	gtcactgtcg	ccagaggaag	cgcagcggat	gcagcaggca	720
agtgaagacg	aatttaacgc	cgcgttaaat	atcgcttttg	ataatcgctt	gggcttatgc	780
aaagttgaga	gcgcgcgtca	ggtgttccca	ctgacggggc	gttatgcgcg	ccagtttgcc	840
tcgcaccgct	tgccgctggg	gggcgacgcc	gcacatacca	ttcaccgcgt	ggcggggcag	900
ggggtaaatc	tcggccttat	ggatgctgca	gagctgattg	ccgaactgaa	acggttgcat	960
cgctcagggg	aagacatcgg	gcagtacatt	tatctgcgtc	gctatgagcg	tagccgcaag	1020
cacagtgcgg	cgttgatgct	ggctgggtat	cagggattcc	gcgatctgtt	ttccggtaac	1080
aatccggcga	aaaaactgct	gcgtgatatt	ggtttgaaac	tggccgacac	gcttctggc	1140
gttaagccgc	aacttatccg	ccaggcaatg	ggattaaacg	atttgctga	atggctgcgt	1200

taa

1203

<210> 111
 <211> 1179
 <212> DNA
 <213> E. Coli

<400> 111

atgagcgtaa	tcacgcgcgg	tggcggcgcg	gcggggcgca	cgctggcgct	ggctatttcc	60
cggttaagtc	acggggcgct	gccgggtacat	ttgattgaag	cgactgcgcc	agagtcacat	120
gtccatccgg	gctttgatgg	acgagcgata	gcgctggcgg	cggttacctg	tcagcaactg	180
gcgcgcacgc	gcgtctggca	atctctggcg	gattgcgcaa	ctgccatcac	caccgtgcat	240
gtcagcgatc	gtggtcacgc	tggatttgct	accctcgccg	cagaagatta	ccaactggcg	300
gcgctgggac	aggttgtcga	attgcacaat	gtcgggcaac	ggctgtttgc	attgctgcgt	360
aaagcacctg	gcgtaacgct	gcattgccct	gacgcgctgg	ctaacgttgc	ccgtactcag	420
agtcacgttg	aagtgcgcgt	ggagagtggc	gagacgctga	cgggccgcgt	gctggttagca	480
gctgatggca	cccattcagc	gttagccacc	gcgtgcggcg	ttgactggca	gcaggagcct	540
tacgaacaac	tggccgtgat	tgccaacgtt	gctacttccg	ttgcgcata	agggcgcgct	600
tttgaacgct	ttacgcaaca	tggcccgcgt	gcgatgttgc	cgatgtctga	cggacgctgt	660
tcgctggctt	ggtgtcatcc	actggaacgg	cgcgaaagag	tgttgtcgtg	gagtgacgag	720
aagttttgcc	gtgaactcca	gtcggccttt	ggctggcgac	ttgggaaaat	taccacgct	780
ggtaaacgca	gtgcttatcc	gctggcgctt	acccacgccg	ccagatctat	taccatcgt	840
accgtgctgg	tgggcaatgc	ggcgcaaat	ctgcaccgca	ttgcggggca	agggtttaac	900
ctcggtatgc	gagatgtgat	gagtccttgc	gaaaccctga	ctcaggcgca	ggagcgcgga	960
gaagacatgg	gggattacgg	cgtattgtgc	cgttatcagc	agcgtcgaca	gagcgatcgc	1020
gaagcaacca	ttggcgctac	ggacagcctt	gtacatcttt	ttggcaaccg	ttgggcaccg	1080
ctggttgtcg	ggcgcaacat	cggtctgatg	acgatggaat	tattcaccct	ggcacgcgat	1140
gtgctggcgc	agcgcacctt	cggttgggtg	gcgcgttga			1179

<210> 112
 <211> 1326
 <212> DNA
 <213> E. Coli

<400> 112

atgagtgaga	tatcccggca	agagtttcag	cgctcgccgc	aggccctggt	ggagcaaatg	60
caaccgcgca	gcgcgcgcgt	gatttttgct	gcaccagaag	taacacgtag	cgccgacagc	120
gaataccctt	atcgtcagaa	cagtgaactt	tggtaactca	ccggctttta	cgaaccggaa	180
gcggtgctgg	tgctgattaa	aagcgatgac	actcataacc	acagcgcttc	gtttaaccgc	240
gttcgcgacc	tgacggcgga	gatctggttt	ggccgtcgct	taggccagga	tgccgcgcca	300
gagaaactgg	gcgttgaccg	cgcaactggca	ttcagcgaaa	tcaatcagca	actttatcaa	360
ctacttaacg	gcctggatgt	ggtttaccat	gcccaggggc	aatatgcata	tgctgatgta	420
atcgtgaaca	gtgcgctgga	aaaactgcgt	aaagggttcg	ggcaaaatct	caccgcaccg	480
gcaacgatga	tcgactggcg	tcctgttggt	catgaaatgc	gcctgttcaa	atcgccagaa	540
gagattgccc	tactccgccc	cgcgggagaa	atcaccccca	tggcacatac	acgggcgatg	600
gaaaaatgcc	gtccgggaat	gttcgagtac	catctggaag	gcgaaattca	ccacgaattt	660
aaccggcacg	gtgcgcgcta	tccgtcctat	aacaccattg	tcggcagcgg	tgaaaacggc	720
tgcatctctg	actacaccga	aaacgagtgt	gaaatgcgcg	acggcgacct	ggtgttgatt	780
gacgcgggtt	gtgaatacaa	aggttacgct	ggcgatatta	cccgcacctt	cccggccaac	840
ggcaaatcca	cccaggccca	gcgtgaaatc	tacgacattg	tgctggagtc	tctcgaaacc	900
agcctgcgcc	tgtatcgtcc	gggaacttcc	attctggaag	tcactggtga	agtgggtgcg	960
atcatggtta	gcggcctggt	aaaactcgcc	atcctgaaag	gtgatgttga	tgaactgatc	1020
gctcagaacg	cccatcgctc	tttctttatg	catggcctta	gccactggtt	aggactggat	1080
gtccatgacg	tgggtgttta	tggtcaggat	cgctcgcgca	ttctggaacc	gggcatggta	1140
ctgaccgtag	agccagggct	gtatattgcg	ccgatgcag	aagtgccaga	acaatatcgc	1200
ggtatcggca	ttcgtattga	agacgacatt	gtgattaccg	aaaccggtta	cgaaaacctc	1260
accgccagcg	tggtgaaaaa	gccggaagaa	atcgaagcgt	tgatggttgc	tgcgagaaag	1320
caatga						1326

<210> 113
 <211> 585

<212> DNA

<213> E. Coli

<400> 113

atgcttatgt	ctatacagaa	cgaaatgcct	ggttacaacg	aaatgaacca	gtatctgaac	60
caacaaggga	cggtctgac	cccagctgag	atgcatggtt	taatcagcgg	gatgatatgt	120
ggcggtaacg	atgacagctc	atggctaccg	ctacttcacg	acctgacgaa	cgaaggcatg	180
gctttcggtc	atgagctggc	acaggcactg	cgtaaaatgc	actctgccac	cagcgatgcc	240
ctgcaggatg	acggcttctt	ttttcagctt	tatctgcctg	atggcgatga	tgtcagcggt	300
ttcgatcggg	ctgatgcatt	ggcagggttg	gtcaatcact	tcctgcttgg	tcttggcggt	360
acgcaaccga	agctggataa	agtgaccggc	gaaaccgggtg	aagctatcga	cgatctgcgt	420
aacattgcgc	aactgggtta	cgacgaagac	gaagatcagg	aagagcttga	aatgtcgcgt	480
gaagagatca	tcgaatacgt	tcgtgttgcc	gcgctgttat	gccacgacac	ctttactcat	540
ccgcaaccga	ccgcgcgaga	agtacaaaaa	ccgactctac	actaa		585

<210> 114

<211> 363

<212> DNA

<213> E. Coli

<400> 114

atgtttaaagc	tatttgcaaa	gtacacctct	attgggtgtgc	tgaacaccct	tatacactgg	60
gtgggttttg	gtgtttgtat	ctatgtcgcg	catacaaaac	aagctcttgc	aaacttcgca	120
ggtttcgttg	tggtctgtgag	ctttagcttc	ttcgcgaatg	caaaattcac	attcaaggca	180
tcgactacaa	cgatgcgcta	catgctatat	gttgggttca	tggggacact	gagtgcctact	240
gttggatggg	ctgctgatag	atgcgcactt	cccccgatga	taactcttgt	caccttctcc	300
gccatcagcc	tggtgtgcgg	tttcgtctat	tcaaagtcca	ttgtctttag	ggatgcgaaa	360
tga						363

<210> 115

<211> 921

<212> DNA

<213> E. Coli

<400> 115

atgaagatat	ctcttgtagt	tcctgtcttc	aatgaagaag	aagcgatacc	aattttttat	60
aaaacggtag	gtgaattcga	agaattgaag	tcatatgaag	tggaaatcgt	tttcataaat	120
gacggcgagca	aagacgctac	ggagtcaatc	attaatgtct	tggtctgttc	agatcctcta	180
gttgttcgcg	tgatcatttac	acgcaacttt	ggtaaagaac	cagcattgtt	tgcagggtta	240
gaccatgcaa	ccgggggatgc	gataatccca	attgatgttg	acctgcaaga	cccgattgag	300
gttattcctc	atcttattga	aaaatggcaa	gcagggtgctg	atatggttct	tgctaaaaga	360
tctgaccgct	caactgatgg	acgcctgaag	cgaaaaacgg	ctgagtgggt	ctataagctc	420
cacaataaaa	taagcaatcc	taaaattgaa	gagaatgttg	gtgatttcag	gctgatgagc	480
cgatgatgtg	tcgaaaatat	taaacttatg	ccagaacgaa	accttttcat	gaaagggtatt	540
ctgagctggg	taggaggaaa	gacagatatt	gttgaatacg	tcgagcgga	aagaattgct	600
ggagatacaa	aatttaaatgg	atggaaaact	tggaaatttag	cacttgaggg	tattacaagc	660
ttttccacat	tccctcttcg	catctggaca	tacatagggt	tagtggtagc	cagtgtagca	720
tttatttatg	ggcgtggat	gatttttagat	actatcatat	ttggaaatgc	tgtaggggga	780
tatccttcac	tacttgtttc	aatactgttt	ttagggtgaa	ttcagatgat	tggaatagga	840
gtatttaggtg	aatatatttg	acgcacatac	attgaaacca	aaaaacgccc	gaaatacatc	900
atcaagagag	tcaaaaaatg	a				921

<210> 116

<211> 1332

<212> DNA

<213> E. Coli

<400> 116

atgaataaag	caataaaagt	atcattgtat	atatcttttg	ttttgattat	ttgcgcctta	60
tctaaaaaca	taatgatgtt	aaatacatct	gatttcggaa	gagccattaa	gccattaatt	120
gaagacatac	cagcatttac	atatgactta	cctttattgt	ataaattgaa	aggatcatatt	180

gattcaattg	atagctatga	gtatataagt	tcatatagtt	atattttgta	tacatacgtc	240
ctgtttatta	gcatttttac	tgaatatctt	gatgctaggg	tggtatcggt	atttctaaaa	300
gtaatatata	tttattcatt	atatgcgata	tttacttcat	atataaaaaac	agaaagggtat	360
gtaactttat	ttacattctt	tatttttagct	tttcttatgt	gttcttctac	aacactgtca	420
atgtttgcat	cattctatca	agagcaata	gttataatct	tccttccatt	tttggtgtat	480
tcattaacat	gcaaaaaaca	taaatctatg	cttttgctat	tttttctggt	gctaataata	540
tctactgcta	aaaatcaatt	tatattaacc	ccactaatag	tgtattcata	ttatatTTTT	600
tttgatagac	acaaactaat	tattaaatct	gtaatatgcg	tggtgtgctt	gcttgcggtca	660
atatttgcaa	tatcttattc	aaaagggtgt	gttgaattaa	ataagtacca	tgcaacatac	720
ttcggtagtt	atctttatat	gaaaaacaac	gggtataaaa	tgccatcgta	tggtgatgat	780
aagtgtgttg	ggtagatgc	ctggggtaat	aaattcgaca	tatcatttgg	cgcaacccca	840
acagaagttg	gaacggaatg	tttcgaatct	cataaagatg	aaacgttttc	gaatgcactc	900
tttttatagg	ttagcaaac	aagcaccatc	ttcaaaactc	catttgatga	tggtgtgatg	960
tctcagtata	aagaaaatta	tttccatgta	tataaaaaac	tacacgtaat	atatggagaa	1020
tcaaacatac	taacgactat	tactaacata	aaagacaata	tatttaaaaa	cattagattt	1080
atatcattgt	tattattttt	tattgcttct	atttttatta	gaaataataa	aataaaggca	1140
tctttatttg	tagtatctct	ttttggaata	tctcaatttt	atgtgtcatt	tttcggggaa	1200
ggatataagag	atttaagcaa	gcattttatt	ggaatgtatt	tttcggtcga	cctttgctta	1260
tacataacag	tcgttttttt	aatttataaa	ataattcaaa	gaaatcaaga	caatagcgat	1320
gtaaagcact	aa					1332

<210> 117
 <211> 249
 <212> DNA
 <213> E. Coli

<400> 117						
atgggcattc	tgatcatggat	tatttttggg	cttattgccc	gtattctggc	gaagtggatc	60
atgccaggta	aagatggagg	tggaattctt	atgactatcc	tgctggggat	agtcgggtgcc	120
gtagtcggcg	gatggatcag	cacgctgttt	ggctttggta	aagtcgatgg	cttcaatttt	180
ggcagcttcg	tggttgccgt	tattggtgcg	attgtcgtgc	tatttatcta	caggaagatt	240
aaaagttaa						249

<210> 118
 <211> 183
 <212> DNA
 <213> E. Coli

<400> 118						
atgggcaaaag	caacgtatac	cgtgaccgtc	accaataaca	gcaatggcgt	ttctgtcgat	60
tatgaaacag	agacgccgat	gactttgctg	gtgccagaag	tgccggctga	agtgataaaa	120
gatctggtga	ataccgtacg	ttcttatgac	acggaaaacg	aacatgatgt	ttgtgggtgg	180
taa						183

<210> 119
 <211> 360
 <212> DNA
 <213> E. Coli

<400> 119						
atgcttcaaa	tcccacagaa	ttatattcat	acgcgctcaa	cgcttttctg	gaataaacia	60
actgcacctg	ccggaatatt	cgaacgtcat	cttgataaag	gaacgcgcc	gggggtttac	120
ccacgccttt	ccgttatgca	tggggcgggc	aaatatctcg	gctacgctga	tgaacacagt	180
gcagagcctg	atcaggtgat	ccttatcgaa	gcggggcagt	ttgcggtgtt	ccctccagaa	240
aagtggcaca	acattgaagc	catgactgac	gatacttatt	tcaacattga	cttcttcgtg	300
gctcctgaag	tcctgatgga	aggtgcgcaa	caacggaaa	tcattcataa	cgggaaatga	360

<210> 120
 <211> 741
 <212> DNA
 <213> E. Coli

<400> 120

gtgaagtcca	aagttatcgc	cctggcgcca	ttaatgggta	ttagcgggat	ggcagcgag	60
gctaacgaat	tgccgatgg	accgcataatt	gtcacctccg	gtacggcaag	cgtggatgag	120
gtgccagaca	ttgccactct	tgcgattgaa	gttaacgtgg	ccgcgaagga	tgccgctact	180
gccaaagaaac	aggcagatga	gcgcgtcgca	caatacattt	ccttccttga	actcaatcag	240
atcgcgaaaa	aagatatcag	ctcagcgaac	ttacgcaccc	agccagatta	tgattatcag	300
gatggtaaaa	gtatccttaa	aggctaccgc	gctgtgagaa	cggtggaagt	cacgctccgt	360
cagttagaca	aactgaattc	cttgctggat	ggcgcgctga	aggcggtct	taacgaaatt	420
cgttctgtgt	cgctgggctg	ggcgagccg	gatgcctata	aagacaaagc	gcgtaaaggca	480
gcgattgata	acgcgattca	tcaggcgca	gaactggcga	acggctttca	tcgtaaactg	540
gggccgggat	atagcgtgag	ctaccatgtt	tccaactatc	agcccagccc	aatggtgagg	600
atgatgaaag	ccgatgccgc	gccggtgtcc	gcccaggaaa	cttacgagca	ggccgctatt	660
cagtttgatg	atcaggtcga	tgtggtcttc	cagttagaac	ctgtggatca	acaacccgct	720
aaaacacctg	cagcacaata	a				741

<210> 121

<211> 1395

<212> DNA

<213> E. Coli

<400> 121

gtgttattac	tggtgagtg	ctcgcaaatg	tgcccgtcat	tcagacgatt	ccagacagtg	60
tttcataatt	cctccatttt	tctcccttat	tggtggcta	cactagtatc	attccgcgaa	120
acgtttcagg	aagagaaact	cttaacgatg	aaaggtagtt	ataaatcccg	ttgggtaatc	180
gtaatcgtgg	tggttatcgc	cgccatcgcc	gcattctggt	tctggcaagg	ccgcaatgac	240
tcccggagtg	cagccccagg	ggcgacgaaa	caagcgagc	aatcgccagc	gggtggtcga	300
cgtggtatgc	gttccggccc	attagccccg	gttcaggcgg	cgaccgccc	agaacaggca	360
gttcgcggtt	acctcaccgg	gcttggcacc	attaccgccc	ctaataccgt	tacggtgccc	420
agccgcgtgg	acggccaaact	gatagcggtta	catttccagg	aaggccagca	ggtcaaagca	480
ggcgatttac	tggcagaaat	tgaccccgag	cagttcaaa	ttgcattagc	acaagcccag	540
ggccaaactg	caaaaagataa	agccacgctt	gccaaacgccc	gccgtgacct	ggcgcggtat	600
caacaactgg	caaaaaaccaa	tctcgtttcc	cgccaggagc	tggtgcccc	acaggcgctg	660
gtcagtgaag	ccgaaggcac	cattaaggct	gatgaagcaa	gcgttgccag	cgcgagctg	720
caactcgact	ggagccggat	taccgcacca	gtcgatggtc	gcgttggtct	caagcaggtt	780
gatgttgata	accaaacttc	cagtgggtgat	accaccggga	tcgtggtgat	caccagagc	840
catcctatcg	atttagtctt	taccctgccc	gaaagcgata	tcgctaccgt	agtgcaggcg	900
cagaaagccg	gaaaaccgct	ggtggtagaa	gcctgggagc	gcaccaactc	gaagaaatta	960
agtgaaggca	cgctgttaag	tctagataac	caaatcgatg	ccactaccgg	tacgattaaa	1020
gtgaaagcac	gctttaataa	tcaggatgat	gcgctgtttc	ccaatcagtt	tgtaaacgag	1080
cgcatgttag	tcgacaccga	acaaaacgccc	gtagtgatcc	caacagccgc	cctgcaaatg	1140
ggcaatgaag	gccattttgt	ctgggtgctg	aatagcgaaa	acaaggtcag	caaacatctg	1200
gtgacgcccg	gcatttcagg	cagtcagaaa	gtgggtgatcc	gtgcaggtat	ttctgcgggc	1260
gatcgcgctg	tgacagacgg	cattgatcgc	ctgaccgaag	ggcggaaggt	ggaagtgggtg	1320
gaagcccaga	gcgccactac	tccggaagag	aaagccacca	gccgcgaata	cgcgaaaaaa	1380
ggagcacgct	cctga					1395

<210> 122

<211> 3123

<212> DNA

<213> E. Coli

<400> 122

atgcaggtgt	tacccccgag	cagcacaggc	ggcccgtcgc	gcctgtttat	tatgcgtect	60
gtggccacca	cgctgctgat	ggtggcgatc	ttactcgccg	ggattatcgg	ttatcgcgcc	120
ctgcccgttt	cggcgctgcc	ggaagtggac	tatccgacca	ttcaggtggg	cacgctctac	180
ccaggtgcca	gcccggatgt	catgacctct	gccgttaccc	cgccgctaga	acgccagttc	240
gggcagatgt	ctggcctgaa	acagatgtcg	tcgcaaatgt	ccggcggtgc	gtcagttatc	300
actttgcagt	tccagctaac	attaccgctc	gatgtcgccg	agcaggaagt	gcaggccgag	360
attaacgctg	cgaccaactt	gttgcggagc	gatctgccta	acccgcccgt	ttacagcaaa	420
gtgaaccggg	cagatccgcc	gatcatgacg	ctcgccgtca	cctcaaccgc	catgccgatg	480

acgcaagtgg	aagatatggt	ggaacccgc	gtcgcgcaga	aaatctcgca	gatttccggc	540
gtcggcctgg	tgacgctttc	cggcggtcag	cgteccggctg	ttcgcggtcaa	acttaacgct	600
caggcgattg	ccgcccctcg	cctgaccagc	gaaaccgtgc	gcaccgccat	taccggcgct	660
aacgttaact	cgcaaaaagg	tagcctcgac	ggcccttccc	gtgcgggtcac	gctttccgcg	720
aacgaccaga	tgcaatccgc	cgaagagtat	cgccagctaa	tcacgccta	ccagaacggc	780
gcgccaattc	gtctgggcga	tgctcgcaact	gtagagcaag	gtgcagaaaa	cagctggctc	840
ggcgcggtgg	cgaacaaaga	acaggccatt	gtgatgaatg	ttcagcgcca	gcccgggtgct	900
aacattatct	ccaccgcccga	cagcattcgg	cagatgctgc	cacagctcac	tgagagtctg	960
ccgaaatcgg	tgaaggtgac	agtgccttcc	gategcacca	ccaatatccg	cgcattccgtc	1020
gatgatactc	agtttgaaat	gatgatggct	atcgcgctgg	tagtcatgat	tatctacctg	1080
tttttcaatc	atattccggc	gaccatcatt	cccgggtgtg	ctgtaccgct	gtcgttaatc	1140
ggcactttcg	cggttatggt	gtttctcgat	ttttcaatca	ataacctgac	actgatggcg	1200
ttactatcgc	ccaccggatt	cgtggctcga	gacgccatcg	tggtgatcga	aaacatttcc	1260
cgctatatcg	aaaaagcgga	aaaaccgttg	gcggcgggcg	tcaagggcg	agggtgaaatc	1320
ggctttacca	ttatctcgct	gaccttctca	ctgattgcgg	tggtgatccc	actgctgttt	1380
atgggcgata	tcgtcggcgg	actgttccgc	gaatttgcta	ttacctggc	ggtagcgatt	1440
ttgatctcag	cgggtggtgc	gctgacctg	acaccgatga	tggtcgcgcg	gatgctcagc	1500
caggagtctg	tgcgtaaaaca	gaaccgcttc	tcctcgctcc	cggaaaaaat	gttcgacagg	1560
ataatcgccg	cctatggtcg	tggaactggc	aaagtgtctga	atcatccgtg	gctgacctta	1620
agcgtggcac	tcagcacgct	gctgcttagc	gtgctgtgtg	gggtgttcat	tccgaaagg	1680
ttcttcccg	tacaggacaa	tggcattatt	cagggcactt	tgcaaggcac	gcaatccagc	1740
tcctttgcc	atatggccca	gcgacaacgc	caggtcgcgg	acgtgatttt	gcaggatccg	1800
gcagtgcaca	gcctgacctc	atttgtttgg	gttgatggca	ctaaccgctc	gctgaacagt	1860
gcacgtttac	aaatcaacct	caaaccgttg	gatgaacgtg	atgatcgggt	gcaaaaagtc	1920
atcgcccgtc	tgcaaacggc	ggtagataaa	gtgccggcg	tcgatctctt	cctgcaacca	1980
acgcaggatc	tgactattga	tactcaggtc	agccgcaccc	agtaccagtt	taccttgacg	2040
gccacgtcac	tggtgctgct	cagtacctgg	gtgccacagt	tgatggaaaa	actccagcaa	2100
ctgccacagc	ttctctgatg	ctccagcgac	tgccaggaca	aagggtggtg	ggcgtatgtc	2160
aatgttgatc	gcgacagcgc	cagccgtctg	gggatcagca	tgccggatgt	cgataacgcc	2220
ctgtacaacg	cgtttggtca	gcggctgatt	tccactattt	atactcaggc	caaccagtat	2280
cgcgtggtg	tggaagcaca	caccgaaaa	accccaggcc	tcgcggcgct	ggataccatt	2340
cgccctgacca	gcagcgacgg	cggcggtggt	ccgctaagct	caattgccaa	aattgagcag	2400
cgttttgccg	cgtcttccat	caaccatctg	gatcagttcc	cggtaacgac	catctccttt	2460
aacgtgccc	ataactatc	gctgggcgat	gcggtgcagg	cgattatgga	caccgaaaa	2520
acgctgaatc	tgccggtgga	tatcaccacg	cagttccagg	gcagcaccc	cgccttccag	2580
tcggcgctgg	gcagcactgt	ctggctgatt	gtcgcggcgg	tggtggcgat	gtatatcgtg	2640
ctcggcattc	tgtacgagag	ctttattcac	ccgatcacca	ttctctcgac	gctaccaccc	2700
gcagggttgg	gcgcactgct	ggcggttgcg	attgctggta	gcgaactgga	tggtatttgc	2760
attatcgcca	ttattttgct	gatcggtatc	gtgaagaaga	acgccatcat	gatgatcgac	2820
ttcgcgctgg	ctgctgagcg	cgagcaaggc	atgtcgccgc	gcgaggcaat	ctaccaggct	2880
tgctctgttc	gttttcgtcc	gacccctgag	accactctgg	cggctctgct	tggcgcgctg	2940
ccgctgatgt	tgagtaccgg	ggtcggcgcg	gaactgcgtc	gtccgttagg	tatcggcatg	3000
gtcgcgggtc	tgattgtcag	ccagggtgct	acgctgttta	ccacgccggt	gatttatttg	3060
ctgttcgacc	gcctggcatt	gtgggaccaa	agccgctttg	cccgtcatga	agaggaggcg	3120
taa						3123

<210> 123

<211> 3078

<212> DNA

<213> E. Coli

<400> 123

gtgaagtttt	ttgccctctt	catttaccgc	ccggtggcga	cgattttact	gtcggttgcc	60
attacctgtg	gcggcatact	gggtctccgt	atgctgccgg	tcgccccgct	gccgcaggtc	120
gattttccgg	tgattatcgt	cagcgccctc	ctgcccgggtg	cgtaaccaga	aacaatggcg	180
tcttccggtg	ccacgccgct	ggagcgctca	cttgggcgca	ttgccggagt	cagtgaatg	240
acctccagca	gttcgctcgg	cagcacgcgt	attattttgc	agtttgattt	tgaccgggat	300
atcaacggcg	cagcgcggtg	tgtagcggcg	gcgatcaacg	ctgcacaaag	tttgotgccc	360
agtgggatgc	ccagccgccc	gacctatcgc	aaagcgaacc	cgtcggtatg	gccaattatg	420
atcttcacgc	tgacgtccga	tacttattcg	cagggtgaac	tgtaacgatt	cgcctcgacg	480
cagctggctc	cgacgatttc	gcaaatcgac	ggtgttgggt	atgtcgatgt	cggaggcagc	540

tcaactgcccg	ccgtacgcgt	cgggctgaat	ccgcaggcgc	tgtttaatca	gggcgtgtcg	600
ctggacgacg	tacgcaccgc	cgtcagcaat	gccaaacgtgc	gtaaaccgca	gggcgcgctg	660
gaagatggca	ctcacgcgtg	gcagatccag	accaatgatg	agctaaaaac	cggcgtgtaa	720
tatcacgcgt	tgattattca	ctacaacaac	ggcggcgcg	ttcgtctggg	cgatgtggcg	780
acggtgaccg	actcagtgca	ggatgtgcgc	aacgccggga	tgaccaacgc	caaacggct	840
attttactga	tgatccgcaa	actgccggaa	gccaatatta	tccagacggt	tgacagcatc	900
cgggcacaaa	taccggaggt	gcaggaaacc	attccggcgg	cgattgatct	gcaaatgtcc	960
caggatcgct	ccccaccat	tcgcgcctcg	ctggaagaag	tcgagcaaac	gctgattatc	1020
tcgggtggcg	tggtgattct	gggtgtgttt	ttattcctgc	gctcgggtcg	cgccactatt	1080
attcccgccg	tttcggtgcc	ggtttcgctg	attggtacgt	ttgcggcgat	gtacctgtgc	1140
ggattcagtc	tcaataacct	ttcgttaatg	gcgctcacca	tcgctactgg	ttcgtgtgtg	1200
gatgacgcca	tcgtggtgct	ggaaaacatt	gcacgtcatc	tggaagcggg	aatgaaaccg	1260
ttgcaagccg	cactgcaagg	tactcgcgaa	gtcggtttta	cgggtgctgtc	gatgagctcg	1320
tcactgggtg	cgggtgttct	gcgcgtgctg	ttgatgggcg	gattgccggg	ccgactgtta	1380
cgcgaaattg	ccgtgacgct	ttctgtcgcc	attggtatat	cgttgctggg	ttctctgaca	1440
ttaacgcgaa	tgatgtgtgg	ctggatgctg	aaagccagca	agccgcgcga	gcaaaagcga	1500
ctgcgtgggt	ttggtcgcat	gttggtagcc	ctgcaacaag	gctacggcaa	gtcactaaaa	1560
tggtgtctca	atcataccgc	ttctggtggc	gtggtgtctg	ttggcaccat	tgcgctgaat	1620
atctcgctgt	atatctcgat	cccgaaaaac	ttcttcccgg	agcaggacac	tggcgtgttg	1680
atggggcgga	ttcaggcgga	tcagagtatt	tcgtttcagg	cgatgcgcgg	taagtgtcag	1740
gatttctatga	aaattatccg	tgacgatccg	gcagtgata	atgtcacccg	ctttacaggc	1800
ggttcgcgag	tgaacagcgg	gatgatgttt	atcacctcca	agccacgcga	cgaacgcagc	1860
gaaacggcgc	agcaaatat	cgacogtctg	cgcgtaaaac	tgcgcaaaaga	accggggcg	1920
aatctgttcc	tgatggcggt	acaggatatt	cgcgttggtg	ggcgctcagtc	gaacgccagc	1980
taccagtaca	cgttgttata	cgacgacctg	gcggcactgc	gagaatggga	gccgaaaatc	2040
cgcaaaaaac	tgggcagctt	gccggaaactg	gcggacgtga	actccgatca	gcaggataac	2100
ggcgcgga	tgaatctggt	ttacgaccgc	gacaccatgg	cacggctggg	aatcgacgta	2160
caagccgcca	acagtctgtt	aaataacgcc	ttcggtcagc	ggcaaatctc	gaccatttac	2220
cagccgatga	accagtataa	agtgtgtgatg	gaagtggatc	cgcgtataac	ccaggacatc	2280
agtgcgtcgg	aaaaaatgtt	cgttatcaat	aacgaaggca	aagcgatccc	gctgtcgtat	2340
ttcgtcaaat	ggcaaccggc	gaatgcccc	ctatcgggtga	atcatcaggg	attatcggcg	2400
gcctcgacca	tttcgtttta	cctgccgacc	ggaaaaatcgc	tctcggacgc	cagtgcggcg	2460
atcgatcgcg	caatgaccca	gcttggtgtg	ccttcgacgg	tgccggcgag	ttttgccggc	2520
acggcgacgg	tggtccagga	gacgatgaac	tcgcaaggta	tcctgattat	cgcggccatc	2580
gccacggtgt	atatcgtgct	gggtatcctt	tacgagagtt	acgtacatcc	gctgacgatt	2640
ctctccaccc	tgccctcggc	gggcgttgga	gcgctgttgg	cgtcggagct	gttcaatgcc	2700
ccgttcagcc	taatcgccct	gataggatc	atgctattaa	tcggcatcgt	gaagaaaaac	2760
gccattatga	tggtcgattt	tgcgcttgaa	gcccaacggc	acggtaacct	gacgcccgag	2820
gaagctatct	tccaggcctg	tctgtctgct	tttcgcccga	ttatgatgac	taccctggcg	2880
gcgctgtttg	gtgcgctgcc	gctggtattg	tcgggcggcg	acggctcgga	gctgcggcaa	2940
ccctcgggga	tcaccattgt	cggcggaactg	gtaatgagcc	agctccttac	gctgtatacc	3000
acgcgggtgg	tgtatctctt	tttcgaccgt	ctgcggctgc	gtttttcgcg	taaacctaaa	3060
caaacggtaa	ccgagtaa					3078

<210> 124

<211> 1416

<212> DNA

<213> E. Coli

<400> 124

atgacagatc	ttcccagacg	caccggttgg	caattgtgga	ttgtggcttt	cggcttcttt	60
atgcagtcgc	tggaaccac	catcgtaaac	accgcccttc	cctcaatggc	gcaaaagcctc	120
ggggaaaagtc	cgttgcatat	gcacatggtc	attgtctctt	atgtgctgac	cgtggcggtg	180
atgtgccccg	ccagcggctg	gctggcggac	aaagtcggcg	tgcgcaatat	tttctttacc	240
gccatcgtgc	tgtttactct	cggttcactg	ttttgcgcgc	tttccggcac	gctgaacgaa	300
ctgttgctgg	cacgcgcgtt	acagggcgtt	ggcggcgcg	tgatgggtgcc	ggtcggcgaga	360
ttgacgggtga	tgaaaatcgt	accgcgcgag	caatatatgg	cggcgatgac	ctttgtcacg	420
ttaccgggtc	aggtcgggtc	gctgctcggt	cggcgctcgc	gcggtctgct	ggtggagtac	480
gcacgtggtg	actggatctt	tttgatcaac	attccgggtg	ggattatcgg	tgcgatcgcc	540
acattgctgt	taatgccgaa	ctacaccatg	cagacgcggc	gctttgatct	ctccgatttt	600
ttattgtctg	cggttggcat	ggcggtatta	accctggcgc	tggaacggcag	taaaagtaca	660

gggttatcgc	cgctgacgat	tgcaggcctg	gtcgcagttg	gcgtgggtggc	actgggtgctt	720
tatctgctgc	acgccagaaa	taacaaccgt	gccctgttca	gtctgaaact	gttcgcgtact	780
cgtacctttt	cgctgggcct	ggcggggagc	tttgccggac	gtattggcag	tgccatgttg	840
ccctttatga	caccgggttt	cctgcaaat	ggcctcggtt	tctcgcggtt	tcattgccgga	900
ctgatgatga	tcccgatggg	gcttggcagc	atgggaatga	agcgaattgt	ggtacaggtg	960
gtgaatcgct	ttggttatcg	tccgggtactg	gtagcgacca	cgctgggtct	gtcgtcggtc	1020
acccgtgtgt	ttatgactac	cgcctcgctg	ggctgggtact	acgttttgcc	gttcgtcctg	1080
tttttacaag	ggatgggtcaa	ctcgacgcgt	ttctcctcca	tgaacaccct	gacgtgaaa	1140
gatctcccg	acaatctggc	gagcagcggc	aacagcctgc	tgtcgatgat	tatgcaattg	1200
tcgatgagta	tccggcgtcac	tatcgccggg	ctgttgctgg	gactttttgg	ttcacagcat	1260
gtcagcgctg	acagcggcac	cacacaaacc	gtctttatgt	acacctggct	tagcatggcg	1320
ttgatcatcg	cccttcgggc	gttcattctt	gccagagtgc	cgaacgatac	gcatacaaat	1380
gtagctattt	cgcggcgaaa	aaggagcgcg	caatga			1416

<210> 125
 <211> 1035
 <212> DNA
 <213> E. Coli

<400> 125						
atggaaattc	gcataatgct	atttatat	atgatgatgg	ttatgcctgt	gagctatgcg	60
gcatgttata	gtgagttatc	tggtcagcac	aacttggttg	ttcaggggga	ttttgcactt	120
actcaaacac	aaatggcgac	atatgagcat	aattttaatg	attcgatcat	cgtaagtaca	180
aatactatca	cccctatgag	cccgctcgat	attattgttg	gactttataa	cgataccata	240
aaattaaatt	tacattttga	atggaccaat	aaaaacaaca	tcacgttgct	aaataatcag	300
accagtttca	ccagtgggta	ttcagttacg	gtgacacctg	cgccagtaaa	tgcaaaagtg	360
aatgtttctg	cggggggcgg	cgggttcagtg	atgattaatg	gtgttgcgac	attatccagt	420
gcttcatcat	cgacacgcgg	gagtgccgca	gtacaatttc	tactgtgttt	attaggtggc	480
aaagtcatggg	atgcatgtgt	aaatagctac	agaaatgcat	tgccacaaaa	tgcaaggtgtc	540
tattccttta	atctgacatt	gtcatacaac	ccgataacca	caacctgcaa	accggacgat	600
ttatttaata	ctttagacag	tattcccggt	tcacaattac	cagccacagg	taacaaagca	660
acaataaata	gtaaacagg	ggatattatt	ctgcgttgta	aaaattttatt	aggtaacaaa	720
aatcaaacat	cacggaaaat	gcagggtgat	ttatcaagtt	ctgacttggt	aaccaacagc	780
aacacaatac	tgaaagggtg	ggaagataat	ggcgtaggat	ttattcttga	aagtaatggt	840
tcgccagtea	cactttttaa	tatcactaac	agcagtaaa	gatatacaaa	tttaaaaggaa	900
gttgccggcga	agtcaaaact	tacagataca	acggtttcaa	ttccgataac	agccagttac	960
tacgtctacg	atacaaacaa	agttaaatct	ggcgcaactg	aggcaaccgc	attaatcaac	1020
gtgaaatac	actaa					1035

<210> 126
 <211> 2481
 <212> DNA
 <213> E. Coli

<400> 126						
atgttgagaa	tgaccccaact	tgcatacaga	atcgtagcgt	tattgctcgg	cattgaagct	60
tatgcagctg	aagaaacctt	tgatacccat	tttatgatag	gtggaatgaa	agaccagcag	120
gttgcaaaata	ttcgtcttga	tgataatcaa	cccttaccgg	ggcagtatga	catcgatatt	180
tatgtcaata	agcaatggcg	cgggaaatat	gagattattg	ttaaagacaa	cccgaagaa	240
acatgtttat	caagagaaagt	tatcaagcgg	ttaggcatta	atagcgataa	cttcgccagc	300
ggtaagcaat	gtttaacatt	tgagcaactt	gttcagggtg	ggagctatac	ctgggatatac	360
gggggttttc	gtctcgattt	cagtgtcccg	caggcctggg	tggaagaact	ggaaagtggc	420
tatgttccac	cggaaaactg	ggagcggggg	attaatgcgt	tttatacctc	ttattatctg	480
agtcagtatt	acagcgacta	taaaacgtcg	ggtaataaca	agagtacata	tgtacgtttt	540
aacagcgggt	taaaatttact	ggggtggcaa	ctgcattctg	atgccagttt	cagtaaaaca	600
aataacaatc	caggggtgtg	gaaaagcaat	accctgtatc	tggaacgtgg	atttgcccaa	660
cttctcggca	cgcttcgcgt	gggtgatatg	tacacatcaa	gcgatatttt	tgattctgtt	720
cgcttcagag	gtgtgcggtt	gtttcgtgat	atgcagatgt	tgccataactc	gaaacaaaat	780
tttacgccac	gggtgcaggg	gattgctcag	agtaacgcgc	tggttaactat	tgaacagaat	840
ggttttgtgg	tttatcagaa	agaggttcct	cctggcccg	tcgcgattac	agatttgag	900
ttggccgggtg	gtggagcaga	tcttgatgtc	agcgtgaaa	aggcggaacg	ctcggtaacc	960

acctatctgg	tgccttatgc	agcgggtgcca	aatatgctgc	aacccggcgt	gtcgaatat	1020
gatttagcgg	cggttcgtag	ccatattgaa	ggggcgagca	aacaaagtga	ttttgtccag	1080
gcggttatc	agtaggttt	taataattta	ttgacgctgt	atgggtggctc	gatggtcgcg	1140
aataattatt	acgcgtttac	tttgggggct	ggctggaata	cacgcattgg	tgccatttcc	1200
gtcgtatgcca	ctaagtcgca	tagtaaacaa	gacaacggcg	atgtgtttga	cgggcaaat	1260
tatcaaattg	cctacaacaa	atattgtgagc	caaacgtcga	cgcgttttgg	tctggcggcc	1320
tgccgttatt	cgctcgctga	ttaccggaca	tttaacgac	acgtttgggc	aaacaataaa	1380
gataattatc	gccgtgatga	aaacgatgtc	tatgacattg	ccgattatta	ccagaacgat	1440
tttgcccgca	aaaatagctt	ttccgccaat	atgagccagt	cattgccaga	aggttggggg	1500
tctgtgtcat	taagtacgtt	atggcgagat	tactgggggc	gtagcggcag	tagtaaggat	1560
tatcagttga	gttattccaa	caacctgcga	cggtataagct	ataccctcgc	ggcaagccag	1620
gcttatgacg	agaatcatca	tgaagagaaa	cgttttaata	tttttatatc	gattcccttt	1680
gattgggggtg	atgacgtttc	gacgcctcgt	cggtcaaatat	atatgtctaa	ctcaacgacg	1740
tttgatgatc	aggggtttgc	ctcaataaat	acgggattat	caggaaacagt	agggagtcgg	1800
gatcagttca	attatggtgt	caacctgagt	catcaacatc	agggaaatga	aacgacagct	1860
ggggcggaatt	tgacctggaa	cgcccggtt	gcgacagtga	atggcagttta	tagtcagtcg	1920
agtaacttatc	gacaggctgg	agccagtgtt	tcagggggca	ttgtcgccctg	gtcgggtggc	1980
gttaaatctgg	cgaaaccgtct	ttccgaaaacg	tttctgtgta	tgaatgcgcc	aggaattaaa	2040
gatgcttatg	tcaatgggca	aaaatatcgc	acaacaaacc	gtaatggagt	ggtgatatac	2100
gacggaaatga	caccttatcg	ggaaaaatcac	ctgatgctgg	atgtgtcgca	aagcgatagc	2160
gaagcagaaat	tacgtggcaa	ccggaaaatt	gccgccctt	atcgccggcg	ggttgtagctg	2220
gttaattttg	ataccgatca	gcgcaagcca	tggtttataa	aagcgttaag	agcagatggg	2280
caatcattaa	cgtttgggta	tgaagtcaat	gatattccatg	gtcataatat	tgccgttggtc	2340
ggccagggaa	gtcagttatt	tattcgacac	aatgaagtac	cgccatcggt	taatgtggca	2400
attgataagc	aacaaggact	ttcatgcaca	atcaccttcg	gtaaagagat	tgatgaaagt	2460
agaaattata	tttgccagta	a				2481

<210> 127

<211> 720

<212> DNA

<213> E. Coli

<400> 127

atggccgcta	tcccattggcg	gccttttaat	ttaagaggca	ttaaaatgaa	aggattatta	60
tctttactca	ttttttctat	ggtccttct	gcacatgccg	gaattgttat	ctacgggacg	120
cgcattattt	acccggcgaga	aaataaagaa	gtgatggtgc	agttgatgaa	ccaggggaaac	180
cggtcttcgc	tgtcgagcg	gtggattgat	gatggcgata	cgctattacc	accagaaaaa	240
ctttcagttc	ctttcatggt	aacgccacca	gtggcaaaaa	taggggcaaa	ttccgggcag	300
caagtataaaa	tcaaaattat	gccgaataaa	ctgcccacta	ataaagaaag	cattttttat	360
ctgaatgttc	tggaatttcc	accaaatagt	ccagagcaag	aaggtaagaa	tgcaactgaag	420
tttgcgatgc	aaaacagaat	taagttgttt	taccggccag	cggttattgc	tccggtaaat	480
aaagcgacat	ttaaaaaatt	gctggtaaat	cgagtgggca	atggtttggt	gataaaaaat	540
gactcagcta	attgggtgac	gatttcggat	gtcaaagcta	ataatgtcaa	agtcatttat	600
gaaactatta	tgattgcccc	cttagaaaag	cagagtgtta	atgtcaaaag	taataatgca	660
aataactggc	atctgaccat	tatcgatgac	catggcaact	atattagtga	caaaatttaa	720

<210> 128

<211> 543

<212> DNA

<213> E. Coli

<400> 128

atgaaacgtt	caattattgc	tgccgctgtc	ttttcttctt	tttttatgag	cgctggagta	60
tttgctgcag	acgttgatac	cggaaacatta	actattaagg	ggaatattgc	agaatctccg	120
tgtaaatctg	aagcgggtgg	tgattcagta	agtattaata	tgccgactgt	accaaccagt	180
gtctttgaag	gtaaagctaa	atattctacc	tatgatgatg	cagtcgggtg	aaccagcagc	240
atgttaaaaa	ttagctgccc	gaaagaagtt	gctgggtgtaa	aactctcggt	gattaccaac	300
gataaaataa	ccggtaacga	taaggcgata	gccagtagca	acgataccgt	gggttactat	360
ctctatttag	gtgataacag	cgatgtcctg	gatgtttctg	caccttttaa	cattgagagt	420
tataaaacag	cggaagggtca	atatgctatt	ccgttttaag	caaaatccct	gaaactgaca	480
gataactcag	tgcaatcagg	tgatgtgtta	tcttctctgg	ttatgcgtgt	ggcgcaggat	540

taa

543

<210> 129
 <211> 339
 <212> DNA
 <213> E. Coli

<400> 129

atgagttcag	agcgagatct	ggtaatttt	cttggcgatt	tttcaatgga	tgtggccaaa	60
gcagttatag	ccggtggtgt	tgcaaccgct	attggaagtc	tggtctcttt	tgctctgtgt	120
agctttggct	ttccagtaat	tcttgtcgga	ggagcaattt	tactgacagg	gatatgtgtg	180
acagttgttt	taaatgaaat	cgatgctcaa	tgccatttat	cagaaaaatt	aaaatatgca	240
attagagatg	gactaaaacg	gcaacaggaa	cttgataaat	ggaaaaggga	aaacatgact	300
ccatttatgt	atgttcttaa	cactccaccc	gtgatatga			339

<210> 130
 <211> 582
 <212> DNA
 <213> E. Coli

<400> 130

atgactgact	acctgttact	gtttgtcgga	actgtactgg	tcaataactt	tgtactggtc	60
aagtttctcg	gtctctgtcc	gtttatgggg	gtttccaaaa	aactggaaac	cgcgatgggc	120
atggggctcg	caacaacggt	tgtgatgacg	ctggcgctta	tttgcgcctg	gcttatcgat	180
acgtggattt	tgatcccaact	taatctgatt	tacctgcgca	ccctggcatt	tattctgggtg	240
attgctgtgg	tcgtgcagtt	caccgagatg	gtgggtgcga	aaaccagccc	ggtgctttac	300
cgctcgtcgg	ggattttttt	gccgcttata	accaccaact	gtgcagtgtc	cggcgtggcg	360
ttgctgaata	tcaatctcgg	gcacaatttc	ttgcagtcgg	cgctgtacgg	tttttccgcc	420
gctgtcggtt	tctcgtcgtg	gatggtgtcc	ttcgccgcca	tccgcgaacg	ccttgcgtgtg	480
gctgatgtcc	cggcaccttt	tcgcggtaat	gccattgcgt	taattaccgc	aggtcttatg	540
tctctggcct	ttatgggctt	tagtggtttg	gtgaagttgt	aa		582

<210> 131
 <211> 579
 <212> DNA
 <213> E. Coli

<400> 131

atgaatgcta	tctggattgc	cggttgcgcg	gtgagcctgc	tgggcctggc	gtttggcgcc	60
attctggggt	atgcctcccg	ccgttttgcg	gtggaagacg	atccggtcgt	tgagaaaatt	120
gacgaaatct	taccgcagag	ccagtgtggt	cagtgcggtt	atcccggtcg	tcgcccctac	180
gcggaagcca	tcagctgtaa	cggtgaaaaa	atcaaccggt	gcgccccagg	tggcgaagct	240
gtgatgctaa	aaattgcccga	gttgcttaat	gtcagagccg	agccgctgga	tggcgaagcg	300
caagagataa	cgccctgcgcg	gatggtggcg	gttattgatg	aaaaataactg	tattggctgc	360
actaaatgta	ttcaggcggtg	tccggtagac	gccatcgttg	gcgctacccg	tgccatgcac	420
acggtaataa	gtgatctctg	tacgggctgc	aatttatgtg	ttgatccgtg	cccgacgcac	480
tgcatctcgt	tgcaaccggt	cgcagaaaca	cctgactcct	ggaaatggga	tctgaacacc	540
attcccggtc	gtatcattcc	cgtggaacac	catgcttaa			579

<210> 132
 <211> 2223
 <212> DNA
 <213> E. Coli

<400> 132

atgcttaagt	tattctctgc	attcagaaaa	aataaaatct	gggatttcaa	cggcggcatc	60
catccaccgg	agatgaaaac	ccagttccaac	ggtacaaccc	tgcgccaggt	acccctggcg	120
cagcgttttg	ttattccact	gaaacagcat	attggcgctg	aaggtgagtt	gtgcgttagc	180
gtcggcgata	aagtattgcg	cggcagcccg	cttaccggtg	gtcggcgcaa	aatgctgcct	240
gttcacgcgc	ccacctcggtg	taccgttacg	gctattgcgc	cccactctac	ggctcactct	300
tcagctttag	ctgaattaag	cgtgattatt	gatgccgatg	gtgaagactg	ctggatcccg	360

cgcgacggct	gggcccatta	tcgcactcgc	agtcgcgaag	agttaatcga	gcgcatacat	420
cagtttgggt	ttgccgggct	gggcggtgca	ggattcccga	caggcggttaa	attgcagggt	480
ggcggagata	agattgaaac	gttgattatc	aacgcgggctg	agtgcgagcc	gtacattacc	540
gccgatgacc	gtttgatgca	ggattgcgcg	gctcaggctcg	tagaggggat	tcgcattctt	600
gcgcataatc	tcgagccacg	cgaattctt	atcggcattg	aagataacaa	accgcaggcg	660
atttccatgc	tcgcgcgggt	gctggcgac	tctaacgata	tttctctgcg	ggtgattcca	720
accaaaatc	cttctggcgg	tgctaaacaa	ttaacctaca	ttctgaccgg	gaagcagggt	780
ccacatggcg	ggcggttcac	cgatatcggc	gtattaatgc	aaaacgtcgg	cactgcttat	840
gcagtgaac	gtgccgttat	tgatggcgag	ccgattaccg	agcgtgttgt	aaccttgact	900
ggcgaagcaa	tcgctcgccc	gggcaacgtc	tgggcacggc	tggggacggc	agtgcgtcat	960
ttattgaatg	atgccggatt	ctgcccctct	gccgatcaaa	tggtgattat	gggtggcccg	1020
ctaattgggt	ttaccttgcc	atggctggat	gtcccggctg	taaagattac	caactgtctg	1080
ttggctccct	ctgccaatga	acttggcgaa	ccacaggaag	aacaaagctg	catccgggtg	1140
agcgccctgt	ctgacgcctg	ccctgcggat	cttttgccgc	aacagttgta	ctgggttcagc	1200
aaaggtcagc	aacacgataa	agctaccacg	cataacattg	ctgattgcat	tgaatgtggg	1260
gcttgcgctg	gggtttgccc	gagcaatatt	ccccgtgtgc	aatatttccg	tcaggaaaaa	1320
gctgaaattg	cggtctattc	tcaggaagaa	aagcgcgccg	cagaagccaa	agcgcgtttc	1380
gaagcgcgcc	aggctcgtct	ggagcgcgaa	aaagcggtc	gccttgaacg	acataagagc	1440
gcagcggttc	aacctgcagc	caaaagataa	gatgcgattg	ctgccgctct	ggcgcggttg	1500
aaagagaaac	aggcccaagg	tacacagcct	attgtgatta	aagcgggcga	acgcccggat	1560
aacagtgcga	ttattgcagc	acgggaagcc	cgtaaaagcg	aagccagagc	gaaacaggca	1620
gaactgcagc	aaactaacga	cgcagcaacc	gttgctgac	cacgtaaaac	tgccgttgaa	1680
gcagctatcg	cccgcgcaaa	agcgcgcaag	ctggaacagc	aacaggtctg	tgccgaacca	1740
gaacaacagc	tcgatccgcg	caaaagccgc	gtcgaagccg	ctattgccc	tgccaaagcg	1800
cgcgaagctg	aacagcaaca	ggctaattgc	gaaccagaag	aacaggtcga	tcgcgcgcaa	1860
gccgcgctcg	aagccgctat	tgcccgtgcc	aaagcacgca	agctggaaca	gcaacagggt	1920
aatgccgagc	cagaacaaca	ggtcgatccg	cgcaaaagcc	ccgtcgaaag	cgctattgcc	1980
cgagccaaag	cgcgcaaacg	ggaacagcaa	ccggctaatt	cggaagcaga	agaacagggt	2040
gatccgcgca	aagctgccc	cgaagcggt	attgcacgcg	ccaaagcagc	caagctggaa	2100
caagcaacagc	ctaattgcgt	accagaagaa	caggttgatc	cgcgcgaaag	ggcagttgcc	2160
gcggctattg	cccgcgctca	ggccaaaaaa	gccgcccagc	agaaggttgt	aaacgaggac	2220
taa						2223

<210> 133
 <211> 1059
 <212> DNA
 <213> E. Coli

<400> 133						
atgggtattca	gaatagctag	ctcccccttat	accataaacc	agcgccagac	atcgcgctatt	60
atgctgttgg	tggtgctcgc	agccgtgccca	ggaatcgag	cgcaactgtg	gttttttgggt	120
tggtgtactc	tcggtcagat	ccgtgttgcca	tcggttagtg	ctctgttagc	cgaagctctc	180
gtactcaaac	tacgcaagca	gtcggtagcc	gcaacggtga	aagataaact	agcatttgctg	240
acaggcttat	tgctggcggt	aagtattccc	cccctcgcg	catggtggat	ggtcgtgctg	300
ggtacgggtg	ttcggtgat	catcgctaaa	cagttgtatg	gcggtctggg	acaaaaccg	360
tttaatcccg	caatgattgg	ttatgtggtc	ttactgatct	cttccccgt	gcagatgacc	420
agctggttac	cgccacatga	aattgcggtc	aacatccctg	gttttatcga	cgccatccag	480
gttattttta	gcggtcatac	cgccagtggt	ggtgatatga	acacactacg	cttaggtatt	540
gatggcatta	gtcaggcgac	accgctggat	acatttaaaa	cctctgtccg	tgccgggtcat	600
tcggttgaac	agattatgca	atatccgatc	tacagcggtg	ttctggcggg	cgctggttgg	660
caatgggtaa	atctcgctg	gctggctggc	ggcgataggt	tgctatggca	gaaagcgatt	720
cgctggcata	ttccccctcag	cttcttagta	acgctggcgt	tatgcgcaat	gttgggctgg	780
ttgtttctac	cagaaacact	ggcagcaccg	caaattcatc	tgctgtctgg	agcgacctg	840
ctcgcgcat	tctttatctt	gactgacccg	gttaccgctt	ctacgaccaa	tcgtggctgt	900
cttatttttc	gcgcgcttgc	gggcttatta	gtctggttga	tcgcaggtt	cgccggctat	960
cctgacggcg	tggtctttgc	cgtcctgctg	gcgaacatca	cgggtccctc	gatcgattac	1020
tacacgcgtc	cgcgctctca	cggccatcgc	aaagggttaa			1059

<210> 134
 <211> 621
 <212> DNA

<213> E. Coli

<400> 134

atgctgaaaa	ctatccgaaa	acacggcatt	acgttggcgc	tatttgcagc	gggttcaaca	60
gggttaactg	cgcccatcaa	ccagatgacc	aaaacgacga	ttgctgaaca	ggccagtctg	120
caacaaaagg	cgttatttga	tcaggtgctg	ccagccgaac	gctataacaa	tgcgctggca	180
cagagttgct	atctggtaac	tgcgccagag	ttaggtaaag	gtgagcatcg	ggtttacatc	240
gccaaaacagg	atgacaaacc	ggtagccgcc	gttctggaag	caaccgcgcc	agatggctat	300
tccggtgcga	ttcagctgct	ggtgggagcc	gattttaacg	gcacggctact	tggcacgcgc	360
gtgacagagc	accacgaaac	gccagggctt	ggcgataaaa	tcgaactgcg	cctttctgac	420
tggatcacc	attttgcggg	taaaaaaatc	agtgggtgcag	atgatgcgca	ctgggcgggtg	480
aagaaaagtg	gtggtgattt	cgaccagttc	accggcgcga	cgattactcc	ccgcgcgggtg	540
gttaatgcgg	taaaacgcgc	cggattgtac	gctcagacgt	taccggcaca	actttctcaa	600
cttctgcct	gtggagaata	a				621

<210> 135

<211> 696

<212> DNA

<213> E. Coli

<400> 135

gtgagcga	ttaaagacgt	tattgttcag	gggttgtgga	aaaacaactc	tgcgctgggtc	60
cagttgctcg	gcctttgtcc	tctgttggcg	gtcacgtcca	ctgccactaa	cgctctgggt	120
ttaggacttg	cgactacgct	ggtactgacg	ctgaccaacc	tgaccatttc	gacgctgcgt	180
cactggacgc	cagccgagat	ccgcattccc	atttacgtga	tgatcatcgc	ctcgggtggte	240
agcgcgtgac	agatgctgat	caacgcctac	gcctttggcc	tgtatcaatc	attagggatt	300
tttatccgcg	tgattgtcac	taactgtatc	gttgtgggcc	gcgctgaagc	cttcgccgcc	360
aaaaaaggtc	cggcgccttc	ggcactggac	ggcttttcaa	ttggtatggg	cgcaacctgc	420
gccatgttgc	tgcctgggttc	actacgcgaa	attatcggca	atggcacatt	gtttgacgggt	480
gcagatgcgc	tgttaggtag	ctgggcacaaa	gtattacgcg	tggagatttt	ccacaccgac	540
tcccccttcc	tgctggcgat	gctgccacca	ggtgcattta	ttggcctggg	actgatgctg	600
gcaggaaaat	acctgattga	tgaagaatg	aaaaagcgcc	gtgctgaagc	agctgcagaa	660
cgtgcattgc	caaacgggtga	aacagggaat	gtctga			696

<210> 136

<211> 636

<212> DNA

<213> E. Coli

<400> 136

atgaataaag	caaaacgcct	ggagatccct	actcgcctgc	gtgagaacaa	tcctcatccc	60
accaccgagc	ttaatttcag	ttcgcccttt	gaattgctga	ttgccgtact	gctttccgct	120
caggcgaccg	atgtcagtgt	taataaggcg	acggcgaaac	tctaccgggt	ggcgaataacg	180
cctgcagcga	tgcttgaact	ggcggttgaa	gggttgaaaa	cctatatcaa	aacgattggg	240
ctttataaca	gcaaagcaga	aaatatactc	aaaacctgcc	gtatcttgct	ggagcagcat	300
aatggcgagg	ttccggaaga	tcgtgctgcg	cttgaagccc	tgcccggcgt	aggtcgtaaa	360
acagccaacg	tcgtattaaa	cactgcattc	ggctggccga	ctattgctgt	cgacacgcac	420
attttccgcg	tttgaatcgc	tactcaattt	gcgcggggga	aaaacgtcga	acaggtagaa	480
gaaaagctac	tgaagtggt	tccagcagag	tttaaagtcg	actgccacca	ttggttgatc	540
ctgcacgggc	gttatacctg	cattgcccg	aagccccgct	gtggctcttg	tattattgaa	600
gatctttgtg	aatacaaga	gaaagttgac	atctga			636

<210> 137

<211> 504

<212> DNA

<213> E. Coli

<400> 137

atgaaaagac	ttcacaagag	gttcctgtta	gctacgtttt	gcgcgttatt	cacagcaact	60
ctccaggccg	ccgatgtcac	tatcactggt	aatggctcgg	tagtcgctaa	accctgcact	120
attcaaacca	aagaagctaa	cgttaatctc	ggggatcttt	atacgcgcaa	tctgcaacaa	180

cctgggtctcg	catctggctg	gcacaatatt	actttgtcat	taaccgattg	tccggttgaa	240
acaagtgcag	tgacggcaat	cggtgacagg	tcaactgaca	atacgggtta	ttacaaaaat	300
gaaggtactg	ccgaaaatat	tcagatagag	ctgagggatg	accaggatgc	tgcgttaaaa	360
aatggcgata	gcaaaacggg	tattgttgat	gagatcactc	gtaatgcaca	gtttccactt	420
aaggcaagag	ctatcacggg	gaatggaaac	gcaagccagg	gaacgatcga	ggcgctaata	480
aatgtgatct	acacctggca	ataa				504

<210> 138
 <211> 531
 <212> DNA
 <213> E. Coli

<400> 138						
atgaaataca	ataacattat	tttcctcggg	ttatgtctgg	ggtaaccac	ctattctgct	60
ttatccgcag	atagcggtat	taaaattagc	gggcgcgctc	tcgattatgg	ctgcacagtc	120
tcacgcgatt	cgcttaattt	taccgtagat	ctccaaaaaa	acagtgccag	acaatttcca	180
acgaccggta	gcacaagtcc	agccgtccct	tttcagatta	cgtaaagtga	atgcagcaaa	240
gggacaacgg	gggttcgggt	tgcatttaac	ggatattgag	atgcagaaaa	taatactttg	300
ttgaaactgg	atgaagggaag	caatcacggc	tccggtttgg	gtatagaaat	attggacgca	360
aatatgcgtc	cgggtgaaact	gaatgatctt	catgccggga	tgacgtggat	cccactggta	420
ccagaacaga	acaatatattt	gccttactcc	gctcgtctga	agtcaactca	gaagtcctgc	480
aatccgggac	tggtgagggc	ttcggcaacc	tttacccttg	aatttcaata	a	531

<210> 139
 <211> 1149
 <212> DNA
 <213> E. Coli

<400> 139						
atgagtgggt	acaccgtcaa	gcctcctacc	ggagacacca	atgagcagac	acaattttat	60
gattatttta	atctgttcta	cagtaagcgt	ggtcaggaaac	aaataagcat	ctctcagcag	120
cttggaattt	acggtacgac	atttttcagt	gccagtcgcc	aaagttaactg	gaacacgtca	180
cgcagcgacc	agcaaatatc	atttgatta	aatgtgccgt	ttggtgatat	tacgacttcg	240
ctgaattaca	gctattccaa	taatatatgg	caaaacgac	gggatcattt	actcgttttt	300
acgcttaaat	ttcccttcag	tcattggatg	cgtacagaca	gtcagtcggc	atttcgtaat	360
tcaaaccgca	gttacagtat	gtcaaacgat	ttgaaaggcg	gcacgaccaa	tctatcgggg	420
gtttatggca	ctctgctgcc	ggataataac	ctgaattata	gcgttcagggt	cggtaacacc	480
cacggagcta	atacatcgtc	tgccaccagt	ggttacagrt	ctcttaatta	tcgtggagct	540
tatggtaata	ctaattgtcg	ttacagtcgg	agtgggtgaca	gcagccagat	ttattacgga	600
atgagtgggt	ggattattgc	tcattgctgat	ggcatcacct	ttggacagcc	gctgggagac	660
acaatgggtc	tggttaaggc	tcctgggtgt	gataatgtca	aaatagagaa	ccagaccgga	720
attcataccg	actggcgctg	ctatgccata	ttaccatttg	cgacagaata	tagagaaaaa	780
cgtgttgctc	ttaacgcgaa	ttcccttgca	gataatgttg	aactggatga	aaccgtggtc	840
actgtcatcc	caactcacgg	tgctattgcc	agagcaacat	ttaatgcaca	aatcggcggg	900
aaagtattaa	tgacgttgaa	gtacggtaat	aagagcgctc	cattcggtgc	aattgtcaca	960
cacggagaga	ataaaaaatg	cagcattgtc	gcggaaaatg	gtcaggttta	tctgactgga	1020
cttccacagt	cagggcaatt	acaggtttca	tggggcgaaag	ataaaaaactc	aaactgtatt	1080
gtcgagtaca	agcttcctga	agtttctcct	ggtaccttac	tgaaccagca	gacagcaatc	1140
tgctgctaa						1149

<210> 140
 <211> 417
 <212> DNA
 <213> E. Coli

<400> 140						
atgattgcga	ttgccgacat	cttgcaagca	ggagaaaagc	taactgctgt	ggcacctttt	60
ctggcgggta	ttcagaacga	ggaacaatac	acccaggcgc	tggaactggg	agatcatctg	120
ctgctcaacg	atcctgaaaa	ccccttgctg	gatctgggtg	gtgccaaaaa	aaccgcgtgg	180
gaagaatcag	cggccgaatt	tgcggaattt	aatgccatgg	ctcaagccat	gcctggcggt	240
atagccgtga	ttcgtaccct	tatggatcaa	tatgggttaa	ccctttccga	tctgccggaa	300

attggcagta aatctatggt gtcacgcggt ttgagcggga agaggaaatt aacgctggaa 360
 caccgtaaaa aattggcaac gcgattcggc atttctcccg ccttgtttat tgattaa 417

<210> 141
 <211> 315
 <212> DNA
 <213> E. Coli

<400> 141
 atgcacctga taactcaaaa agcattgaaa gatgctgcgg aaaaataccg gcaacataaa 60
 acggagttgg tggctctggg gaacacgatt gctaagggat atttcaaaaa acctgagtca 120
 ttaaaagcag tattcccatc tctggataac ttcaaatatc tggataagca ttatgttttc 180
 aatgttgggg gcaatgaatt acgtgttgta gcaatggctc tttttgaatc gcaaaagtgc 240
 tacatacgtg aagttatgac gcataaagaa tacgatttct ttaccgctgt tcatcgctact 300
 aaggggaaaa aatga 315

<210> 142
 <211> 7152
 <212> DNA
 <213> E. Coli

<400> 142
 ttgctatcag tatttacatt ttttcgctgt gctagaaagg gcgcatttat gttagctcgt 60
 tcagggaagg taagcatggc tacgaagaag agaagtggag aagaaataaa tgaccgacaa 120
 atattatgcg ggatgggaat taaactacgc cgcttaactg cgggtatctg tctgataact 180
 caacttgctg tccctatggc tgcggcagca caaggtgtgg taaacgcccg aaccacaaca 240
 ccagttcctg cacaatttgc cattgcaaat gccaatacgg tgcctacac ccttgagcgg 300
 ttggaatcgg cccaaagcgt tgcggaacgt ttcggtattt cgggtggctga gttacgcaa 360
 ctcaaccagt ttctgacgtt tgctcgaagt ttgataatg tccgcagggg tgatgaactg 420
 gatgtcccgg cacaagttag tgaaaaaaa ttaaccccg cgccgggtaa tagcagtgc 480
 aacctcgagc aacagatagc cagtacttca cagcaaatcg ggtctctgct cgccgaagat 540
 atgaacacgg agcaagcggc aaatatggcg cgtggatggg cctcttctca ggcttcaggg 600
 gcaatgacag actggttaag ccgcttcggt accgcaagaa tcacgctggg cgtggatgaa 660
 gatttttagcc tgaagaactc ccagttcgat ttctctccatc cgtggatga aacgcctgat 720
 aatctctttt tcagtcagca tactctccat cgtactgacg agcgtacgca gattaacaac 780
 ggcttaggtt ggcgtcattt cactcccaca tggatgtcgg gcatcaactt ctttttcgac 840
 cagcatctta gccgttacca ctcccgcggc ggcattggcg cggagtactg gcycgactat 900
 ctaaaattaa gcagtaacgg ctatttgcca ctgaccaact ggcgcagcgc acctgaactg 960
 gacaacgatt atgaagcagc cccggccaat ggctgggatg tacgcgcaga aagctggcta 1020
 cccgcctggc cgcaccttgg cggtaaaactg gcttatgaac agtattatgg cgatgaagtg 1080
 gccctgttgc ataaagacga tcggcaaaat aatcctcatg ccataaccgc tggacttaac 1140
 tataccccct tcccgtgat gaccttcagc gcggagcaac gccagggtta acagggcgaa 1200
 aatgacaccc gttttgccgt cgattttacc tggcaacctg gcagcgcaat gcagaaacag 1260
 cttgaccgga atgaagtgcg tgcacggcgt agccttgca gacgcccgtta tgatctggtg 1320
 gatcgcaaca acaatatcgt tctggaatat cgcataaaag aactggttcg cctgaccctg 1380
 acagaccccg tgacagggaa gtcaggagaa gtgaatcac tggtttcgtc gctacaaacc 1440
 aaatatgccc tgaaaggcta taacgtcgaa gccaccgcac tggaaactgc cgggtggcaa 1500
 gtggtcaca cgggttaaaga tattctggtt accctgccgg cttaccggtt caccagtacg 1560
 ccagaaaccg ataacacctg gccgattgaa gtcaccgccc aagatgtcaa aggcaatttg 1620
 tcgaatcgtg aacagagcat ggtggtcgtt caggcaccta cgctaagcca gaaagattcc 1680
 tccgtatcgt taagtaccca aacattgaac gcggattccc attcaaccgc cactactgact 1740
 tttattgcgc atgatgcagc aggtaatcct gttgtcgggc tgggtctctc gacgcgtcac 1800
 gaaggtgttc aggacatcac cctttctgac tggaagata atggtgacgg aagctatacc 1860
 cagatcctga ccacaggagc gatgtctggc acgctgacgc tgatgccaca gctgaatggg 1920
 gtggatgcgg ctaaagcccc cgccgtggtg aatatcattt ctgtttctgc atccccgaact 1980
 cactcgtcaa ttaagattga taaggaccgt tatctctccg gcaatcctat cgaggtgacg 2040
 gtagaactga gagatgaaaa tgacaaacct gtttaaggaa aaaaacagca actgaataac 2100
 gcagtcagca tcgacaacgt gaaaccagga gtcactacag actggaaaaga aaccgcagat 2160
 ggcgtctata agcgaccta taccgcctat accaaaggca gtggacttac tgcgaagcta 2220
 ttaatgcaa actggaatga agatttgcac accgctggat ttatcatcga cgccaaccg 2280
 cagtcagcga aaattgcgac attatctgcc agcaataatg gtgtgctcgc caatgagaat 2340

gcagcaaa	ccgtctcggt	caatgtcgct	gatgaaggaa	gcaacccaat	caatgatcat	2400
accgtcacgt	ttgcggtatt	aagcgggatcg	gcaacttcct	tcaacaatca	aaacaccgca	2460
aaaacggatg	ttaatgggtct	ggcgactttt	gatctgaaaa	gtagtaagca	ggaagacaac	2520
acggttgaag	tcacccttga	aaatggcggtg	aaacaaacgt	taatcgctcag	ttttgtcggc	2580
gactcgagta	ctgcgcaggt	tgatctgcag	aagtcgaaaa	atgaagtgggt	tgctgacggc	2640
aatgacagcg	tcacaatgac	cgcgaccgtc	cgggatgcaa	aaggcaacct	gctcaatgac	2700
gtcatgggtca	ctttcaatgt	taattcagca	qagggcgaac	tgagccaaac	cgaaagtgaat	2760
agccacgacg	ggatcgccac	agctacgctg	accagtttga	aaaatgggtga	ttatagggtt	2820
acggcctctg	tgagctctgg	ttccagggt	aatcaacagg	tgaattttat	cggtgatcaa	2880
agtactgtcg	ccctgaccct	cagtgtgcct	tcaggtgata	tcaccgtcac	caacacagct	2940
ccgcaatata	tgactgcaac	cttgacggat	aaaaatggca	accactaaa	agataaagaa	3000
atcaccttct	ctgtgccaaa	cgacgtcgca	agtaagtctt	cgattagcaa	cgagggaana	3060
ggcatgacgg	atagtaacgg	ggttgcaatc	gcctccctga	ccggcagctt	agcgggacgt	3120
catatgata	tggtctcgct	ggctaacagc	aatgtcagcg	atgcacagcc	aatgacgttt	3180
gtggcgagata	aagacagagc	ggttgcgtt	ttgcaaacat	cgaaagcgga	aatcattggg	3240
aatggcggtg	atgagacaac	tctgacagca	acagtgaag	atccgtcgaa	tcattccggtg	3300
gcggggataa	cggtaaactt	caccatgcc	caggacgttg	cgcaaaactt	tacccttgaa	3360
aataacggta	ttgccatcac	tcaggccaat	ggggaagcgc	atgtcacgct	gaaaggtaaa	3420
aaagcgggca	cgcatacggt	taccgcaacg	ctgggtaata	acaataccag	tgattcgag	3480
ccggtaacat	ttgtggcgga	caaagcctcg	gtcaggttg	tcctgcagat	atcaaaagat	3540
gagatcacag	gtaattggcg	cgatagcgca	acgctaactg	caacgggtta	agatcagttc	3600
gacaatgagg	tgaataatct	tccggtaaac	ttcagctcag	cctcttcagg	actcaccctg	3660
accccgggag	taagtaatac	caacgagtct	ggcatcgcg	aggccactct	cgcagggcgt	3720
gcctttggtg	agaagacggt	tactgcatca	ctggctaata	atgggtgccag	cgacaacaaa	3780
actgtgcatt	ttattggcga	cacagcgcg	gcaaaaatta	tcgagttggc	gcctgtccca	3840
gacagcataa	tcgccgggtac	ccgcgagaac	agctccggca	gcgtcatcac	cgccacagtc	3900
gttgataata	atggctttcc	ggtgaaaggt	gtgactgtga	acttcaccag	caacgcagcg	3960
acagccgaaa	tgacgaacgg	cggtcaagcc	gtgacgaacg	aacagggtta	ggctaccgtc	4020
acttatacca	atacccgctc	ctcgatagaa	tcaggagcga	gaccggatac	cgttgaggcc	4080
agtcctgaaa	atggtagctc	acagcttagc	acatcaatta	atgtcaacgc	tgatgcgtct	4140
acggcacatc	tcaccttgct	acaggcactt	tttgatacag	tctccgcagg	cgagacaacc	4200
agtcctgtata	ttgaggtgaa	ggataattac	ggcaacgggtg	tccccagca	ggaggttaacc	4260
ctcagcggtt	caccaagtga	aggcgtgacc	cccagtaata	acgctatata	tactaccaac	4320
cacgacggca	atttttacgc	aagctttacc	gctacaaaag	ccgggggtta	tcaattgacg	4380
gcaacccctc	aaaatggcga	ttcgatgcaa	caaacagtga	cctatgtgcc	gaacgtcgcg	4440
aatgctgaaa	tcacgctggc	agcctcgaag	gatccgggtga	ttgccgacaa	taacgatctc	4500
acgcaactaa	cagcaacagt	cgctgatata	gagggcaatg	cgatagccaa	cactgaggta	4560
acatttactc	tgccggaaga	tgtgaaggcg	aacttcacgc	tgagcgatgg	cggtaaagtg	4620
attactgatg	ctgaaggcaa	agcgaaagtc	acgctgaaag	gtacaaaagc	aggcgctcat	4680
actgttacag	catcgatgac	tggcggttaag	agtgaagcag	tgggtggtgaa	ctttattgcg	4740
gatacgtca	ctgcgcaggt	taatcttaac	gttacogagg	acaattttat	cgctaataac	4800
gtcgggatga	ccaggctgca	ggcaacagtg	actgatggaa	acggcaaccc	gttagccaat	4860
gagggcggtga	cattcacgct	accggcagat	gtgagcgcaa	gctttactct	cggaacaaggc	4920
ggttccgcca	ttactgatat	caacggcgaag	gctgaagtta	cactgagcgg	tacaaaatcc	4980
ggcacctacc	ccgtgacagt	tagcgtgaac	aattatgggt	tcagtatac	gaaacagggtg	5040
actttgattg	ccgatgctgg	taccgcaaaa	ctagcctcct	taacctctgt	atactcattc	5100
gtcgtcagca	cgaccgaggg	cgcaaccatg	acggcaagcg	tcactgacgc	taacggcaac	5160
ccggtagaag	gcataaaaagt	taatttccgc	ggaacctccg	tcacgctaag	cagcaccagc	5220
gttgaaacgg	atgatcgggg	tttcgctgaa	attcttgtga	caagcaccga	ggtcggactg	5280
aaaacagttt	cagcctctct	ggcagataaa	cctactgaag	tcactctcgcg	attactgaat	5340
gccagtgcag	atgttaattc	tgcgacgatt	accagctctg	agataccgga	aggtcaggta	5400
atggtcgcac	aagacgtagc	agttaaagct	cacgttaacg	accagtttgg	caacccgggt	5460
gcgcataca	ccgtgacatt	cagtgcagag	ccatcctcgc	aaatgatcat	cagccagaat	5520
acggtctcta	ctaatacgca	gggtgtagcc	gaggtcacca	tgacgcccga	aagaaaagggt	5580
tcgtatatgg	tgaagcatc	cctgcccgaat	ggagcctcac	ttgagaaaca	actggagggt	5640
attgatgaaa	aactgacact	cacggcgctc	agtcggctta	tcgggtgcta	tgccctaca	5700
ggcgctactc	tgacggcaac	gctaacctct	gcaaatggca	ctccagtgga	gggtcaggtc	5760
atcaacttta	gcgtaacgcc	agaaggggcg	acgttaagtg	gcggaaaagt	gagaactaac	5820
tcctcaggtc	aggctccagt	cgttttgacc	agcaataaag	tcgggtacata	tacggtgact	5880
gcactcttcc	ataacggcgt	aacaatacag	acacagacaa	ccgtgaaagt	cactggcaac	5940
tcaagcaccg	cccatgttgc	tagctttatc	gctgatccat	cgactatcgc	cgccaccaac	6000

actgatttaa	gtaccttaaa	ggcaacgggt	gaggatggca	gtggtaacct	gatcgaaggt	6060
ctcactgtgt	acttcgcctt	aaaaagcggc	tctgccacat	taacgtcatt	aacagcgggtg	6120
accgatcaaa	acggaatcgc	gacaacaagc	gtgaaaaggag	cgatgacagg	tagcgtcacg	6180
gtaagcgca	tcacgaccgc	tgggtggaatg	caaacagtag	atataacgct	ggtggctggc	6240
ccggcagaca	cctcgcagtc	cgtccttaag	agcaatcggg	catcactgaa	aggggactat	6300
accgatagtg	ctgaattacg	tcttgttctg	cacgatatat	caggcaatcc	gatcaaaagt	6360
tctgaaggga	tggaatttgt	gcaatcaggt	actaacgtgc	cctatataaa	aattagcgca	6420
attgattaca	gtctaataat	caacgggtgat	tacaaagcca	ctgttacagg	aggcggagag	6480
ggtatcgcaa	cgtgatccc	tgtattgaat	ggtgttcac	aagctggtct	gagtaccaca	6540
atacaattca	ctcgcgcaga	agacaaaata	atgagcggta	cagtatcagt	caatgggtact	6600
gacctaccga	caactacatt	cccttcgcag	gggttcaccg	ggcgtatta	tcagttaga	6660
aatgacaact	ttgccccagg	aaaaacggcg	gctgattatg	agttttcaag	ctctgcctcc	6720
tgggtcgatg	ttgatgctac	cggtaaaagt	acatttataa	atgtcggcag	caattcggaa	6780
aggattacgg	cgacgcca	atcaggaggc	cctagctatg	tatacgaaat	ccgtgtgaag	6840
agttggtggg	tgaacgccgg	cgaggcttcc	atgatataca	gccttgctga	aaatttttgc	6900
agcagcaatg	gctacacgct	ccccagagca	aactatttaa	accactgtag	ttcccagagg	6960
atcgggtcac	tgtacagtga	atggggagat	atggggcatt	acacgactga	cgctggtttt	7020
caatacaata	tgtattgggtc	atctagtccc	gcaaaactcaa	gcgaacaata	cgtagtttcc	7080
ctggcaacag	gtgatcaaa	cgtatttgaa	aagcttgggt	ttgcttatgc	gacatgttat	7140
aaaaacctgt	ga					

7152

<210> 143
 <211> 186
 <212> DNA
 <213> E. Coli

<400> 143	
atgagcaaa	gcgcaattata
tgaatttaac	aatccagatc
aactgaaaat	acctctccct
cataaacaca	tagcgtcaac
attcaatgac	ataatgagta
aagatgttgg	ttatgcatac
gtatcattac	tctatgcctg
tcccttaaaa	acccactcat
taagactgaa	tccattcagc
aaatga	

60

120

180

186

<210> 144
 <211> 1197
 <212> DNA
 <213> E. Coli

<400> 144	
atgcagggtg	ctgaacagcg
cattcagcta	gctgaagccc
aggcgaaggc	agttgccact
caggatggtc	cgcagatcga
cttttcggcg	gatatggagc
ggcaaaaaat	gtcggcagaa
ggccttaatg	ggccgtttgc
tctgaacgat	ccggccgcag
gtaccaccgg	cccggtgtac
accacaggtg	cttttggtct
aacggcgggc	tggcatctcg
atatctgggg	aaagaatcgg
gcggaggtta	ctgcccgcct
gggtacgggt	aaagcacggg
cgccggaacg	cgagcaaaac
cgccaattgc	tggctggcag
cgtagcccg	ctgtactggg
agtggcaaac	ccaggcggcg
ttaaacacgg	tcttgcagca
aatagaaaaa	gagcagaaca
ccattatcgc	gaccgatcgc
cagctatatc	agaacgggat
tacttcttca	gttgaagggt
tggaaaaccg	tattaatgcc
agcaaaaccc	ggcagcagct
caacgatgtc	gcggggaaaa
tgaatttat	tgaggcacgg
ttaaagcgac	ttacaaataa
ccagacaaag	tcattgaagc
ttaaaaccgg	cgcgttgccg
aaagtggcaa	gccagcttcc
tgatgaactg	gggtactcct
tactggcccc	gcgggcagat
ttgcaggcgg	cgcactggta
cgttgagtca	tgcctaagca
ccattgatgc	ggcaaaagcg
gcattttatc	ctgacatcaa
cctgatggcc	ttcctgcaac
aggatgcgtt	gcacttaagc
gatctgttcc	gtcattccgc
gcagcaaatg	ggcgttacgg
caggcctgac	gctaccatt
ttcgatagtg	gtcgtcttaa
cgccaatctc	gatatcgcaa
aagccgaaag	caacttgtct
atcggcagct	acaacaaagc
ggtggttgaa	gcgggtgaatg
acgtggcgcg	ggcagccagt
caggttcaga	cactggcgga
gaaaaaccag	catcaggcgc
aaattgagcg	cgatgccttg
cgtgtggtag	gtccttgcga
ggcgcgcttt	aacgcgggca
tcattgctgg	ttcccgcgtc
agcgaagcca	gaatccccgc
gctgcgtgag	cgggccaatg
gcctgttatt	gcaagggcag
tggctggatg	cctccattca
actcactggt	gcgttgggcg
gggggtacaa	acgctga

60

120

180

240

300

360

420

480

540

600

660

720

780

840

900

960

1020

1080

1140

1197

<210> 145
 <211> 291
 <212> DNA

<213> E. Coli

<400> 145

atgtattgcc	acgcgaaact	aaaaaatata	tcgcaacaca	cggtaatctc	cgcgcacctt	60
ttcttacctg	attattcccc	catgaatcgt	gattcctttt	atccagccat	cgctgtttt	120
ccgctgttac	tgatgctggc	cggtgtgctg	cctatgcatg	aaaccgcca	ggcgtaagc	180
cagcaaacgc	ccgctgcaca	agttgacacc	gcattacca	cgcgctgaa	aatggttgc	240
cagacagcca	atggtggctg	gagtatcacg	ataatcaact	cattcctta	a	291

<210> 146

<211> 948

<212> DNA

<213> E. Coli

<400> 146

atgcgtgtgt	tactggcacc	gatggagga	gtgcttgact	ctctggtgctg	tgaattgctg	60
accgaagtta	acgactacga	tctgtgcac	accgagtttg	tccgcgtggt	ggatcaactg	120
ctgccggtaa	aagtctttca	tcgcatttgc	cctgagctac	aaaacgccag	ccggacacca	180
tctggtacgc	tggtgctgct	gcagttgtta	ggtcagttcc	cacaatggct	ggcagagaac	240
gccgcccgtg	cggtggagtt	aggttcctgg	ggcgtggatc	tcaattgctg	ctgcccgtcg	300
aaaacggtta	acggtagcgg	cgccggggcg	acgttactca	aagatcctga	actcatctac	360
caggggtgcaa	aagcgatgcg	tgaagctgta	ccggcgcatt	tgcccgtcag	cgtgaaagtg	420
cgtctgggct	gggacagcgg	tgagaagaaa	tttgaatcgc	ccgatgcggt	tcaacaggct	480
ggcgctacgc	agctggtggt	gcattggcgg	acgaaagagc	agggttaccg	cgcggagcat	540
attgactggc	aggcgattgg	cgatattcgc	cagcggctga	atattccggt	gattgccaac	600
ggtgaaatct	gggactggca	gagcgcgcga	caatgcattg	cgatcagcgg	ctgcgacgca	660
gtgatgattg	gtcgcggggc	gctcaatatt	cccaacctga	gccgggtggt	aaaatataac	720
gaaccgcgaa	tgccgtggcc	ggaggtggtt	gctttgctgc	aaaaatatac	ccgtctggaa	780
aagcagggcg	ataccgggtt	atatcacggt	gcgcggatta	aacagtggtt	gagttatttg	840
cgtaaaaat	acgatgaagc	aacggaatta	tttcagcatg	ttcgggtggt	gaataattcc	900
cctgatattg	caagggctat	tcaggcaatt	gatatcgaga	aactctaa		948

<210> 147

<211> 891

<212> DNA

<213> E. Coli

<400> 147

atgacaatat	cgacaacttc	cacgcccgat	gatgcgggat	ttaaatcttt	tttacgccat	60
ccagacaccg	cgcgggattt	tattgatatt	catcttcccg	cgcgcgtgctg	caaaactgtg	120
gatttaacga	cgcttaaaact	ggaaccaaac	agttttattg	atgaagacct	gcggcaatat	180
tattccgacc	tcttgtggtc	tgtgaaaacg	caggaggagag	tggtttatat	ttatgtagt	240
atagagcacc	aaagtaagcc	ggaagaatta	atggcttttc	gcattgatgctg	ttattccatt	300
gcggcaatgc	aaaaccatct	tgatgcgggc	tataaagagc	ttccattggt	gctcccgatg	360
ctgtttttatc	atggtttcag	aagtccttat	ccttattcac	tctgctggct	tgatgaattt	420
gccgagcctg	ctatagcccg	caaaatatat	tcacgcgctt	ttccgttgggt	ggatattacc	480
gtggtgccgg	atgacgagat	tatgcaacac	cgcaaaatgg	cgctgttggga	gttaattcag	540
aaacatattc	gtcagcgcca	tctgttggtg	ttagtcgacc	aaattgtttc	gctgctagt	600
acagggaaca	ctaatagacag	acagctaata	gccctgttta	attacgtatt	acaaacagg	660
gatgcccagc	gttttcgtgc	atttattggt	gagatagcgg	aacgcgcacc	acaagaaaag	720
gagaaactga	tgaccattgc	tgacagatta	cgtgaagaag	gcgcaatgca	gggcaaacac	780
gaagaagccc	tgcttattgc	tcaggagatg	ctggatagag	gtttagacag	agagttagt	840
atgatggtga	cccgaacttc	accagacgat	cttatcgcgc	aaagccacta	a	891

<210> 148

<211> 1668

<212> DNA

<213> E. Coli

<400> 148

gtggctcaat	tcgtttat	catgcatcgt	gtcggcaaa	tggttccgcc	gaaacgtcat	60
------------	----------	------------	-----------	------------	------------	----

```

atattgaaaa acatctctct gagttctctt cctggggcaa aaattgggtg cctgggtctg 120
aatggcgcg gtaagtccac cctgctgcgc attatggcgg gcattgataa agacatcgaa 180
ggtagaagcgc gtccgcagcc agacatcaag attgggttatc tgccgcagga accgcagctg 240
aaccgcgaac acaccgtgcg tgagtcctatt gaagaagcgg ttccagaagt ggtaaacgcc 300
ctgaaacgcc tggatgaagt gtatgcgctg tacgcgcgac cggatgccga ttttgacaag 360
ctggccgctg aacaaggccg tctggaagag atcattcagg ctccacgacg tcataatctg 420
aacgtacagc tggagcgtgc ggcggatgcg ctacgtctgc cggactggga cgcgaaaatc 480
gctaacctct ccggtgggtga acgtcgtcgc gtagcgttgt gccgcctgct gctggaaaaa 540
ccagacatgc tgctgctcga cgaaccgacc aaccacctgg atgccgaatc cgtggcctgg 600
ctggaacgct tctcgcacga cttcgaaggc accgttgtgg cgattacca cgaaccgttac 660
ttcctcgata acgttgcaag ctggatcctc gaacttgacc gcggtgaagg tattccgtgg 720
gaaggtaact actcctcctg gctggagcag aaagatcagc gcctggcgca ggaagcttca 780
caagaagcgg cgcgtcgtaa gtcgattgag aaagagctgg aatgggtacg tcaaggtact 840
aaaggccgtc agtcgaaaag taaagcacgt ctggcgcgct ttgaagaact gaacagcacc 900
gaatatcaga aacgtaacga aaccaacgaa ctgtttattc cacctggacc gcgtctgggc 960
gataaagtgc tggaaagtca caacctgcgt aaatcctatg gcgatcgtct gctgattgat 1020
gacctgagct tctcgatccc gaaaggagcg atcgtcggga tcacgcgtcc gaacggtgcg 1080
ggtaaatacga cctgttccg tatgatctct ggtcaggaac agccggacag cggcaccatc 1140
actttgggtg aaacggtgaa actggcgctg gttgatcagt tccgtgactc aatggataac 1200
agcaaaaaccg tttgggaaga agtttccggc gggctggata tcataagat cggcaaacacc 1260
gagatgccaa gccgcgccta cgttgcccg ttttaactta aaggggttga tcagggtaaa 1320
cgcgttggtg aactctccgg tggtagcgcg ggtcgtctgc atctggcgaa gctgctgcag 1380
gttgccggca acatgctgct gctcgacgaa ccaaccaacy acctggatat cgaaccctg 1440
cgcgcgctgg aaaaacgccc gctggagttc ccgggctgtg cgatggttat ctgcacgac 1500
cgttggttcc tcgaccgtat cgccacgcac attctggatt accaggtatg aggtaaagt 1560
gagttctctg aaggtaaact taccgagtac gaagagtaca agaaacgcac gctgggcgca 1620
gacgcgctgg agccgaagcg tatcaagtac aagcgtattg cgaagtaa 1668

```

<210> 149
<211> 522
<212> DNA
<213> E. Coli

```

<400> 149
atgtcaaaagc caaatacccc ttttgaagg cgccttgaag tcgtgaatca ctacttcaca 60
actgatgatg gttacaggat catctcggca cgttttggtg tcccccgaa ccaggtcagg 120
acatgggttg cctctctatg aaaacatgga gaaaaagggt taattcccaa acctaaaggc 180
gttagtgctg atccagagtt gcgtattaag gtcgtgaaag ctgtgatcga gcagcacatg 240
tccttaatac aggtctgctg tcaactttatg cttgctggta gtggttctgt agccagggtg 300
ctgaagggtct atgaagagcg cggagaagct ggtttacgcg cgctcaagat tggcaccaaa 360
agaaacattg caatatcagt tgatccagaa aaagcggcat cagcattgga gctgtcaaaa 420
gaccgacgca ttgaggatct tgaaggcaa gttcgatttc ttgaaacgcg gcttatgtat 480
ctaaaaaagc tgaagccctt agctcatccc acgaaaaagt ga 522

```

<210> 150
<211> 852
<212> DNA
<213> E. Coli

```

<400> 150
gtgaaagtac tcaacgagct aaggcagttt tatcctcttg atgagcttct cagggtgctg 60
gagataccgc gcagtaagtt ttattatcat cttaaaggctc tcagcaagcc tgacaagtat 120
gcggacgtta aaaagcgat tagtgagatt tatcacgaga atagaggccg atacggatac 180
cgtagggtta cgtgtctctc tcatcgagaa gggaaacaga ttaaccataa agctgttcag 240
cgctgatgg gaacctctc acttaaaagca gcgattaagg tcaagcgata ccgctcttac 300
agaggagagg tagggcaaac cgccctaat gttctccaaa gagatttcaa ggctacgctg 360
ccaaacgaga agtgggttac cgatgttact gaatttgtag tcaatggcg caagctgtat 420
ttgtctccag taatagatct cttcaacaac gaagttattt cttacagcct ttcggaaaga 480
ccagtgtatg acatggttga gaatatgctc gatcaggcat tcaaaaagct taatcctcac 540
gagcatcctg ttctgcactc tgaccaggga tggcagtatc gtatgagaag atatcaaaat 600

```

atccttaaaag aacatggtat taaacaaagc atgtccagaa aaggcaattg tctggataat	660
gctgtggtgg agtgttttctt tggaaacctta aagtcggagt gtttttatct tgatgagttc	720
agtaataataa gcgaactgaa ggtgctgtt acggaatata ttgaatacta caacagcaga	780
agaatttagcc tgaattataa aggtctgact ccaattgaat atcggaatca gacctatatg	840
cctcgtgttt aa	852

<210> 151

<211> 117

<212> DNA

<213> E. Coli

<400> 151

atgaaagttc gtgcttccgt caagaaatta tgccgtaact gcaaaatcgt taagcgtgat	60
gggtgcatcc gtgtgatttg cagtgcggag ccgaagcata aacagcgcca aggtcga	117

<210> 152

<211> 1332

<212> DNA

<213> E. Coli

<400> 152

atggctaaac aaccgggatt agattttcaa agtgccaaag gtggccttagg cgagctgaaa	60
cgagactgc tgtttgttat cgggtgcgctg attgtgttcc gtattggctc ttttattccg	120
atccctggta ttgatgccgc tgtacttgcc aaactgcttg agcaacagcg aggcaccatc	180
attgagatgt ttaacatgtt ctctgggtgt gctctcagcc gtgcttctat ctttgcctcg	240
gggacatgc cgtatatctt ggcgtcgatc attatccagc tgctgacggg ggttcaccca	300
acgttggcag aaattaagaa agaaggggag tctggtcgtc gtaagatcag ccagtaacac	360
cgctacggta ctctggtgct ggcaatattc cagtcgatcg gtattgctac cggctcgccg	420
aatatgcctg gtatgcaagg cctggtgatt aaccggggct ttgcatttcta cttcaccgct	480
gttgtaagtc tggtcacagg aacctgttct ctgatgtggt tgggcgaaca gattactgaa	540
cgaggtatcg gcaacgggat ttcaatcatt atcttcgccc gtattgtcgc gggactcccg	600
ccagccattg cccatactat cgagcaagcg cgtcaaggcg acctgcactt cctcgtgttg	660
ctgttgggtg cagtattagt atttgcagtg acgttctttg ttgtatttgt tgagcgtggg	720
caacggcgca ttgtggtaaa ctacgcgaaa cgtcagcaag gtcgtcgtgt ctatgctgca	780
cgagacacac atttaccgct gaaagtgaat atggcggggg taatcccggc aatcttcgct	840
tccagtatta ttctgttccc ggcgaccatc cgcgtatggt tcgggggccc tactggttgg	900
aactggctga caacaatttc gctgtatttg cagcctgggc aaccgcttta tgtgttactc	960
tatgcgtctg caatcatctt cttctgttct ttctacacgg cgttgggttt caaccgcgt	1020
gaaacagcag ataacctgaa gaagtcgggt gcatttgtac caggaattcg tccgggagag	1080
caaacggcga agtatatcga taaagtaatg acccgccctga cctggttgg tgcgtgtat	1140
attaccttta tctgcctgat cccggagtct atgctgatg caatgaaagt accgttctac	1200
ttcgggtgga cctcactgct tatcgttgtt gtcgtgatta tggactttat ggctcaagt	1260
caaacctctg tgatgtccag tcagtatgag tctgcattga agaaggcgaa cctgaaaggc	1320
tacggccgat aa	1332

<210> 153

<211> 435

<212> DNA

<213> E. Coli

<400> 153

atgcgtttaa atactctgtc tccggccgaa ggctccaaaa aggcgggttaa acgcctgggt	60
cgtgggtatcg gttctggcct cggtaaaacc ggtggtcgtg gtcacaaaagg tcagaagtct	120
cgttctggcg gtggcgtagc tcgcgggttc gaggtgtgtc agatgcctct gtaccgtcgt	180
ctgcggaat tcggcttcac ttctcgtaaa gcagcgatta cagccgaaat tcgtctgtct	240
gacctggcta aagtagaagg cgggttagta gacctgaaca cgctgaaaag ggctaacatt	300
atcggtatcc agatcaggtt gcggaagtg atcctggctg gcgaagtaac gactccggt	360
actgttcgtg gcctgcgtgt tactaaaagg gctcgtgctg ctatcgaaag tgcgtggcgt	420
aaaatcgagg aataa	435

<210> 154

<211> 180
 <212> DNA
 <213> E. Coli

<400> 154

atggcacaaga	ctattaaaaat	tactcaaaacc	cgcaqtgcaa	tcggctcgtct	gccgaaacac	60
aaggcaacgc	tgcttggcct	gggtctgcgt	cgtattggtc	acaccgtaga	gcgcgaggat	120
actcctgcta	ttcgcgggat	gatcaacgcg	gtttccttca	tcggttaaagt	tgaggagtaa	180

<210> 155
 <211> 504
 <212> DNA
 <213> E. Coli

<400> 155

atggctcaca	tcgaaaaaca	agctggcgaa	ctgcaggaaa	agctgatcgc	ggtaaacgcg	60
gtatctaaaa	ccgttaaagg	tggtcgtatt	ttctccttca	cagctctgac	tgtagttggc	120
gatggtaacg	gtcgcgttgg	ttttggttac	ggtaaagcgc	gtgaagtccc	agcagcgatc	180
cagaaacgca	tggaaaaaagc	ccgtcgcaat	atgattaacg	tcgcgctgaa	taacggcact	240
ctgcaacacc	ctgttaaagg	tggtcacacg	ggttctcgcg	tattcatgca	gccggcttcc	300
gaaggtaccg	gtatcatcgc	cggtgggtgca	atgcgcgcgcg	ttctggaagt	cgctgggggt	360
cataacgttc	tggtctaaagc	ctatgggtcc	accaacccga	tcaacgtggt	tcgtgcaact	420
attgatggcc	tggaataat	gaattctcca	gaaatggctg	ctgccaaagc	tggtaaatcc	480
gttgaagaaa	ttctggggaa	ataa				504

<210> 156
 <211> 354
 <212> DNA
 <213> E. Coli

<400> 156

atggataaga	aatctgctcg	tatccgtcgt	gcgacccgcg	cacgccgcaa	gctccaggag	60
ctggggcgcaa	ctgccttggg	ggtacatcgt	accccgcgtc	acatttacgc	acaggtaatt	120
gcaccgaacg	gttctgaagt	tctggtagct	gcttctactg	tagaaaaagc	tatcgctgaa	180
caactgaagt	acaccggtaa	caaagacgcg	gctgcagctg	tggtgtaaagc	tgctcgctgaa	240
cgcgctctcg	aaaaaggcat	caaagatgta	tcctttgacc	gttccggggt	ccaatatcat	300
ggctcgtgtcc	aggcactggc	agatgctgcc	cgtgaagctg	gccttcagtt	ctaa	354

<210> 157
 <211> 534
 <212> DNA
 <213> E. Coli

<400> 157

atgtctcgtg	ttgctaaagc	accggctcgtt	gttcctgcgcg	gcgttgacgt	aaaaatcaac	60
ggtcagggtta	ttacgatcaa	aggtaaaaac	ggcgagctga	ctcgtactct	caacgatgct	120
gttgaagtta	aacatgcaga	taataacctg	accttcggtc	cgcgtgatgg	ttacgcagac	180
ggttgggcac	aggcttggtac	cgcgcggtgcc	ctgctgaact	caatggttat	cggtgttacc	240
gaaggcttca	ctaagaagct	gcagctgggt	gggtgtaggtt	accgtgcagc	gggttaaaggc	300
aatgtgatta	acctgtctct	gggtttctct	catcctgttg	accatcagct	gcctgcgggt	360
atcactgctg	aatgtccgac	tcagactgaa	atcgtgctga	aaggcgctga	taagcagggtg	420
atcggccagg	ttgcagcgga	tctgcgcgcc	taccgtcgtc	ctgagcctta	taaaggcaag	480
ggtgttcgtt	acgccgacga	agtcgtgcgt	accaaagagg	ctaagaagaa	gtaa	534

<210> 158
 <211> 393
 <212> DNA
 <213> E. Coli

<400> 158

atgagcatgc	aagatccgat	cgcggatatg	ctgacccgta	tccgtaacgg	tcaggccgcg	60
------------	------------	------------	------------	------------	------------	----

WO 00/44906

PCT/US00/02200

aacaaagctg	cggtcacccat	gccttcctcc	aagctgaaag	tggcaatcgc	caacgtgctg	120
aaggagaag	gttttattga	agattttaaa	gttgaaggcg	acaccaagcc	tgaactggaa	180
cttactctga	agtatttcca	gggcaaagct	gttgtagaaa	gcattcagcg	tgtcagccgc	240
ccaggtctgc	gcattctataa	acgtaaagat	gagctgccga	aagttatggc	gggtctgggt	300
atcgagcttg	ttttacctc	taaaggtgtt	atgactgac	gtgcagcgcg	ccaggctggg	360
cttgggtggc	aaattatctg	ctacgtagcc	taa			393

<210> 159

<211> 306

<212> DNA

<213> E. Coli

<400> 159

atggcctaagc	aatcaatgaa	agcacgcgaa	gtaaaacgcg	tagcttttagc	tgataaatac	60
ttcgcgaaac	gcgctgaact	gaaagcgatc	atctctgatg	tgaacgcttc	cgacgaagat	120
cgttggaacg	ctgttctcaa	gctgcagact	ctgccgcgtg	attccagccc	gtctcgtcag	180
cgtaaccgct	gccgtcaaac	aggctcgccg	catggtttcc	tgccggaagt	cggtttgagc	240
cgtattaagg	tccgtgaagc	cgtatgcgc	ggtgaaatcc	cgggtctgaa	aaaggctagc	300
tggttaa						306

<210> 160

<211> 540

<212> DNA

<213> E. Coli

<400> 160

atggcgaaac	tgcatgatta	ctacaaagac	gaagtagtta	aaaaactcat	gactgagttt	60
aactacaatt	ctgtcatgca	agtcctctcg	gtcgagaaga	tcaccctgaa	catgggtgtt	120
gggtgaagcga	tcgctgacaa	aaaactgctg	gataaacgcag	cagcagacct	ggcagcaatc	180
tccgggtcaaa	aaccgctgat	caccaaagca	cgcaaatctg	ttgcaggctt	caaaatccgt	240
cagggctatc	cgatcggtcg	taaagtaact	ctgcgtggcg	aacgcagtgt	ggagttcttt	300
gagcgctga	tactatttgc	tgtacctctg	atccgtgact	tccgtggcct	gtccgctaag	360
tctttcgacg	gtcgtggtaa	ctacagcatg	ggtgtccgtg	agcagatcat	cttccagaa	420
atcgactacg	ataaagtcga	ccgcgttcgt	ggtttggata	ttaccattac	cactactgcg	480
aaatctgacg	aagaaggccg	cgctctgctg	gctgcctttg	acttcccgtt	ccgcaagtaa	540

<210> 161

<211> 315

<212> DNA

<213> E. Coli

<400> 161

atggcagcga	aaatccgtcg	tgatgacgaa	gttatcgtgt	taaccggtaa	agataaaggt	60
aaacgcggta	aagttaagaa	tgtcctgtct	tccggcaagg	tcattgttga	aggtatcaac	120
ctgggttaaga	aacatcagaa	gccgggttccg	gccctgaacc	aaccgggtgg	catcgttgaa	180
aaagaagccg	ctattcaggt	ttccaacgta	gcaatcttca	atgcggcaac	cggcaaggct	240
gaccgtgtag	gcttttagatt	cgaagacggt	aaaaaagtc	gtttcttcaa	gtctaacagc	300
gaaactatca	agtaa					315

<210> 162

<211> 372

<212> DNA

<213> E. Coli

<400> 162

atgatccaag	aacagactat	gctgaacgtc	gccgacaact	ccggtgcacg	tcgcgtaagt	60
tgtatcaagg	ttctgggtgg	ctcgcaccgt	cgctacgcag	gcgtaggcga	catcatcaag	120
atcaccatca	aagaagcaat	tccgcgtggg	aaggtcaaaa	aaggtgatgt	gctgaaggcg	180
gtagtgggtc	gcaccaagaa	gggtgttcgt	cgcccgacg	gttctgtcat	tcgcttcgat	240
ggtaatgctt	gtgttcttct	gaacaacaac	agcgagcagc	ctatcggtac	gcgtattttt	300
gggccggtaa	ctcgtgagct	tcgtagttag	aagttcatga	aaattatctc	tctggcacca	360

gaagtactct aa

372

<210> 163
 <211> 567
 <212> DNA
 <213> E. Coli

<400> 163

atgtttaaag	gacaaaaaac	attggccgca	ctggccgtat	ctctgctgtt	cactgcacct	60
gtttatgctg	ctgatgaagg	ttctggcgaa	attcacttta	agggggaggt	tattgaagca	120
ccttgtagaa	ttcatccaga	agatattgat	aaaaacatag	atcttggaca	agtcacgaca	180
acccatataa	accgggagca	tcatagcaat	aaagtggccg	tcgacattcg	cttgatcaac	240
tgtgatctgc	ctgcttctga	caacggtagc	ggaatgccgg	tatccaaagt	tgccgtaacc	300
ttcgatagca	cggctaagac	aactgggtgt	acgcctttgt	tgagcaaac	cagtgagggc	360
gaagcaactg	gggtcgggtg	acgactgatg	gacaaaaatg	acggtaacat	cgtattaggt	420
tcagccgcgc	cagatcttga	cctggatgca	agctcatcag	aacagacgct	gaactttttc	480
gcctggatgg	aacaaattga	taatgcagtc	gatgtcacgg	caggtgaagt	aaccgctaac	540
gcaacctacg	tgctggatta	taaataa				567

<210> 164
 <211> 1284
 <212> DNA
 <213> E. Coli

<400> 164

atggctgata	caaaagcaaa	actcaccctc	aacggggata	cagctgttga	actggatgtg	60
ctgaaaggca	cgctgggtca	agatgttatt	gatatccgta	ctctcgggtc	aaaagggtgtg	120
ttcacctttg	accagggctt	cacttcaacc	gcacccctcg	aatctaaaa	tacttttatt	180
gatggtgatg	aagggtat	gctgcacgcg	ggtttcccg	tcgatcagct	ggcgaccgat	240
tctaactacc	tggaagt	ttacatcctg	ctgaatgggtg	aaaaaccgac	tcaggaacag	300
tatgacgaat	ttaaaactac	ggtgacccgt	cataccatga	tcacgagca	gattaccgct	360
ctgttccatg	ctttccgtcg	cgactcgcgt	ccaatggcag	tcattgtgtg	tattaccggc	420
gcgctggcgg	cgcttctatca	cgactcgcgt	gatgttaaca	atctcgttca	ccgtgaaatt	480
gcccgcgttc	gcctgctgtc	gaaaatgccg	accatggccg	cgatgtgtta	caagtattcc	540
attggtcagc	catttgttta	cccgcgcaac	gatctctcct	acgcgggtaa	cttctgaat	600
atgatgttct	ccacgcctg	cgaacccgtat	gaagttaac	cgattcttga	acgtgctatg	660
gaccgtatct	tgatcctgca	cgctgaccat	gaacagaacg	cctctacctc	caccgtgcgt	720
accgcctggc	cttcgggtgc	gaacccgttt	gcctgtatcg	cagcaggtat	tgcttccactg	780
tggggacctg	cgcacggcgg	tgctaacgaa	ggcgcgctga	aaatgctgga	agaaatcagc	840
tccgttaaac	acattccgga	atttgttcgt	cgctcgaaag	acaaaaatga	ttctttccgc	900
ctgatgggct	tcggtcaccg	cgtgtacaaa	aattacgacc	cgcgccgcac	cgtaatgcgt	960
gaaacctgcc	atgaagtgtc	gaaagagctg	ggcacgaagg	atgacctgct	ggaagtggct	1020
atggagctgg	aaaacatcgc	gctgaacgac	ccgtacttta	tcgagaagaa	actgtacccg	1080
aacgtcgatt	tctactctgg	tatcatcctg	aaagcgatgg	gtattccgtc	ttccatgttc	1140
accgtcattt	tcgcaatggc	acgtaccggt	ggctggatcg	cccactggag	cgaaatgcac	1200
agtgcgggta	tgaagattgc	ccgtccgcgt	cagctgtata	caggatatga	aaaacgcgac	1260
tttaaaagcg	atatcaagcg	ttaa				1284

<210> 165
 <211> 1434
 <212> DNA
 <213> E. Coli

<400> 165

atgaaagtaa	cgctgccaga	gtttgaacgt	gcaggagtga	tggtggttgg	tgatgtgatg	60
ctggatcggt	actggtacgg	ccccaccagt	cgatctctgc	cggaagcgcc	ggtgcccggtg	120
gttaaagtga	ataccatcga	agaacgtccg	ggcggcgcgg	ctaacgtggc	gatgaatc	180
gcttctctcg	gtgctaagtc	acgcctgggtc	gggttgacgg	gcattgacga	tgacgcgcgc	240
gcgctgagta	aatctctggc	cgacgtcaac	gtcaaatgct	acttcgtttc	tgtaccgacg	300
catccgacca	ttaccaaatt	acgggtactt	tcctcgcaacc	aacagctgat	ccgtctggat	360
tttgaagaag	gtttcgaagg	tggtgatccg	cagccgctgc	acgagcggtat	taatcagggc	420

ctgagttcga	ttggcgcgct	gggtctttct	gactacgcca	aaggtgcgct	ggcaagcgta	480
cagcagatga	tccaactggc	gcgtaaagcg	gggtgtccgg	tgctgattga	tccaaaaggt	540
accgattttg	agcgctaccg	cggtcgctacg	ctgttaacgc	cgaatctctc	ggaatttgaa	600
gctgttgctg	gtaaatgtaa	gaccgaagaa	gagattgttg	agcgcgccat	gaaactgatt	660
gccgattacg	aactctcggc	tctgttagtg	acccgttccg	aacagggtat	gtcgtgctg	720
caaccgggta	aagcgccgct	gcatacgcca	acccaagcgc	aggaagtgtg	tgacgttacc	780
gggtgcggcg	acacggtgat	tggtcgctctg	gcggcaacgc	tggaacgggg	taattcgctg	840
gaagaagcct	gcttctttgc	caatgcggcg	gctggcggtg	tggtcgga	actgggaacc	900
tccacgggtt	cgccgatcga	gctggaaaaa	gctgtacgtg	gacgtgcaga	tacaggcttt	960
ggcgtgatga	ccgaagagga	actgaagctg	gccgtagcgg	cagcgcgtaa	acgtgggtgaa	1020
aaagtgggtg	tgaccaacgg	tgcttttgac	atcctgcacg	ccgggcacgt	ctcttatctg	1080
gcaaatgccc	gcaagctggg	tgaccgcttg	attgttgccg	tcaacagcga	tgccctccacc	1140
aaacggctga	aaggggattc	ccgcccggta	aaaccactcg	aacagcgatg	gattgtgctg	1200
ggcgcaactg	aagcggtcga	ctgggttagtg	tcgtttgaag	aggacacgcc	gcagcgcttg	1260
atcgccggga	tcttgccaga	tctgctgggtg	aaaggcggtg	actataaacc	agaagagatt	1320
gcccggagta	aagaagctcg	ggccaacggt	ggcgaaagtgt	tggtgctcaa	ctttgaagac	1380
ggttgctcga	cgaccaacat	catcaagaag	atccaacagc	ataaaaaagg	ctaa	1434

<210> 166

<211> 2841

<212> DNA

<213> E. Coli

<400> 166

atgaagccgc	tctcttcacc	gttacagcag	tactggcaga	ccgttggtga	gcggctgcca	60
gagcctttag	ccgaggaatc	acttagcgca	caggcggaagt	cagtacttac	ttttagtgtg	120
tttgtgcagg	acagcggtgat	tgcgcatcca	gagtggtgga	cggaaactgga	aagccaaccg	180
ccgcagggcg	acgaatggca	gcattacgcg	gcattggtgc	aggaggcgct	ctgtaatgtg	240
agtgcagaa	ccgggttaat	gcgcgaagctg	cggtatttcc	ggcgccgcat	tatggtgcgc	300
atcgctctgg	cgcaaacgct	ggcactggtt	actgaagaga	gcataattgca	gcagctcagc	360
tatctggcgg	agacgctgat	tgttgccggcg	cgtgactggc	tgtatgacgc	ctgctgccgc	420
gagtgaggaa	cgccgtgcaa	tgccgagggc	gaagcgcaac	cgctgctgat	tttaggcattg	480
ggtaagctcg	gcgggtggga	gctgaatttc	tcctctgata	tcgatctgat	ttttgcctgg	540
ccggaacatg	gttgtacgca	gggtggacgc	cggaactgg	ataacgcgca	gttttttacc	600
cgcatggggc	agcggctgat	ttaaagtgctg	gatcaaccaa	cgaggatgg	cttcgtctat	660
cgctgggata	tgccggctcg	tcctgtttgc	gaaagtggcc	cgctggtgct	gagctttgcc	720
gcgttggaag	attattacca	ggagcagggg	cgcgactggg	agcgttacgc	gatggtcaag	780
gcgcggatta	tgggcgatag	cgaaggcgctc	tatgctaacc	agttgcgtgc	gatgctgcgc	840
ccgtttgttt	tcctgcgtta	catcgatttc	agcgtgatcc	agtcgctgcg	caacatgaaa	900
gggatgattg	cccgtaaggt	gcgtcgacgt	ggtttgaccg	acaatatcaa	actcggcgca	960
ggcggcattc	gcgaaattga	atttatcgtt	cagggtgtcc	agctcattcg	cggcggacgc	1020
gaaccgctcg	tgcaatcgcg	ctctttactg	ccaacgctca	gcgccattgc	cgagctgcat	1080
ctgctttctg	aaaacgatgc	tgaacaattg	cgaaggcgct	atctgttcc	gcggcgctcg	1140
gaaaaacctgc	tgcaaaagcat	taacgacga	caaaaccaga	cgcttctctc	tgatgagctt	1200
aatcgtgcgc	ggctggcggtg	ggcgatggac	tttgctgact	ggccgcaact	gaccggggcg	1260
ctgacccgac	atatgaccaa	gtgctgccc	gtgtttaatg	aattgattgg	cgacgatgaa	1320
agtgaaactc	aggaagagtc	gctgtcggaa	cagtggcggtg	agctgtggca	ggatgcgttg	1380
caggaaagtg	acactacgcc	agtgctggcg	catcttagcg	aggatgatcg	caaacaggtg	1440
ctaaccgctga	ttgccgattt	ccgcaaaagag	ctggataaag	gcaccatcgg	gccgcgagga	1500
cgtcaggtgc	tcgaccatct	gatgccgcat	ctgctaagtg	atgtctgtgc	gcgtgaagac	1560
gctgcccgtta	cgctgtcgcg	cattacggcc	ttgctggtgg	ggattgttac	ccgcaccacc	1620
tatttagaat	tgctcagtga	attccccgcg	gcgcttaaac	atttgatttc	tctgtgtgcc	1680
gcgtgcggca	tgattgccag	ccagctggcg	cgttatccat	tattgctgga	tgaattgctc	1740
gatccaaaca	ccctttacca	gccgacggcg	accgatgcct	accgcgatga	gttgccgacg	1800
tatttgctgc	gcgtgccgga	agatgacgaa	gagcaacagc	ttgagggcgt	gcgtcagttc	1860
aaacaggcgc	agctgttacg	catcgccgca	cgggatatcg	ccggtacgct	accggtgatg	1920
aaagtgcgag	atcacttaac	ctggctggcg	gaagccatga	tagatgccgt	cgttcagcag	1980
gcgtgggttc	aaatgggtgc	ccgctacggt	aagccgaatc	acctgaacga	acgcgaaggg	2040
cggtgggttc	cggtgggtcg	ctacggcaag	ctggcgggct	gggagttagg	ctacagttcc	2100
gatcttgacc	ttatcttcc	ccatgattgc	ccaatggatg	cgatgactga	cggtgagcgg	2160
gaaatcgacg	ggcggcagtt	ttatctcgct	ctggcgcaac	gcattatgca	tctgttcagt	2220

WO 00/44906

PCT/US00/02200

acgcgtacct	cttcggcat	tttgatgaa	gtggatgctc	gactgcgtcc	gtccggggcg	2280
gcgggaatgc	tggtagacatc	cgcagaagca	tttgccgatt	atcagaaaaa	cgaggcctgg	2340
acgtgggaac	atcaggcgct	ggtgctgctg	cgtgtagtgt	acggcgatcc	gcagctcacc	2400
gcgcactttg	acgcagtgcg	tcgcgagatt	atgacgctgc	cgcgtagaag	taaaactctg	2460
caaacggaag	tgcgggaaat	gcgcgagaaa	atgcgcgtc	atctcggcaa	taaacatcgc	2520
gatcgctttg	atatcaaaag	tgatgaagg	ggaattaccg	atctcgaatt	tattacccaa	2580
tatctggtgt	tgcgctacgc	tcataaaaa	ccgaagttaa	cgcgctggtc	agacaacgtg	2640
cgtattctgg	aactactggc	gcaaaacgac	attatggaag	agcagggaag	gatggcgctg	2700
accgctgctt	acactacgct	tcgcgatgaa	cttcacatc	tggcattaca	ggaattgccg	2760
ggccatgtgt	cgaggattg	cttcaccgca	gagcgtgaac	tggtagcggg	aagctggcag	2820
aagtggctgg	tggaagaatg	a				2841

<210> 167
 <211> 1302
 <212> DNA
 <213> E. Coli

<400> 167

atggctcagg	aaatcgaatt	aaagtttatt	gttaatcaca	gtgccgttga	ggcgttgctg	60
gaccatctca	atacgtctgg	cgccgagcac	catgaccccg	tgcagttgct	gaatatttac	120
tacgaaacgc	cggataactg	gctgctgggg	cacgatatgg	gcttacgtat	tcgtggcgaa	180
aacggtcgct	atgagatgac	catgaaagt	gcagggaagag	tgacaggcgg	cttacatcag	240
cgcccggaat	ataacgtggc	gttgagcgaa	ccgacgctcg	acctggcgca	gttaccgacg	300
gaagctctgg	cgaacggcga	attgcccgcc	gatctcgct	cccgctgca	gccgtgttc	360
agcaccgatt	tttatcgca	aaaatggctg	gtggcggtcg	atggtagcca	aattgaaatc	420
gccctcgacc	agggggaagt	gaaagcggtg	gaatttgctg	aacctatctg	tgagctggaa	480
ctggaaactgc	ttagcggcga	cacgcgcgcg	gtgctgaaac	tggcgaaacca	actggtatcg	540
caaacccgat	tacgccaggg	cagcctgagc	aaagcggcgc	gtggctatca	tctggcgag	600
ggcaatccgg	cgcgtgaaat	caaacccgac	accattttgc	atgttgccgg	aaaagccgat	660
gtggaaacag	ggctggaagc	ggcgctcgag	ctggcgtag	cgcaatggca	gtatcatgaa	720
gaactgtggg	tacggcgcaa	cgatgcggcg	aaagaacagg	tgctggcagc	cattagcctg	780
gtccgtcata	cgctgatgct	gttcggtggt	attgtgcgcg	gtaaagcgag	cactcactta	840
cgtgatctgc	tgactcaatg	cgaggcgacc	attgcttctg	cggtgtctgc	cgtgacggcg	900
gtctactcta	ccgaaacggc	aatggcgaa	ctggcgtag	ccgaatggtt	ggtaagcaaa	960
gcatggcagc	catttttaga	tgccaaagcg	cagggcaaaa	tcagcgactc	cttcaaacgc	1020
tttgccgata	tcacatcttc	ccgcatgcc	gctgaactga	aaagcgtttt	ctgccagccg	1080
ttagggcgatc	gctaccgtga	ccagttgcca	cgcctgacgc	gtgatattga	ctcaatactg	1140
ttgctggcgg	gttactatga	tcctgtcgtc	gcgcaagcct	ggctggagaa	ctggcagggg	1200
ctgcatcacg	ctattgcgac	cgggcaacgc	atcgaaattg	aacatttccg	taatgaggca	1260
aaacaatcag	aaccgttctg	gttcacacag	ggaaaacgtt	aa		1302

<210> 168
 <211> 213
 <212> DNA
 <213> E. Coli

<400> 168

atgtccggta	aaatgactgg	tatcgtaaaa	tggttcaacg	ctgacaaaag	cttcggcttc	60
atcactcctg	acgatggctc	taaaagatgtg	ttcgtacact	tctctgctat	ccagaacgat	120
ggttacaaat	ctctggacga	aggtcagaaa	gtgtccttca	ccatcgaaaag	cggcgctaaa	180
ggcccggcag	ctggtaacgt	aaccagcctg	taa			213

<210> 169
 <211> 1572
 <212> DNA
 <213> E. Coli

<400> 169

atgagggaca	ttgtggaccc	tgtattctct	atcggtatct	catcattatg	ggatgagctg	60
cgacatatgc	cagcaggcgg	cgtctgggtg	tttaacgtcg	atcgccatga	agatgctatc	120
agtctggcga	atcaaaacat	tgcatcccag	gctgaaaccg	cacacgtcgc	ggtcattagc	180

atggacagcg	atccggcgaa	aatctttcaa	ttagatgatt	ctcaagggcc	ggaaaaaata	240
aaattatatt	caatgctaaa	tcatgaaaaa	ggtctatact	atgtgacccg	tgatttgacg	300
tggttctatt	atccccataa	ttaccttttt	attcttgttt	gcgcaataa	cgcatggcaa	360
aacattccct	ccgagcggct	tcgctcatgg	ttggataaaa	tgaataaatg	gagcaggtta	420
aaccattgtt	cgcttttggt	aattaatccc	ggaaataata	acgataaaca	attttcattg	480
ttgcttgagg	aataccgttc	actttttggt	cttgccagtt	tgctgtttca	gggtgaccaa	540
catttgctgg	atattgcctt	ctgggtgcaac	gaaaaagggg	tcagcgcccg	tcagcagctt	600
agcgttcagc	aacaaaaatg	tatctggaca	ttagttcaaa	gcgaagagcg	ggagatccaa	660
ccacgcagcg	acgaaaaacg	cattctgagt	aatgttgctg	tactggaagg	tgccgcgcgc	720
ctatcggaac	actggcaact	gttcaacaat	aacgaagtcc	tggtcaatga	agcccgtagc	780
gctcaggcgg	cgacggtggt	cttttcttta	cagcaaaatg	cgcaaatcga	gccactggcc	840
cgacgcatc	ataccctgcg	tcgcccagcg	ggtagtgcga	tgaaaaatcct	cgtagcggaa	900
aataccgcta	gcctgcgcgc	caccgatgaa	cggttggtat	tgccctgctg	tgcaaatatg	960
gttattccgt	ggaatgcgcc	actctcccgt	tgcttgacga	tgatcgaaag	cgtagcaagg	1020
cagaagttaa	gtcgtctatg	gccggaagat	atcactacct	tgctgtcaat	gacccagccg	1080
ctcaaatg	gtggtttcca	gaagtgggat	gtgttctgta	atgccgtcaa	caacatgatg	1140
aataaccctc	tattacctgc	ccacggtaaa	ggcgttctgg	ttgccctacg	tcgggtaccg	1200
ggtatccgcg	ttgaacaagc	cctgacgctg	tgctgcctta	accgtaccgg	cgatatcatg	1260
accattggcg	gtaatcggtt	ggtgctgttt	ctctcattct	gtcggattaa	cgatctggat	1320
accgcgttga	atcatatttt	cccatgtcct	actggcgaca	ttttctcaaa	ccgtatggtc	1380
tggtttgaag	atgatcaaat	cagtgcgcag	ctgggtgcaga	tgctgttgcg	tgccccagaa	1440
caatggggca	tgccgctgcc	tttaacgcaa	agttctaaac	cggtcatcaa	tgccgagcac	1500
gatggtcgcc	actggcgacg	aataaccagaa	cccatgcgac	tgtagatga	tgctgtggag	1560
cgctcatcat	ga					1572

<210> 170

<211> 189

<212> DNA

<213> E. Coli

<400> 170

atgaccatca	gcgatatcat	tgaaattatt	gtcgtttgcy	cactgatatt	tttcccgtcg	60
ggctatctcg	cgcggcactc	tttgcgacgc	attcgcgaca	ccttaacgttt	gttctttgct	120
aaacctcggt	atgttaaacc	ggccgggacg	ttacgcccga	cgaaaaaagc	cagggcaacc	180
aaaaaatga						189

<210> 171

<211> 1680

<212> DNA

<213> E. Coli

<400> 171

atgactcaat	ttacgcaaaa	taccgccatg	ccttcttccc	tctggcaata	ctggcgcggc	60
ctttccggct	ggaacttcta	ttttctgggt	aagttcggcc	tggtgtgggc	gggatattctt	120
aacttccatc	cgctcctcaa	tttggtgttt	gccgcgtttc	tgctgatgcc	ccttccgcgc	180
tacagcctgc	atcgcttgcg	ccactggatt	gccctgccga	tcggcttgcg	tttgttctgg	240
catgacacct	ggttgccctg	cccggaaagc	ataatgagcc	agggttcgca	ggtggcgggg	300
ttcagtaccg	attatttaat	cgaccttgct	acacgcttta	ttaactggca	gatgattggg	360
gccatttttg	ttttattagt	ggcctgggta	ttcctgtcac	aatggattcg	cattaccggt	420
tttgtgtgtg	ccatactgct	atggctgaac	gtacttaacc	tgccgggacc	aagtttctcc	480
ttgtgtgccg	ccggacaacc	gacgaccact	gtaacaacga	cggttggtaa	cgacgcgcca	540
accgttgccg	cgacgggtgg	cgacccggta	gtgggtgata	tgcccgcaca	aactgcaccg	600
ccaacaacgg	cgaaccttaa	cgcttggtcg	aataatttct	ataacgcgga	ggcgaaacgt	660
aaatcgacct	tcccgtcttc	gctgcccgct	gatgctcagc	catttgaact	actggtgatt	720
aacatctgtt	cgctttccctg	gtcggatata	gaagccgcgc	ggttgatgtc	gcattccactg	780
tggtcgcatc	tcgatattga	gttcaagaac	tttaactccg	ccacctccta	cagtggcccg	840
gcggcgatcc	gtttactgcg	cgccagctgc	gggcagactt	cgcacactaa	tctgtatcaa	900
ccggcaataa	acgactgcta	tctgtttgat	aacctttcga	aactgggctt	taccagcac	960
ctgatgcagg	gacataacgg	ccagttcggc	ggttttttga	aagaagttcg	cgaaaaatggc	1020
ggcatgcaga	gcgaattgat	ggatcaaca	aatctgcggg	ttattttgct	gggtttgat	1080
ggttcgccgg	tttatgacga	taccgctgtg	cttaaccgct	ggctggacgt	taccgaaaaa	1140

gataaaaaaca	gccgtagtgc	cacgttctac	aacacgccttc	cactgcatga	cggaaccat	1200
tatccggggg	tcagcaaaac	agcggattac	aaagcgcggg	cgcagaaatt	ctttgatgaa	1260
ctggacgcct	tctttactga	acttgagaaa	tcgggtcgta	aagtgatggt	ggcgtgggtg	1320
ccggaacacg	gcggcgcgct	gaaggcgac	agaatgcagg	tatctggcct	acgtgatatc	1380
cctagcccg	ctatcaccca	cgccccgtt	ggggtgaaat	tcttcggcat	gaaggcaccg	1440
catcaggggg	caccgattgt	catcgaacaa	ccgagcagct	tcctggctat	ctccgatctg	1500
gtggttcg	ttctcgatgg	caagattttc	accgaagaca	atgttgactg	gaaaaaactc	1560
accagtggt	tgccacaaac	agcacgggtc	tccgagaact	caaatgcagt	agttattcaa	1620
taccagata	aaccgtacgt	tcgcctgaac	ggcgcgact	gggtgcctta	cccgcagtaa	1680

<210> 172
 <211> 384
 <212> DNA
 <213> E. Coli

<400> 172						
atggaagggt	caagaatgaa	ataccgcac	gctttagctg	tttctctctt	tgctcttagt	60
gccggtagtt	atgccactac	cctgtgtcag	gaaaaggagc	aaaatatcct	taaggagatc	120
agctatgccg	aaaaacacca	aaaccagaat	cgtattgacg	gtctgaataa	agccctgagt	180
gaagtcgggg	ccaactgttc	agatagccag	ctgcgtgccg	atcatcagaa	gaaaatcgca	240
aagcagaaaag	atgaggtggc	ggaacgccag	caagattttag	ccgagggcga	gcaaaaaggc	300
gatgccgata	agattgccaa	acgcgaacgg	aaactggcag	aagcgccagg	agagctgaaa	360
aagctggaag	gcgcgcgacta	ctaa				384

<210> 173
 <211> 306
 <212> DNA
 <213> E. Coli

<400> 173						
atgtcgaaaag	aacacactac	ggaacatctg	cgctgctgagt	tgaaatccct	ttccgatacg	60
ctggaagagg	tgcttagctc	atctggcgag	aagtcgaaag	aagagttgag	taagattcgt	120
agcaaaagcgg	agcaggcact	gaaacagagc	cgttatcgcc	tggttgaaac	cggtgatgcc	180
attgccaaaac	aaaccctgtg	cgcgccggcg	cgctgccgatg	agtatgtgcg	cgaaaatccg	240
tgacggggcg	tgggcattgg	cgctgcaatc	ggtgtagtgc	tcggcggttct	gctgtcgcgt	300
cgtaa						306

<210> 174
 <211> 405
 <212> DNA
 <213> E. Coli

<400> 174						
atggcgagaca	ctcatcacgc	acaagggccc	ggtaaaagcg	ttctgggcat	cgggcagcga	60
attgtttcta	tcatgggtga	aatggtagag	acacgtctcg	ggctggcggt	ggtggagctg	120
gaagaggaaa	aagcgaatct	ctttcaactt	ttactgatgc	tgggcctgac	gatgcttttc	180
gctgcatttg	gtcttatgag	cctgatgggtg	ctaattattt	gggcgggttg	ccgcgaatat	240
cgctgaatg	cgatgattgc	caccaccggtg	gtgttgctgc	tactggcact	gattggcggt	300
atctggagcg	tacgtaaaac	gcgtaagtct	acgttgctgc	gccatacacg	ccatgagtta	360
gcaaacgata	ggcagctgct	cgaggaggag	tcccgtgagc	agtaa		405

<210> 175
 <211> 300
 <212> DNA
 <213> E. Coli

<400> 175						
gtgagcagta	aagtcgaacg	tgaacgacgt	aaggcgcaac	tgcttagcca	gatccagcaa	60
caacggctgg	atctttccgc	cagtcgtcgt	gaatggctgg	agacaacagg	cgcttacgat	120
cgctcgctga	atatgctgct	aagtctgcgc	tcctggggcg	tggttgccag	tagcgtgatg	180
gcgatctgga	cgattcgcca	tcctaatatg	ctggtccgct	gggccagacg	cggttttggc	240

gtatggagcg cctggcgctct gggtaaaaacg accctcaagc agcaacagct tcgcggttaa 300

<210> 176
<211> 483
<212> DNA
<213> E. Coli

<400> 176

atgattctct	ccatcgacag	caacgacgct	aataccgcgc	cattgcacaa	aaaaacaatc	60
agcagcctga	gtggcgagc	ggagagtatg	atgaaaaaat	tagaagatgt	tggtgtactg	120
gtagcgcgca	ttttaatgcc	gattctgttt	attaccgctg	gctggggaaa	aattactggc	180
tacgcggtga	cccaacaata	tatggaagca	atgggcgtcc	cgggttttat	gctgccactg	240
gtgattctgc	ttgagtttgg	tggtgggtctg	gcaatcctgt	tcggtttcct	gactcgcacc	300
acagccctgt	ttactgcggg	ctttacgctg	ctgacggcat	ttttatttca	cagcaacttt	360
gctgaaggcg	tcaactcgct	gatgttcatt	aaaaacctga	caatttctgg	cggattcctg	420
ctgctggcaa	ttaccggctc	gggcgcgtat	agcatcgacc	gcctgctgaa	taaaaagtgg	480
taa						483

<210> 177
<211> 891
<212> DNA
<213> E. Coli

<400> 177

atgatcaaga	agacaacgga	aattgatgcc	atcttggttaa	atctcaataa	ggctatcgat	60
gcccactacc	agtggctggt	gagtatgttt	cacagcgtgg	tcgcgagaga	tgccagtaag	120
ccagaaaata	cggataacca	ttcttatgga	ctgtgccagt	ttggtcgggtg	gattgatcat	180
ctggggccac	tcgataacga	tgaattacct	tacgttcggc	taatggattc	tgcccaccaa	240
catatgcata	actgtggctg	ggaattaatg	ctggtctattg	ttgaaaatca	ctggcaggac	300
gcgcatttgc	acgcctttca	ggaggggttg	ctttctttta	ctgcggcatt	aaccgattac	360
aaaattttat	tgctgacgat	ccgtagcaat	atggatgttt	tgacgggatt	gccgggtcgt	420
cgggttcttg	atgaatcctt	tgatcatcag	ttacgcaacg	ctgagcctct	gaatctttat	480
ttaatgttgt	tggtatttga	ccgattttaa	ttggttaatg	atacctacgg	gcattttaatc	540
ggcgatgtag	tattacgcac	cctggcaact	tacttagcca	gttgagcgcg	tgattacgaa	600
acggtttatc	gctacggggg	cgaagaattt	atcattattg	tcaaaagcggc	taatgatgaa	660
gaagcatgtc	gtgcagggtg	cagaatttgc	cagttagtcg	ataaccatgc	catcacacat	720
tctgaaggcg	atatcaacat	taccgtgaca	gcagggtgtga	gtcgcgcatt	tcctgaagag	780
cctctggatg	tggtcatttg	aagagcggac	cgggcaatgt	atgagggttaa	gcaaaccgga	840
agaaatcgct	gcattgtttat	tgacgaacaa	aatgtgatta	accgagttaa	a	891

<210> 178
<211> 612
<212> DNA
<213> E. Coli

<400> 178

atgcgccttc	gtgttggtgcc	cgggttttatt	tcaccacctc	cgggcttcgg	tggtctcggc	60
tataccctta	cagcgagagc	ttgtgttaac	atttcaatac	ccttacagtt	gagagtattt	120
gatattgttg	atgtatttac	tccattgttg	aaactttttg	ctaacgagcc	actcgaaaga	180
cttatgtata	cgattatcat	ttttgggtctc	actctctggc	tgataccgaa	agagtttact	240
gtcgcattca	atgcttatac	tgaaatacct	tggtctcttc	agattatcgt	ttttgccttt	300
tctttcgtgg	tcgccatttc	cttctcaaga	ttgcgagcac	atattcaaaa	gcattattca	360
ttactaccag	agcaacgagt	attgcttcgt	ttatctgaga	aagaaatcgc	tgtattttaa	420
gatttcctta	aaacaggaaa	tcttattatc	acttctcctt	gccgtaacct	ggttatgaaa	480
aaattagaac	ggaagggcac	cattcaacat	cagagtgata	gcgcaaacct	ttcttattat	540
ctcgtcaccg	aaaaatactc	ccattttatg	aagttattct	ggaacagcag	gagtagacgt	600
tttaatcggt	ag					612

<210> 179
<211> 177
<212> DNA

<213> E. Coli

<400> 179

gtgcttctcc	aaccatcggc	gcgcaccagt	ttcggtttta	aatgttttgc	ttttggtata	60
cgctcatggca	gtgaacgttc	catcctgggt	ggggaacacg	ccgcacacca	gggattcggt	120
gttgccgagg	tcgatttttt	gcatttttgcg	aatctcacat	cttgttgcta	cgtatag	177

<210> 180

<211> 4281

<212> DNA

<213> E. Coli

<400> 180

atgagcggaa	aaccagcggc	gcgtcagggg	gatatgactc	agtatggcgg	tcccatgtgc	60
cagggttcgg	cagggtgaag	aattggcgcg	cccaccggcg	tggegtgtct	ggtgtgtccg	120
ggcgggatga	cttcgggcaa	cccggtaaat	ccgctgctgg	gggcgaaggt	gctgcccggc	180
gagacggacc	ttgcgtgcc	cgcccgctg	ccgttcattc	tctcccgac	ctacagcagc	240
taccggacga	agacgcctgc	accggtgggc	gttttcggcc	ccggctggaa	agcgccttct	300
gatatccgct	tacagctacg	tgatgacgga	ctgataactca	acgacaaacg	cgggcgagac	360
attcactttg	agccgctgct	gccgggggag	gcggtgtaca	gccgcagtga	gtcaatgtgg	420
ctgggtgcgc	gtggaaggg	agcacagccg	gacggccata	cgctggcgcg	gctgtggggg	480
gcgctgcgcg	cgatatccg	gttaagcccg	catctttacc	tgggcgaccaa	cagcgcacag	540
gggcccgtgt	ggatactggg	gtggtctgag	cggtgtcccg	gtgctgagga	cgtactgcca	600
gcgccgctgc	cgccgtaccg	ggtgcttacc	gggatggcgg	accgcttcgg	gcggacgctg	660
acgtaccggc	gtgaggccgc	cggtgacctg	gccggggaaa	tcaccggcgt	gacggacggg	720
gccggggcgg	agttccgtct	ggtgtgtacc	acgcaggcgc	agcgtgcgga	agaggcccg	780
acctcttcgc	tatcttcttc	tgacagttcc	cgccctctct	cagcctcagc	gttccccgac	840
acactgccc	gtaccgaata	cgccccgac	aggggtatcc	gcctttcggc	ggtgtggctg	900
atgcacgacc	cgccataccc	ggagagcctg	cccgtctgcg	cactggtgcg	gtacacgtat	960
acggaaagcc	gtgaactgct	ggcggtatat	gaccgcagca	atacgcaggt	gcgcgcttct	1020
acgtatgacg	cgagcagccc	gggcccggat	gtggcgaccc	gttacgcggg	aaggccggag	1080
atgcgctacc	gctacgacga	tacggggcgg	gtggtggagc	aactgaaccc	ggcagggtta	1140
agctacogct	atctttatga	gcaggaccgc	atcacogtca	ccgacagcct	gaaccggcgt	1200
gaggtgctgc	atacagaagg	cgggggccgg	ctgaaacggg	tggtgaaaaa	agaactggcg	1260
gacggcagcg	tcacgcgcag	cggttatgac	gcggcaggaa	ggctcacggc	gcagacggac	1320
gcggcgggac	ggaggacaga	gtacggtctg	aatgtggtgt	ccggcgatat	cacggacatc	1380
accacaccgg	acggggcggg	gacgaaattt	tactataaac	acgggaacca	gctgacggcg	1440
gtggtgtccc	cgagcgggct	ggagagccgc	cggaatatg	atgaaccggg	caggctggta	1500
tcggagacat	cgcgacggcg	ggagacagta	cgctaccgct	acgatgacgc	gcacagttag	1560
ttaccggcga	cgacaacgga	tgcgacgggc	agcaccgggc	agatgacctg	gagccgctac	1620
gggcagttgc	tgccgttcac	cgactgctcg	ggctaccaga	cccgttatga	atacagaccgc	1680
ttcgcccaga	tgacggcggt	ccaccgcgag	gaaggcatca	gcctttaccg	ccgctatgac	1740
aaaccgtggc	ggttaacctc	ggtgaaagac	gcacagggcc	gtgaaacgcg	gtatgaatac	1800
aaacgcgcag	gcgacctgac	tgccgttatc	accccggaag	gcaaccggag	cgagacacag	1860
tacgatgcgt	ggggaagggc	ggtcagcacc	acgcaggggc	ggctgacgcg	cagtatggag	1920
tacgatgcgt	ccggacgtgt	catcagcctg	accaacgaga	acggcagcca	cagcgtcttc	1980
agttacgatg	cgctggaccg	gctggtacag	cagggcggct	ttgacggggc	gacgcaacgt	2040
tatcattatg	acctgaccgg	aaaactcaca	cagagttagg	atgagggaat	tgtcatcctc	2100
tggtactacg	atgaatcgga	ccgtatcact	caccgcacgg	tgaacggcga	accggcagag	2160
cagtggcagt	atgatggcca	cggtggctg	acagacatca	gccacctgag	cgaaggccac	2220
cggtgttccg	tccactatgg	ctatgacgat	aaaggccgcc	tgaccggcga	atgccagacg	2280
gtggagaacc	cgagacggg	ggaactgtgt	tggcagcatg	agacgaaaca	cgcatacaac	2340
gagcaggggc	tgcaaaaccg	cgtcacgcgc	gacagcctgc	cgccgggtga	gtggctgacg	2400
tatggcagcg	gttacctggc	gggaatgaag	ctgggcggga	cgccgctggt	cgagtatacg	2460
cgggacaggg	tgaccctgga	gacggtgcgc	agcttcggca	gcatggcagg	cagtaatgcc	2520
gcatacgaac	tgaccagcac	atacaccccc	gcaggccagt	tacagagcca	gcacctgaac	2580
agcctggtat	atgaccgtga	ctacgggtgg	agtgacaacg	gcgacctggt	gcgcacagc	2640
ggcccgcgac	agacgcggga	atacggctac	agcggccagg	gcaggctgga	gagtgtgcgc	2700
accctcgacc	cagacctgga	catccgcata	ccgtatgcca	cggacccggc	gggcaaccgg	2760
ctgccggacg	cggagctgca	cccggacagt	acactcacag	tgtggccgga	taaccgcata	2820
gcggaggatg	cgcactatgt	ctaccgccac	gatgaatacg	gcaggctgac	ggagaagacg	2880

gaccgcatcc	cgggcggtgt	gatacggacg	gacgacgagc	ggacccacca	ctaccactac	2940
gacagccagc	accgcctggt	gttctacacg	cggatacagc	atggcgagcc	actggtcgag	3000
agccgctacc	tctacgaccc	gctgggacgg	cgaatggcaa	aacgggtctg	gcggcgggag	3060
cgtgacctga	cggggtggat	gtcgtctgctg	cgtaaaccgg	aggtgacgtg	gtatggctgg	3120
gacggagaca	ggctgacgac	gggtcgagact	gacaccacac	gtatccagac	ggtatacgag	3180
ccgggaaagt	tcacgccgct	catccgggtc	gagacagaga	acggcgagcg	ggaaaaagcg	3240
cagcggcgca	gcctggcaga	gacgctccag	caggaaggga	gtgagaacgg	ccacggcggtg	3300
gtgttcccg	ctgaactggt	gcggctgctg	gacaggctgg	aggaagaaat	ccgggcagac	3360
cgcgtgagca	gtgaaagccg	ggcgtggctt	gcgcagtgctg	ggctgacggt	ggagcaactg	3420
gccagacagg	tggagccgga	atacacaccg	gcgcgaaaag	ctcatcttta	tactgcgac	3480
caccggggag	tgcgcgtggc	gcttatcagc	gaagacggca	atacggcggtg	gagcgcggaa	3540
tatgatgaat	ggggcaacca	gcttaatgag	gagaaccgcg	atcatgtgta	tcagccgtac	3600
cgtctgccag	ggcagcagca	tgatgaggaa	tcagggtctgt	actataaccg	tcaccggtag	3660
tacgatccgt	tgacggggcg	gtatattact	caggaccgga	tggggttgaa	agggggatgg	3720
aattttatct	agtatccctt	aaatccacta	caacaaattg	accctatggg	attattgcag	3780
acttgggatg	atgccagatc	tggagcatgt	acggggggag	tttgtggtgt	tctttcacgt	3840
ataataggac	caagtaaatt	tgatagtact	gcagatgctg	cgttagatgc	tttgaagaa	3900
acgcagaata	gatctctatg	taatgatatg	gaatactctg	gtattgctgt	taaagatact	3960
aatggaaaat	attttgcac	taaggcagaa	actgataatt	taagaaagga	gtcatatcct	4020
ctgaaaagaa	aatgtcccac	aggtacagat	agagttgctg	cttatcatatc	tcacgggtgca	4080
gatatgtcatg	gcgattatgt	tgatgaattt	ttttcaagta	gcgataaaaa	tcttgtaaga	4140
agtaaagata	ataatcttga	agcattttat	ctcgcaacac	ctgatggacg	atttgagcg	4200
cttaataata	aaggagaata	tatttttatc	agaaatagtg	tcccgggatt	gagttcagta	4260
tgcataccgt	atcatgatta	a				4281

<210> 181

<211> 369

<212> DNA

<213> E. Coli

<400> 181

atgaaatata	gttcaatatt	ttcgatgctt	tcatttttta	tactatttgc	ctgtaatgag	60
acagctgttt	acggttctga	tgaaaaacatt	atrtttatga	ggtagtgga	aaaattacat	120
ttagataaat	actctgttaa	aaatacggta	aaaactgaaa	caatggcgat	acaattagct	180
gaaatataatg	ttaggtatcg	ctatggcgaa	cggattgcag	aagaagaaaa	accatattta	240
attacggaaac	taccagatag	ttgggttgtt	gagggagcaa	agttacctta	tgaagttgag	300
ggtggtgtat	ttattataga	aatttaataag	aaaaatggat	gtgttttgaa	tttctacat	360
agtaataaa						369

<210> 182

<211> 711

<212> DNA

<213> E. Coli

<400> 182

atgctggcgc	tgatggatgc	ggatggaaac	attgcgtgga	gcggggagta	tgatgagtgg	60
ggcaaccagc	tgaatgaaga	gaaccgcgat	cacctgcacc	agccgtaccg	gctgccgggg	120
cagcagtag	ataaggagtc	ggggctgtac	tacaaccgga	accggtacta	cgatccgttg	180
caggggcggt	atatcactca	ggaccgcgata	gggctggagg	ggggatggag	tctgtatgag	240
tatccgctga	atccggtgaa	tggtattgat	ccattagggg	taagtccgcg	agatgtagcg	300
ctaataagaa	gaaaagatca	actaaaccat	caaagagcat	gggatataat	atctgatact	360
tatgaagata	tgaagagatt	aaatttaggt	gggactgac	aatttttcca	ttgtatggca	420
ttttgtcgag	tgtctaaatt	aaatgacgct	ggtgttagcc	gatcgccgaa	agggctgggt	480
tatgaaaaag	agattagaga	ttacgggtta	aatctgttcg	gtatgtacgg	cagaaaagta	540
aagctatccc	attctgaaat	gattgaagat	aataaaaaag	acttggctgt	aaatgacct	600
gggttgacat	gtccatcaac	aacagattgc	tcagatagat	gtagtgatta	tattaatcca	660
gagcataaaa	aaacgataaa	ggctttacaa	gatgctggct	atctcaagta	a	711

<210> 183

<211> 261

<212> DNA

<213> E. Coli

<400> 183

atgctgggcta	tctcaagtaa	tctatcaaag	atgataatat	ttatttttgc	tattataatc	60
attgttgttt	tatgcgtaat	tacttatctt	tatttataca	aagatgaatc	tcttgtaagt	120
aaacattaca	taaactatat	ggcaatacca	gaaaatgatg	gagtttttac	atggctoccca	180
gatttttttc	cgcacgtagc	ggtgcatata	tcaatatata	caaatgtaga	agatgattat	240
ttttttctta	ttttcccta	a				261

<210> 184

<211> 192

<212> DNA

<213> E. Coli

<400> 184

gtgagggcca	gggaacaagt	ggcgaaaatc	gtatcaaaga	atgatccaga	tacaaaaaaa	60
gtgtgggtga	aatatggtaa	gataccaggg	caaggggatg	gtgtaaacct	ttttttgtt	120
ggtgaaatta	atgttacgca	ttattttata	acaaatattg	gagctggatt	gcctgatgct	180
tgtgcagagt	aa					192

<210> 185

<211> 504

<212> DNA

<213> E. Coli

<400> 185

atgccgggca	acagcccgcga	ttatgggcgt	tgccctcaac	acgattttac	gtcacttaaa	60
aaactcaggg	cgcagtcggt	aacctcgcgc	atacagccgg	gcagtgacgt	catcgtctgc	120
gcggaaatgg	acgaacagt	gggctatgct	ggggctaaat	cgcgccagcg	ctggctgttt	180
tacgcgtatg	acagtctccg	gaagacggtt	gttgcgcacg	tattcgggtga	acgcactatg	240
gcgcgcgtgg	ggcgtcttat	gagcctgctg	tcaccctttg	acgtgggtgat	atggatgacg	300
gatggctggc	cgctgtatga	atcccgcctg	aagggaagc	tgcacgtaat	cagcaagcga	360
tatacgcagc	gaattgagcg	gcataacctg	aatctgaggg	agcacctggc	acggctggga	420
cgggaagtgc	tgtcgtttct	aaaatcgggt	gagctgcatg	acaaagtcac	cgggcattat	480
ctgaacataa	aacactatca	ataa				504

<210> 186

<211> 276

<212> DNA

<213> E. Coli

<400> 186

gtggcttctg	tttctatcag	ctgtccctcc	tggtcagcta	ctgacggggg	ggtgcgtaac	60
ggcaaaagca	ccgccggaca	tcagcgctat	ctctgctctc	actgccgtaa	aacatggcaa	120
ctgcagttca	cttacaccgc	ttctcaaccc	ggtacgcacc	agaaaatcat	tgatatggcc	180
atgaatggcg	ttggatgccg	ggcaacagcc	cgcattatgg	gcgttggcct	caacacgatt	240
ttacgtcact	taaaaaactc	aggccgcagt	cggtaa			276

<210> 187

<211> 417

<212> DNA

<213> E. Coli

<400> 187

atgatgacta	aaaccctaat	aaataaatta	ataaaaaatga	tgaatgattt	agactatcca	60
tttgaagcac	cgctcaagga	atcattttatt	gaaagtataa	tccaaataga	atttaattot	120
aattcaacta	attgcctgga	gaagttatgt	aatgaagtta	gtattctttt	taagaatcaa	180
cctgattatc	ttactttttt	aagagcaatg	gatggattcg	aagttaatgg	attacgatta	240
tttagcctct	cgattccaga	accttcagtt	aaaaaccttt	ttgccgtaaa	tgaattttat	300
agaaataatg	atgatttcat	aaaccctgat	ctacaagaac	ggttagtgat	cggggattat	360
agcattttcaa	tatttactta	tgacattaaa	ggtgatgctg	ccaacttact	gatttag	417

<210> 188
 <211> 1179
 <212> DNA
 <213> E. Coli

<400> 188
 atgagtaata ttgtttacct gacagtaacg ggagaacaac aaggaagcat ctccgcaggt 60
 tgtgggactt ctgagtcctac aggtaatcgt tggcagagcg ggcatgagga tgaaatattt 120
 acattctcac tcttaataaa tattaataat acggggcttg gttcacagtt ccatgggtata 180
 acattttgtg aatttaattga taaaagcact ccattattta ttaattccat taacaataat 240
 gaacaattat ttatgggatt tgacttctat cgaataaata gatttggtag attggaaaag 300
 tattattata tacaactaag aggcgcgttt ttatcggcta ttcatcacca gatcattgaa 360
 aaccaactgg atacagaaac aataactatt agttatgaat ttatcctctg tcaacatctt 420
 atcgcaataa ccgagttcag ctatttgcca ctccctgaaa attataaccg tttgttttta 480
 ccaaattcaa aaaaccaaac aaataatcgt ttcaaaacgt taaacagcaa agctattggc 540
 aggcactctg ctgctggtgg cgtatacaat gggaacattg aaggattcag agatactgcy 600
 gaaaaactgg gtggagatgc aataaaagcg tatgatcaaa tactaaatga aaaaacagcg 660
 ggcatagcga tagcaacagc atctattctt ttaacaaagc gttctaattg tgatacatat 720
 acagaaataa atagttactt aggcacactt agaggtcaac aaaaacttct tgatgggtata 780
 gacataatag aaataatata cattaagaga ccttcaaaag acttagctaa cttacgaaag 840
 gagtttaata aaactgtaag aaaaaatttt cttatcaaac ttgcaaaaac ctccgaagca 900
 tctggaagat tcaacgcgca agacctttta agaatgagaa agggcaattg tcctcctaaa 960
 tataatgttc accataaact atctctagat gatgggtgga ctaatgattt cgaaaattta 1020
 gtattaatcg aaaacgaacc atatcataaa gtttttacta acatgcaatc acgaatagct 1080
 aagggaatat tagtaggtga aagcaaaatc actccctggg ccattccatc tggctcaatt 1140
 tatcctcca tgaaaaatat tatggaccac acaaaatga 1179

<210> 189
 <211> 666
 <212> DNA
 <213> E. Coli

<400> 189
 atgggtactg ctttgaacta taatatgcac ggagttaata ttcgctcaga gaatgcagca 60
 aaacctcata cgatgccctc tagatatctt tgcgagtata ttagaagcat tgagaaaaat 120
 ggccacgccc ttgattttgg ctgcggaaaa cttagatatt ctgatgaatt aatcagtata 180
 tttgatgaag ttacttttct agactcgaaa aggcaacttg aaagagagca aattattaga 240
 ggaattaaaa ctaaaattat tgactatgtc ccacgatatt ataaaaatgc aaatacagtt 300
 gctttcgagg atgtcgacaa aataattggg ggttacgatt tcatcctttg ctctaattgt 360
 ctctctgcgc ttcttgtcgc ggatacaatc gacaaaatag ttcttagcat caagagatta 420
 ctaaaatcag gaggtgagac tcttattgta aatcaatata aaagctcata cttcaaaaaa 480
 tacgaaacag gaagaaaaca tctttacgga tacatttaca aaaattcaaa aagtgtttct 540
 tactatggat tactcgatga actcgagtg caagaaatat gttcttcaca tggccttgaa 600
 atattaaagt cgtggagtaa agcaggaagt tcatatgtca ctgttgggag ttgtaatgca 660
 atataa 666

<210> 190
 <211> 705
 <212> DNA
 <213> E. Coli

<400> 190
 gtgaataata tgttcgaacc ccccaaaaat tataatgaaa tgttgccctaa acttcataaa 60
 gcaactttct taaatacgct aatatattgc atacttctag ttatttcaga atacatccct 120
 ttaataacat taccaaccaa gtatgtccca cctattaaag atcatgagag ctttattaat 180
 tgggcactat cttttggtat attaccttgt gcttttgcca tttttgcata ttttaattagc 240
 ggtgcgttag acctacataa caatgcagcc aaactacttc gggtgcgata tctttgggat 300
 aagcatctaa ttataaaacc gttatcacgg agagctggag tcaacagaaa attaaataaa 360
 gatgaagctc acaatgtaat gagcaatcta tattaccctg aagtaagaaa aattgaagac 420
 aaacattata ttgaactctt ctggaataaa gtatactatt tttggatatt ttttgaattt 480

tcgataattg	cattaatttc	cttcctaata	atcttttttt	gcaaacaaat	ggatattttt	540
catgttgaag	gttctttgct	gtcttttatt	ttttttgtaa	ttttatcatt	ctcagtgagt	600
ggtattatct	ttgctttgac	agttaagccc	agaactgaaa	gtcaagtcgg	aaaaatcccc	660
gacgataaaa	taaaagaatt	tttctactaaa	aataacatta	attga		705

<210> 191
 <211> 285
 <212> DNA
 <213> E. Coli

<400> 191

atgtttacta	tcaacgcaga	agtagcgtaaa	gagcagggtta	aggggtgcgag	ccgccgcctg	60
cgtgccgcta	acaagttccc	ggcaatcatc	tacggtggca	aagaagcggc	gctgggtatc	120
gagctggatc	acgacaaagt	catgaacatg	caagctaaag	ctgaattcta	cagcgaagtt	180
ctgaccatcg	ttgttgacgg	taaaagaaatc	aaagttaaa	ctcaggacgt	acagcgtcac	240
ccgtacaaac	cgaagctgca	gcacatcgac	ttcgttcgcg	cttaa		285

<210> 192
 <211> 1977
 <212> DNA
 <213> E. Coli

<400> 192

atggtattgt	tttatcgggc	acactggcgc	gactataaaa	acgatcaagt	gaggatcatg	60
atgaattctga	cgactctgac	ccaccgcgat	gcgttggtgc	tgaatgcgcg	ctttaccagc	120
cgtgaagagg	ccatccacgc	gttgactcaa	cgcttggtgc	ctctggggaa	aatttccagt	180
actgagcaat	ttctggaaga	agtgtatcgc	cgtgaaaagc	ttggcccggc	cgcccttaggt	240
gaaggggttg	ctgtgccgca	tggcaaaact	gctgcggtta	aagaagcggc	gtttgcggtc	300
gccacactca	gcgagccgct	tcagtgggaa	ggcgttgatg	gcccgggaagc	agttgattta	360
gtggtgctgc	tggcgattcc	ccccaatgaa	gcgggtacta	cgcatatgca	actgctgaca	420
gcgctgacca	cgcgccctgc	ggatgatgag	attcgggcgc	gtatacagtc	ggcgacgacg	480
cctgatgagt	tgctctcgcc	gctggatgac	aaggggagca	cgcaaccttc	tgccctcttt	540
tccaacgcgc	caactatcgt	ctgcgtaacg	gcctgtccgg	cgggtattgc	tcacacctat	600
atggctgcgg	aatatctgga	aaaagccgga	cgcaaaactc	gcgtaaatgt	ttacgttgaa	660
aaacaaggcg	ctaacggcat	tgaagggcgt	ttaacggcgg	atcaactcaa	tagtgcaacc	720
gcctgtattt	ttgcggctga	agtgcgccat	aaggagagtg	agcgttttaa	tggcattccc	780
gcgctttcag	tgccctgttc	cgagccgatt	cgccatgcag	aagcgttgat	ccaacaagcg	840
cttaccctca	agcgtagcga	tgagacgcgt	accgtacagc	aagatacgca	accggtgaaa	900
agtgtcaaaa	cggagctgaa	acaggcactg	ttgagcggaa	tctcttttgc	cgtaccggtg	960
attgtcgcgg	ggggcaccgt	gctggcggtc	gcggtattac	tgtcgcaaat	cttcgggcta	1020
caagatctgt	ttaatgaaga	aaactcctgg	ctgtggatgt	accgcaagct	ggcgggcggg	1080
ctgctcggaa	ttttgatggt	accggtgctc	gcggccctata	ccgcctattc	tctggcagat	1140
aaaccggcgt	tagcgccagg	ctttgcggtc	ggacttgccg	ccaacatgat	cggctccggg	1200
tttctcgccg	cggctcgttg	cggattgata	gccggttact	tgatgcgctg	ggtgaaaaat	1260
cacttgcgctc	ttagcagtaa	attcaatgga	ttcctgacct	tttatctcta	cccgggtgctc	1320
ggtacgttgg	gagcgggcag	tctgatgctg	tttgtgtgtg	gggaacctgt	cgccctggatc	1380
aataactcgc	ttaccgcctg	gctgaacggt	ctgtcaggaa	gtaacgcgct	ggtgctgggt	1440
gccattctcg	gttttatgtg	ttcctttgac	cttggaaggc	cagtgaataa	agccgcttat	1500
gcattctgcc	tgggcgcaat	ggcgaacggc	gtttacggcc	cgtatgccaat	tttcgcctcc	1560
gtcaaaatgg	tttcggcatt	taccgtaacc	gcttccacga	tgctcgaccc	gcgcctgttt	1620
aaagagtttg	aaattgagac	cgggaaatcc	acctggctgt	tagggctggc	aggtattacc	1680
gaagggggcga	tcccgatggc	gattgaagat	ccgctgcggg	ttattggttc	gtttgtgctg	1740
ggctctatgg	taacgggcgc	tattgtcggg	gcgatgaata	tcggcccttc	gacacccggg	1800
gccggcattt	tctcgctctt	tttacttcat	gataatggcg	cgggcgggtg	tatggcggca	1860
attggctggt	ttggcgcggc	attgggtggg	gctgcaatct	cgactgcaat	tctcctgatg	1920
tggcggcgctc	acgcggttaa	gcatggcaac	tatctgactg	atggcgtaat	gccataa	1977

<210> 193
 <211> 2634
 <212> DNA
 <213> E. Coli

<400> 193

atgaaagcag	tatctcgcgt	tcacatcacc	ccgcatatgc	actgggatcg	agagtgggtat	60
ttcaccaccg	aagagtcaag	tattctgctg	gtcaataata	tggaagagat	cctgtgccga	120
ctggaaacag	acaacgaata	caaatattac	gtactcgacg	ggcaaacggc	gacccctcgaa	180
gattatttcg	cggtgaaacc	ggaaaacaaa	gaccgtgtga	agaaacaggt	agaagccggc	240
aagttgatta	tcggccctcg	gtataccacg	accgatacca	cgattgttct	tcggaatcc	300
atcgctcgta	atctgatgta	cggaatgcgt	gactgcctcg	cgtttgccga	gccgatgaaa	360
ataggttatt	taccagattc	ctttggcatg	tcggggcaac	tgccgcataat	ctacaatgga	420
tttggcatta	cccgcaccat	gttctggcgc	ggatgttcgg	agcgccacgg	tactgataaa	480
accgagtttt	tgtggcaaaag	cagtgcaggt	agcgaagtga	cgggccaggt	gctgccgctg	540
ggctacgcca	tcggtaagta	cttacctgcc	gacgaaaacg	gattacgtaa	acgcctcgac	600
agttattttg	acgtgctgga	aaaagcgctt	gtaaccaaag	agattttgct	gccgaatggg	660
catgaccaga	tgccattgca	gcaaaatata	ttcgaagtga	tggaataagct	acgtgagatc	720
taccctcaac	gtaagtttgt	gatgagccgc	tttgaagagg	tatttgagaa	gatcgaagcg	780
cagcgagata	atctggcaac	cctgaaaggg	gaattttattg	atggcaataa	tatgcgcgtg	840
catcgacaca	tcggttctac	gcgtatggat	atcaaaattg	cccacgcgcg	tattgaaaaa	900
aagattgtta	atctgctgga	accgctggca	acactggcct	ggacgttggg	ttttgaatac	960
caccacggct	tgctggagaa	aattgtgaaa	gagatcttaa	aaaatcatgc	ccacgacagt	1020
atcggtgct	gctgtagtga	caaagttcat	cgcgaaatcg	tcgcccgcct	cgaactggct	1080
gaagacatgc	cgataaatct	gattcgtttc	tacatgcgca	aaattgccga	caacatgccg	1140
cagagcgacg	ccgacaaact	cgtcctgttt	aacctgatgc	cctggccgcg	tgaagaagtt	1200
atcaaacacca	ctgtgcggct	gcgcgccacg	cagtttaatt	tcgcccgcga	tcgcggtcag	1260
cctgtaccgt	attttattcg	ccatgcccg	gagatcgatc	caggccta	cgatcggcaa	1320
atagttcatt	acggttaatta	cgatcccttt	atggagtttg	atatacagat	caaccagatt	1380
gtcccttcta	tggtctatcg	cacgctttat	atcgaagcga	atcagcctgg	caacgtaatt	1440
gcggcaaaaa	gtgacgctga	agggatactg	gaaaatgctt	tctggcaaat	tgcgctcaat	1500
gaggtatggt	ctctgcaact	ggtagataaa	gacagcggtg	tgcgctatga	ccgggtattg	1560
caaatggaag	aaagctctga	tgatggtgat	gaatatgact	attcaccggc	aaaagaagag	1620
tggtgtaatta	ccgcagcgaa	cgcaaaacgc	caatgcgata	ttattcatga	agcctggcag	1680
agcagggctg	ttatccgcta	tgacatggca	gtgcgcgtca	atttgtcaga	acgcagcgcc	1740
cggaacaacca	ctggcagagt	aggggtgtgt	ttggttgtca	ctcttagtca	taacagcagg	1800
cgtattgatg	tgatatcaaa	tcttgataac	caggctgacg	atcatcgctt	tcgtgtcctg	1860
gtccctacac	cttttaacac	cgacagtgtt	ctggcagata	cgcagttttg	ttcgctaacc	1920
cgcccgctga	acgacagtgc	aatgaacaac	tggcagcaag	aaggctggaa	agaagccggc	1980
gttccggtag	ggaatatgct	caactatggt	gccttacagg	aagggcgtaa	cggcagtggt	2040
gtcttttagcg	aagggttacg	tgaatttgaa	gtcatcggtg	aagagaagaa	aacctttgcc	2100
attacgttgc	tcgctggcgt	gggttactg	ggcaaaagaa	atctgctttt	aaggcctggg	2160
cgcccttcgg	gaattaaaaa	gccagtcctg	gactcacaac	tacgtggtct	gctttcttgt	2220
cgccctaagtt	tattgagtta	taccggtacg	ccaaccggcg	ctggtgtagc	tcagcagggc	2280
cgagcatggc	tgactccagt	acagtgttac	aacaaaatcc	catgggatgt	gatgaagctc	2340
aacaaagccg	gattcaacgt	gccggaaagt	tatagtttgt	tgaaaatgcc	cccagtgagg	2400
tgccgtgataa	gcgcacttaa	gaaagctgaa	gaccgacaag	aagtgatatt	acggctgttt	2460
aatccggctg	aatcagcaac	ctgtgatgcg	actgttgctt	tcagtcgcga	ggtgatattc	2520
tgctcagaaa	cgatgatgga	tgaacacatt	accaccgagg	aaaatcaagg	ttcaaatcta	2580
tcggggcctt	ttttaccggg	ccagtcacgg	acgttcagtt	accggcttgc	ctga	2634

<210> 194

<211> 1572

<212> DNA

<213> E. Coli

<400> 194

atgatgttag	atatagtcga	actgtcgcgc	ttacagtttg	ccttgaccgc	gatgtaccac	60
ttcctttttg	tgccactgac	gctcgggtatg	gcgttcctgc	tgccatttat	ggaaacggtc	120
tacgtcctct	ccggcaaaaca	gatttataaa	gatatgacca	agttctgggg	caagttgttt	180
ggtatcaact	tcgctctggg	tgtggctacc	ggctcgacca	tggaattcca	gttcgggact	240
aactggtctt	actattccca	ctatgtaggg	gatattctcg	gtgcgcgcgt	ggcaatcgaa	300
ggtctgatgg	ccttcttcct	cgaatccacc	ttttaggtgc	tgcttctctt	cggttggtat	360
cgctcgggta	aagttcagca	tatgtgtgtc	acctggctgg	tgccgctcgg	ttcaaacctg	420
tcgcgactgt	ggattctggt	tgcaaacggc	tggtatgcaa	acccaatcgc	gtccgatttc	480

aactttgaaa	ctatgcgtat	ggagatggtg	agcttctccg	agctggtgct	taaccgggtt	540
gctcaggatga	aattcggtca	cactgtagcg	tctggttatg	tgactggcgc	gatgttcac	600
ctcggatatca	gcgcattgta	tatgctgaaa	ggtcgtagct	tcgccttcgc	taaaccgtcc	660
tttgctatcg	ctgccagctt	cggatggtg	gctgttctgt	ctgttattgt	tctgggtgat	720
gaatccggct	acgaaatggg	cgacgtgcag	aaaaccaaac	tggtcgctat	tgaagccgag	780
tgggaaacgc	aacctgcgcc	tgctgccttt	actctgttcg	gcattcctga	tcagggaagag	840
gagacgaaca	aatttgcgat	tcaqatccct	tacgcactgg	ycatcattgc	aacgcgttcc	900
gtggataccc	cggttatcgg	cctgaaagag	ctgatggtgc	agcatgaaga	acgcattcgt	960
aacgggatga	aggcgactc	tctgctcgaa	caactgcgtt	ctggttctac	cgaccaggcg	1020
gttcgtgacc	agttcaatag	catgaagaaa	gacctcgggt	acggtctgct	gctgaaacgc	1080
tatacgccaa	acgtggctga	tgcgactgaa	gcgcagattc	aacaggcaac	caaagactcc	1140
atccccgctg	tagcgccgct	gtactttcgg	ttccgtatca	tggtggcggtg	tggcttcctg	1200
cttctggcaa	tcatcgcgct	ctctttctgg	agtgtcatcc	gcaaccgcat	tggcgagaaa	1260
aaatggcttc	tgccgcgcgc	gctgtacggt	attccgctgc	cgtggattgc	tgtagaagcg	1320
ggctgggttcg	tggtgaaata	tgccgcgcaa	ccgtgggcta	tcggtgaaat	gctgccgaca	1380
gctgtggcga	actcgtcact	gaccgcagcg	gatctcatct	tctcaatggt	gctgatttgc	1440
ggcctgtata	ccctgttccct	ggtggcgaga	ttgttcttaa	tgttcaagtt	tgccagccctc	1500
ggcccaagca	gcctgaaaac	cggtcgctat	cactttgagc	agtcttccac	gactactcag	1560
ccggcacgct	aa					1572

<210> 195

<211> 1140

<212> DNA

<213> E. Coli

<400> 195

atgatcgatt	atgaagtatt	gcgtttttatc	tggtggctgc	tggttggcgt	tctgctgatt	60
ggttttgcag	tcactgacgg	tttcgacatg	gggggtgggca	tgctcaccgc	tttctcgggt	120
cgtaacgaca	ccgagcgctc	aattatgatt	aactccattg	caccacactg	ggacggtaac	180
cagggtttggc	tgatcaccgc	gggcggcgca	ctctttgctg	cctggccgat	ggctctatgcc	240
gctgcgttct	ccggttctta	tgtggcgatg	atcctcgtgc	tggtcgtctt	gttcttccgt	300
ccggtcggtt	ttgactaccg	ctccaagatt	gaagaaaccc	gctggcgtaa	catgtgggac	360
tggtggcatct	tcattggtag	cttcgttccg	ccgctggtaa	ttggtgtagc	gttcggtaac	420
ctgtttgcagg	gcgtaccggt	caacgttgat	gaatatctgc	gtctgtacta	caccggtaac	480
ttcttccagt	tgcttaaccc	gttcggcctg	ctggcaggcg	tggtgagcgt	agggatgac	540
attactcagg	gcgcaaccta	tctgc aaatg	cgtaccgtgg	gcgaactgca	cctgcgtacc	600
cgttgcaacg	ctcaggtggt	tgccgtggtg	acactggtct	gtttcgcact	ggctggcgta	660
tggttgatgt	acgggtatcga	tggttatgtc	gtgaaatcga	caatggacca	ttacgcagcc	720
tctaaccacc	tgaataaaga	agtgtgtcgt	gaagctggcg	catggtcggt	taacttcaac	780
aacacgccaa	ttctgtgggc	tattccggca	ctgggtgtgg	ttctgcgcgt	gctgaccatc	840
ctgactgcac	gtatggataa	agccgcgtgg	gcgttttgtt	tctcctccct	gacgctggcc	900
tgcatcatcc	tgacagccgg	tatcgcaatg	ttcccggttg	tgatgccgtc	cagcaccatg	960
atgaacgcaa	gtctgacaat	gtgggatgca	acttccagcc	agctgacgct	taacgtcatg	1020
acctgggttg	cgtgtgttct	ggtaccgatc	attctgctct	acaccgcctg	gtgttactgg	1080
aaaatgttcg	gtcgtatcac	caaagaagat	attgaacgta	acaccactc	tctgtactaa	1140

<210> 196

<211> 1371

<212> DNA

<213> E. Coli

<400> 196

atggaaattat	cctcactgac	cgccgtttcc	cctgtcgatg	gacgctacgg	cgataaagtc	60
agcgcgctgc	gcgggatttt	cagcgaatat	ggtttgctga	aattccgtgt	acaagttgaa	120
gtacgttggc	tgcaaaaact	ggccgcgcac	gcagcgatca	aggaagttcc	tgcttttgct	180
gccgacgcaa	tcggttacct	tgatgcaatc	gtcgccagtt	tcagcgaaga	agatgcggcg	240
cgcatcaaaa	ctatcgagcg	taccactaac	cacgacgtta	aagcggttga	gtatttcctg	300
aaagaaaaag	tgccggagat	cccggaaactg	cacgcggttt	ctgaattcat	ccactttgcc	360
tgtacttccg	aagatatcaa	taacctctcc	cacgcattaa	tgctgaaaac	cgccggtgat	420
gaagtgatcc	tgccatactg	gcgtcaactg	attgatggca	ttaaagatct	cgccgttcag	480
tatcgcgata	tcccgcgtct	gtctcgtacc	cacgggtcagc	cagccacgcc	gtcaaccatc	540

```

ggtaaagaga tggcaaacgt cgcttaccgt atggagcgcc agtaccgcca gcttaaccag 600
gtggagatcc tcggcaaaat caacggcgcg gtcggtaact ataacgcccc catcgccgct 660
taccgggaag ttgactggca tcagttcagc gaagagttcg tcacctcgct gggatttcag 720
tggaaccggt acaccacca gatcgaaccg cagactaca ttgccgaact gtttgattgc 780
gttgcgcgct tcaacactat tctgatcgac tttgaccgtg acgtctgggg ttatatcgcc 840
cttaaccact tcaaacagaa aaccattgct ggtgagattg gttcttccac catgccgcat 900
aaagttaacc cgatcgactt cgaaaaactcc gaagggaatc tgggcctttc caacgcggta 960
ttgcagcatc tggcaagcaa actgccggtt tcccgctggc agcgtgacct gaccgactct 1020
accgtgctgc gtaacctcgg cgtgggtatc ggttatgcct tgattgcata tcaatccacc 1080
ctgaaaaggcg tgagcaaaact ggaagtgaac cgtgaccatc tgctggatga actggatcac 1140
aactgggaag tctggtgctga accaatccag acagttatgc gtcgctatgg catcgaaaaa 1200
ccgtacgaga agctgaaaga gctgactcgc ggtaagcgcg ttgacgccga aggcatagaag 1260
cagtttatcg atggtctggc gttgccagaa gaagagaaa cccgcctgaa agcgatgacg 1320
ccggctaact atattggtcg agctatcacg atggttgatg agctgaaata a 1371

```

<210> 197
 <211> 186
 <212> DNA
 <213> E. Coli

<400> 197

```

atgctgattc tgactcgtcg agttggtgag accctcatga ttggggatga ggtcaccgtg 60
acagtttttag gggtaaaagg caaccaggta cgtattggcg taaatgcccc gaaggaaagt 120
tctgttcacc gtgaagagat ctaccagcgt atccaggctg aaaaatcccc gcagtcacgt 180
tactaa 186

```

<210> 198
 <211> 93
 <212> DNA
 <213> E. Coli

<400> 198

```

ggtaggtggtg ccgagaggct gaaggcgctc ccctgctaag ggagtatgcg gtcaaaagct 60
gcacccggggg ttcgaatccc cgcctcaccg cca 93

```

<210> 199
 <211> 603
 <212> DNA
 <213> E. Coli

<400> 199

```

atgaagaata aggctgataa caaaaaaagg aacttcctga cccatagtga aatcgaatca 60
ctcctttaaag cagcaaatat cgggcctcat gcagcacgta attattgtct gactttgctt 120
tggtttattc atggtttccg ggcgagtga atttgtcgat tgaggatttc ggatattgat 180
cttaaggcaa agtgtatata tatccatcga ttaaaaaaag gcttttcaac aacgcacccg 240
ctattgaata aagaagttca ggctttaaaa aactggttga gtatccgtac ttcgtacccg 300
catgctgaga gccagtgggt atttttatca cgtaaagggga atccgctttc tcggcaacag 360
ttttaccata ttatctcgac ttccggtggt aatgccgggt tgtcactgga gattcatccg 420
cacatgttac gccattcgtg tggttttgct ttggcgaata tgggaataga tacgcgactt 480
atccaggatt atcttgggca tcgcaatatt cgtcatactg tctggtatac cgccagcaat 540
gcaggggcgtt ttacggcat ctgggataga gccagaggac gacagcgtca cgtgtttta 600
tag 603

```

<210> 200
 <211> 597
 <212> DNA
 <213> E. Coli

<400> 200

```

gtgagtaaac gtcgttatct taccggtaaa gaagttcagg ccatgatgca ggcggtttgt 60
tacggggcaa cgggagccag agattattgt cttattctgt tggcatatcg gcatgggatg 120

```

WO 00/44906

PCT/US00/02200

cgtatttagtg	aactgcttga	tctgcattat	caggaccttg	accttaatga	aggtagaata	180
aatattcgcc	gactgaagaa	cggattttct	accgttcacc	cgttacgttt	tgatgagcgt	240
gaagccgtgg	aacgctggac	ccaggaacgt	gctaactgga	aaggcgctga	ccggactgac	300
gctatatatta	tttctcgccg	cgggagtcgg	ctttctcgcc	agcaggccta	tcgcattatt	360
cgcgatgcgg	gtattgaagc	tggaaccgta	acgcagactc	atcctcatat	gttaaggcat	420
gcttgcggtt	atgaattggc	ggagcgtggt	gcagatactc	gtttaattca	ggattatctc	480
gggcatcgaa	atattcgcca	tactgtgcgt	tataccgcca	gtaatgctgc	tcgttttgcc	540
ggattatggg	aaagaataa	tctcataaac	gaaaaattaa	aaagagaaga	ggtttga	597

<210> 201

<211> 549

<212> DNA

<213> E. Coli

<400> 201

atgaaaatta	aaactctggc	aatcgttgtt	ctgtcggctc	tgccctcag	ttctacagcg	60
gctctggccg	ctgccacgac	ggttaatggt	gggaccgttc	actttaaagg	ggaagttgtt	120
aacgccgctt	gcgcagttga	tgcaggctct	gttgatcaaa	ccgttcagtt	aggacagggt	180
cgtaccgcat	cgtgggcaca	ggaaggagca	accagttctg	ctgtcgggtt	taacattcag	240
ctgaatgatt	gcgataccaa	tgttgcatct	aaagccgctg	ttgcctttt	aggtacggcg	300
attgatgcgg	gtcataccaa	cgttctggct	ctgcagagtt	cagctcgggg	tagcgcaaca	360
aacgttgggt	tgcatatcct	ggacagaacg	ggtgctgcgc	tgacgctgga	tggtgcgaca	420
tttagttcag	aaacaacccr	gaataacgga	accaatacca	ttccgttcca	ggcgcggtat	480
tttgcaaccg	gggcccgaac	cccgggtgct	gctaattgcg	atgcgacctt	caagggttcag	540
tatcaataa						549

<210> 202

<211> 648

<212> DNA

<213> E. Coli

<400> 202

gtgctgctaa	tgccgatgcg	accttcaagg	ttcagtatca	ataacctacc	caggttcagg	60
gacgtcatta	cgggcaggga	tgcccacctt	tgtagcgtaa	aaataacgat	gaaaagggaag	120
agattatttc	tattagcgtc	gttgctgcca	atgtttgctc	tgcccgga	taaatgggaat	180
accacgttgc	ccggcgga	tatgcaattt	caggcgctca	ttattgcgga	aacttgccgg	240
attgaagccg	gtgataaaca	aatgacggtc	aatatggggc	aaatcagcag	taaccggttt	300
catgcggttg	gggaagatag	cgcaccgggtg	ccttttggtta	ttcatttacg	ggaatgtagc	360
acgggtggtga	gtgaacgtgt	aggtgtggcg	tttcacgggtg	tcgcggtatgg	taaaaatccg	420
gatgtgcttt	ccgtgggaga	ggggccaggg	atagccacca	atattggcgt	agcgttggtt	480
gatgatgaag	gaaacctcgt	accgattaat	cgtcctccag	caaactggaa	acggctttat	540
tcaggctcta	cttcgctaca	tttcacgcgc	aaatatcgtg	ctaccgggcg	tcgggttact	600
ggcggcacgc	ccaatgccca	ggcctgggtc	tctttaacct	atcagtaa		648

<210> 203

<211> 726

<212> DNA

<213> E. Coli

<400> 203

gtgagtaata	aaaacgtcaa	tgtaaggaaa	tcgcaggaaa	taacattctg	cttgctggca	60
ggtatcctga	tggtcatggc	aatgatgggt	gccggacgcg	ctgaagcggg	agtggcctta	120
ggtgcgactc	gcgtaattta	tccggcaggg	caaaaacaag	agcaacttgc	cgtgacaaat	180
aatgatgaaa	atagtagccta	tttaattcaa	tcatgggtgg	aaaatgccga	tggtgtaaaag	240
gatggctcgt	ttatcgtgac	gcctcctctg	tttgcatga	agggaaaaaa	agagaatacc	300
ttacgtattc	ttgatgcaac	aaataaccaa	ttgccacagg	accgggaaaag	tttattctgg	360
atgaacgtta	aagcgattcc	gtcaatggat	aaatcaaaat	tgactgagaa	tacgctacag	420
ctcgcaatta	tcagccgcat	taaactgtac	tatcgcccgg	ctaaattagc	gttgccaccc	480
gatcaggccg	cagaaaaatt	aagatttctg	cgtagcgcca	attctctgac	gctgattaac	540
ccgacaccct	attacctgac	ggtaacagag	ttgaatgccg	gaaccggggt	tcttgaaaat	600
gcattggtgc	ctccaatggg	cgaaagcacg	gttaaatgac	cttctgatgc	aggaagcaat	660

attactttacc gaacaataaa tgattatggc gcactttacc ccaaaatgac gggcgtaatg 720
gaataa 726

<210> 204
<211> 2637
<212> DNA
<213> E. Coli

<400> 204

atgtcatatc tgaatttaag actttaccag cgaacacac aatgcttgca tattcgttaag 60
catcggtttgg ctgggtttttt tgtccgactc gttgtcgccct gtgctttttgc cgcacaggca 120
cctttgtcat ctgccgacct ctattttaat ccgcgctttt tagcggatga tccccaggct 180
gtggccgatt tatcgcgttt tgaataatgg caagaattac cgcacaggac gtatcgcgtc 240
gatatctatt tgaataatgg ttatatggca acgctgtgat tcacatttaa tacgggcgac 300
agtgaacaag ggattgttcc ctgcttgaca cgcgcgcaac tcgccagtat ggggctgaat 360
acggcttctg tcgcgggtat gaatctgtg gcggatgatg cctgtgtgcc attaacaca 420
atggtccag acgctactgc gcatctggat gttgtcagc agcgactgaa cctgacgatc 480
cctcaggcat ttatgagtaa tcgcgcgctt ggttatattc ctccgtgatt atgggatccc 540
ggatattaat cgggattgct caattataat ttcagcggaa atagtgtaca gaatcggatt 600
gggggtaaca gccattatgc atatttaaac ctacagagtg ggttaaatat tgggtcgtgg 660
cgttttacgac acaataccac ctggagttat aacagtagcg acagatcatc aggtagcaaa 720
aataaatggc agcatatcaa tacctggcct gagcgagaca taataccggt acgttcccgg 780
ctgacgctgg gtgatggtta tactcagggc gatattttcg atggtattaa ctttcgcggc 840
gcacaattgg cctcagatga caatatgta ccgatatgta aaagaggatt tgccccgggtg 900
atccacggta ttgctcgtgg tactgcacag gtcactatta aacaaaatgg gtatgacatt 960
tataatagta cgggtgccacc ggggcctttt accatcaacg atatctatgc cgcaggtaat 1020
agtgtgact tgcaggtaac gatcaaaagc gctgacggca gcacgcagat tttaccgta 1080
ccctattcgt cagtcgccct tttgcaacgt gaagggcata ctctgtattc cattacggca 1140
ggagaatacc gtagtggaat tgccgacgag gaaaaaaccc gctttttcca gtagtacct 1200
ctccacggcc ttccggctgg ctggacaata tatggtggaa cgcaactggc ggtcgttat 1260
cgtgctttta atttcggtat cgggaaaaac atggggggc tgggcgctct gtctgtggat 1320
atgacgcagg ctaattccac acttcccgat gacagtcagc atgacggaca atcgggtcgt 1380
tttctctata acaaatcgct caatgaatca ggcacgaata ttcagttagt gggttaccgt 1440
tattcgacca cgggatattt taatttcgct gatcaaacat acagtcgaat gaatggctac 1500
aacattgaaa cacaggacgg agttattcag gttaaqccga aattcaccga ctattacaac 1560
ctcgtttata acaaacgcgg gaaattacaa ctcaccgta ctcagcaact cgggcgcaca 1620
tcacaactgt atttgagtgg tagccatcaa acttattggg gaacgagtaa tgcgatgag 1680
caattccagg ctggattaaa tactgcgttc gaagatatca actggacgct cagctatagc 1740
ctgacgaaaa acgcttgga aaaaaggacg gatcagatgt tagcgcttaa cgtcaatatt 1800
cctttcagcc actgctcgc ttctgacagt aaatctcagt ggcgacatgc cagtgcacg 1860
tacagcatgt cacacgatct caacggctcg atgaccaatc tggctggtgt atacggtacg 1920
ttgctggaag acaacaacct cagctatagc gtgcaaacgg gctatgccg gggaggcgat 1980
ggaaatagcg gaagtacagg ctacgccag ctgaattatc gcgggtggtta cggcaatgcc 2040
aatatcggtt acagccatag cgatgatatt aagcagctct attacggagt cagcgggtggg 2100
gtactggctc atgccaatgg cgtaacgctg gggcagccgt taaacgatac ggtggtgctt 2160
gttaaagcgc ctggcgcaaa agatgcaaaa gtcgaaaacc agacgggggt gcgtaccgac 2220
tggcggtggt atgcccgtgct gccttatgcc actgaatatc gggaaaaatag agtggcgctg 2280
gataccaata ccctggctga taacgtcgat ttagataacg cggttgctaa cgttgttccc 2340
actcgtgggg cgatcgtgag agcagagttt aaagcgcgcg ttgggataaa actgctcatg 2400
acgctgaccc acaataataa gccgctgccc ttggggcgca tgggtgacatc agagagttagc 2460
cagagtagcg gcattgttgc ggataatggt caggtttacc tcagcggaat gcctttagcg 2520
ggaaaagtgc aggtgaaatg gggagaagag gaaaaatgctc actgtgtcgc caattatcaa 2580
ctgccaccag agagtcagca gcagtattat acccagctat cagctgaatg tcgttaa 2637

<210> 205
<211> 531
<212> DNA
<213> E. Coli

<400> 205

atgagaaaca aaccttttta tcttctgtgc gcttttttgt ggctggcggg gagtcacgct 60

ttggctgcgg	atagcacgat	tactatccgc	ggctatgtca	gggataacgg	ctgtagtgtg	120
gccgctgaat	caaccaat	tactgttgat	ctgatggaaa	acgcggcgaa	gcaatttaac	180
aacattggcg	cgacgactcc	tggtgttcca	tttcgtat	tgctgtcacc	ctgtggtaat	240
gccgtttctg	ccgtaaaggt	tgggtttact	ggcgttgca	atagccacaa	tgccaacctg	300
cttgcaactg	aaaatacgg	gtcagcggct	tcgggactgg	gaatacagct	tctgaatgag	360
cagcaaaatc	aaataccct	taatgctcca	tcgtcccgcc	tttcgtggac	gaccctgacg	420
ccgggtaaac	caaatcgc	gaatttttac	gcccggttaa	tgccgacaca	ggtgcctgtc	480
actgcggggc	atatcaatgc	cacggctacc	ttcactcttg	aatatcagta	a	531

<210> 206

<211> 504

<212> DNA

<213> E. Coli

<400> 206

atgaatgggt	gcaaacgtgg	gtatgtattg	gcggcaatat	tgccgctcgc	aagtgcgacg	60
atacaggcag	ccgatgtcac	catcacgggtg	aacggtaagg	tcgtcgcgaa	accgtgtacg	120
gtttccacca	ccaatgccac	ggttgatctc	ggcgatcttt	attctttcag	tcttatgtct	180
gccggggcgg	catcgccctg	gcatgatgtt	gcgcttgagt	tgactaattg	tccgggtggga	240
acgtcgaggg	tcactgccag	cttcagcggg	gcagccgaca	gtaccggata	ttataaaaaac	300
caggggacgc	cgcaaaacat	ccagttagag	ctacaggatg	acagtggcaa	cacattgaat	360
actggcgcaa	ccaaaacagt	tcaggtggat	gattccctcac	aatcagcgca	cttcccgtta	420
caggtcagag	cattgacagt	aaatggcgga	gccactcagg	gaaccattca	ggcagtgatt	480
agcatcacct	atacctacag	ctga				504

<210> 207

<211> 903

<212> DNA

<213> E. Coli

<400> 207

atgaaacgag	ttattaccct	gtttgctgta	ctgctgatgg	gctggctcgg	aaatgcctgg	60
tcattcgcct	gtaaaaaccg	caatggtacc	gctatcccta	ttggcggtgg	cagcgccaat	120
gtttatgtaa	acccttgcgc	cgctcgtgaat	gtggggcaaa	acctggctcg	ggatctttcg	180
acgcaaatct	tttgccataa	cgattatccg	gaaaccatta	cagactatgt	cacactgcaa	240
cgaggctcgg	cttatggcgg	cggttatctc	aatttttccg	ggaccgtaaa	atatagtggc	300
agtagctatc	catttctctac	caccagcgaa	acgcgcgcgc	ttgtttataa	ttcgagaacg	360
gataagccgt	ggccgggtgg	gctttatgtg	acgcctgtga	gcagtgcggg	cggggtggcg	420
attaaagctg	gctcattaat	tgcctgtgct	attttgcgac	agaccaacaa	ctataacagc	480
gatgatttcc	agttttgtgt	gaatatattac	gccaatatg	atgtggtggg	gcctactggc	540
ggctgcgatg	tttctgctcg	tgatgtcacc	gttactctgc	cggactaccc	tggttcagtg	600
ccaattcctc	ttaccgttta	ttgtgcgaaa	agccaaaacc	tggggtatta	cctctccggc	660
acaaccgcag	atgcggggcaa	ctcgattttc	accaataccg	cgtcggtttc	acctgcacag	720
ggcgtcggcg	tacagttgac	gcgcaacgg	acgattattc	cagcgaataa	cacggtatcg	780
ttaggagcag	tagggacttc	ggcggtgagt	ctgggattaa	cggcaaat	tgacagtaac	840
ggagggcagg	tgactgcagg	gaatgtgcaa	tcgattattg	gcgtgacttt	tgtttatcaa	900
taa						903

<210> 208

<211> 1631

<212> DNA

<213> E. Coli

<400> 208

gtgctgtcaa	aactaccccg	tagactccga	tcttttcaaa	catattgcac	catccgtgta	60
catcggggtg	aggatatgaa	atcaatggat	aagttaacaa	caggtgttgc	ctatggcaca	120
tcggcggtga	atgctggttt	ctgggcattg	cagttactcg	ataaagtaac	tccgtcacag	180
tggtgtgcaa	tcggtgtgct	gggtagcctg	gtttttggcc	tgctgacgta	tctgacaaat	240
ctttatttca	agattaaaga	agacaggcgt	aaggctgcga	gaggagagta	atccaatgac	300
tcaagactat	gaactggtg	tgaaaggagt	ccgtaatttt	gagaataaag	ttacggtaac	360
tgtagcctta	caggacaaag	aacgccttga	cgtgaaatt	tttgacctgg	atgtcgccat	420

ggaccgtggt	gaaggagctg	cgctggagtt	ttatgaggca	gcagccagaa	ggagcgctccg	480
gcaagtcttc	ctggaagtag	cagaaaaatt	gtcagaaaaa	gttgagtcct	atctgcagca	540
tcagtactcc	tttaagattg	aaaatcctgc	caataagcac	gagcgctcct	atcataaata	600
tctatgaaca	caaaaatcac	atacgccctg	tcggctgccc	ttctggcgct	gattggtgct	660
ggcgcatctg	ctcctcagat	acttgaccag	tttctggacg	aaaaagaagg	taaccacaca	720
atggcatacc	gcatgggttc	tggcatatgg	accatctgtc	ggggtgccac	agtgggtgat	780
ggaaaaaccg	ttttcccaa	tatgaaactg	tcgaaggaaa	aatgcgacca	ggtcaacgcc	840
attgagcgtg	ataaggcgct	ggcatgggtg	gagcgcaata	ttaaagtacc	actgaccgaa	900
ccacaaaaag	cggttatcgc	gtcattttgt	ccctataaca	ttggccccgg	taagtgttcc	960
ccgtcgacgt	tttataagcg	gctgaatgct	ggtgatcgta	aaggtgcatg	cgaagcgatt	1020
cgctgggtgg	ttaaggatgg	cggaacgcgt	tgccgcattc	gttcaataaa	ctgttacggt	1080
caggttattc	gtcgtgacca	ggagagcgca	ttaacctgct	gggggataga	acagtgaatc	1140
agatattcat	gggtattttt	ctcgtgttgt	caggatttat	cgctggaaat	gtctggagcg	1200
accgaggatg	gcacaaaaaa	tgggcggaac	gtgatgctgc	cgcatatca	caagaggtaa	1260
atgctcaatt	tgctgctcga	ataattgaac	agggcggaac	tatagccctg	gatgaggctg	1320
ttaaagatgc	gcaacagaaa	tctgtgaaa	tttctgccag	ggctgcttat	ctgtctgata	1380
gtgttaacca	gttgctgccc	gaagcaaaaa	aatatgccat	acgccttgac	gcagcgaagc	1440
ataccgcaga	tcttcccgct	gccgtcagag	gcaaaacaac	caaaaccgcc	gaagggaatgc	1500
tcaccaacat	gctcggagat	attgcagcag	aagctcagct	ttatgctgaa	attgctgacg	1560
aacgctacat	cgcaggagtg	acttgtcaac	agatctatga	atctttaaga	gataaaaaagc	1620
atcaaatgta	g					1631

<210> 209

<211> 534

<212> DNA

<213> E. Coli

<400> 209

atgaacacaa	aaatcagata	cgccctgtcg	gctgccgttc	tggcgctgat	tggtgctggc	60
gcattctgtc	ctcagatact	tgaccagtgt	ctggacgaaa	aagaaggtaa	ccacacaatg	120
gcataccgcg	atgggttctg	catatggacc	atctgtcggg	gtgccacagt	ggtggatgga	180
aaaaccgttt	ttcccaatat	gaaactgtcg	aaggaaaaat	gcgaccaggt	caacgccatt	240
gagcgtgata	aggcgtggcg	atgggtggag	cgcaatatta	aagtaccact	gaccgaacca	300
caaaaagcgg	gtatcgcgtc	attttgtccc	tataacattg	gccccggtaa	gtgtttcccg	360
tcgacgtttt	ataagcggct	gaatgctggt	gatcgtaaa	gtgcatcgca	agcgattcgc	420
tggtggatta	aggatggcgg	acgcgattgc	cgcatctggt	caaataactg	ttacggtcag	480
gttattctgc	gtgaccagga	gagcgcatta	acctgtcggg	ggatagaaca	gtga	534

<210> 210

<211> 312

<212> DNA

<213> E. Coli

<400> 210

atgactcaag	actatgaact	ggttgtgaaa	ggagtccgta	atcttgagaa	taaagttacg	60
gtaactgtag	ccttacagga	caaagaacgc	tttgacgggt	aaatttttga	cctggatgtc	120
gccatggacc	gtgttgaaag	agctgcgctg	gagttttatg	aggcagcagc	cagaaggagc	180
gtccggcaag	tcttctctga	agtagcagaa	aaattgtcag	aaaaagttga	gtcttatctg	240
cagcatcagt	actcctttaa	gattgaaaaa	cctgcccaata	agcagcagcg	tcctcatcat	300
aaatatctat	ga					312

<210> 211

<211> 291

<212> DNA

<213> E. Coli

<400> 211

gtgctgtcaa	aactaccccc	tagactccga	tcttttcaaa	catattgcac	catccgtgta	60
catcgggggt	aggatatgaa	atcaatggat	aagttaacaa	caggtgttgc	ctatggcaca	120
tcggcgggta	atgtgtgttt	ctgggcattg	cagttactcg	ataaagtaac	tccgtcacag	180
tgggctgcaa	tcggtgtgct	gggtagcctg	gtttttggcc	tgctgacgta	tctgacaaat	240

ctttatttca agattaaaga agacaggcgt aaggctgcga gaggagagta a 291

<210> 212
<211> 216
<212> DNA
<213> E. Coli

<400> 212
atgtcaaata aaatgactgg tttagtaaaa tggtttaacg ctgataaagg tttcggcttt 60
atcttcctcg ttgatggtag taaagatgtg tttgtgcatt tttctgcgat tcagaatgat 120
aattatcgaa ccttatttga aggtcaaaa gttaccttct ctatagagag tgggtgctaaa 180
ggtcctgcag cagcaaatgt catcattact gattaa 216

<210> 213
<211> 1017
<212> DNA
<213> E. Coli

<400> 213
atgtttgtca tctggagcca tagaacaggg ttcacatga gtcacaaact taccttcgcc 60
gacagtgaat tcagcagtaa gcgcgcgcag accagaaaag agattttctt gtcccgcatg 120
gagcagattc tgccatggca aaacatgggt gaagtcacg agccgtttta ccccaggcgt 180
ggtaatggcc ggccgacctta tccgctggaa accatgtac gcattcactg catgcagcat 240
tggtacaacc tgagcgatgg ccgcatggaa gatgctctgt acgaaatcgc ctccatgcgt 300
ctgttttgccc ggttatccct ggatagcgcc ttgcccggacc gcaccacat catgaatttc 360
cgccacctgc tggagcagca tcaactggcc cgccaattgt tcaagacat caatcgctgg 420
ctggccgaag caggcgctcat gatgactcaa ggcaccttgg tcgatgccac catcattgag 480
gcacccagct cgaccaagaa caaagagcag caacgcgatc cggagatgca tcagaccaag 540
aaaggcaatc agtggcactt tggcatgaag gccacacattg gtgtcgatgc caagagtggc 600
ctgaccacaca gcctgggtcac caccgcggcc aacgagcatg acctcaatca gctgggtaat 660
ctgctgcatg gagaggagca atttgtctca gccgatgccg gctaccaagg gggccacag 720
cgccaggagc tggccgaggt ggatgtggac tggctgatcg ccgagcgccc cggcaaggta 780
agaaccttga aacagcatcc acgcaagaac aaaacggcca tcaacatcga atacatgaaa 840
gccagcatcc gggccagggt ggagcaccga tttcgcatca tcaagcgaca gttcggcttc 900
gtgaaagcca gatacaagggt gttgctgaaa aacgataacc aactggcgat gttattcacg 960
ctggccaacc tgtttcgggc ggaccaaagt atacgtcagt gggagagatc tcactaa 1017

<210> 214
<211> 474
<212> DNA
<213> E. Coli

<400> 214
atgggtatata taataatcgt ttcccacgga catgaagact acatcaaaaa attactcgaa 60
aatcttaagt ctgacgatga gcaactacaag attatcgtag gcgacaacaa agactctcta 120
ttattgaaac aaatatgcca gcattatgca ggccctggact atattagtgg aggtgtatac 180
ggcttttggtc ataataataa tattgcggtg gcgtatgtaa aggaaaaata tagaccgca 240
gatgatgatt acattttgtt tttgaatccc gatatcatca tgaagcatga tgatttgctg 300
acatatatta aatatgtcga aagtaagcgt tatgctttta gtacattatg cctgttccga 360
gatgaagcga aatctttaca tgattattcc gtaagaaaat ttccctgtgct ttctgatttt 420
atttgtgcat ttatgttagg gattaaggaa ggtgcgaaca agtcctctgat atga 474

<210> 215
<211> 1119
<212> DNA
<213> E. Coli

<400> 215
atgggaaaaa gcatagtcgt tgtttctgcg gtcaatttta ccactggcgg tccattttacc 60
attttgaaaa aatttttggc agcaactaat aataaagaaa atgtcagttt tatcgcat 120
gtccattctg ctaaagagtt aaaagaaagt tatccatggg ttaaatcat tgagtttcc 180

gaggttaaag	ggtcgtggct	aaaacgtttg	cactttgaat	atgtagtttg	taaaaaactt	240
tcaaaagagc	tgaatgctac	gcattggatt	tgtctgcatg	atattacggc	caatgtcgtc	300
actaaaaaaa	gatatgtgta	ttgtcataac	cctgcacctt	tttataaagg	aattttatct	360
cgtgaaattc	ttatggagcc	tagctttttc	ttatttaaaa	tgctatacgg	gctgatatat	420
aaaataaaca	ttaaaaaaa	tactgcagtg	tttgttcaac	aattctggat	gaaagaaaaa	480
tttatcaaga	aatattctat	aaataacatc	attgtcagtc	ggccagaaat	taaattatct	540
gataaaagcc	aacttactga	tgatgattct	caatttaaga	ataacccttc	tgagttgaca	600
atattttacc	ctgctgttcc	acgagtattt	aaaaattacg	agcttattat	tagtgcagca	660
aggaaattga	aagaacaatc	caatattaaa	tttctgctta	ctatcagtg	tacagaaaat	720
gcgtatgcaa	aatatattat	cagtcttgca	gaaggactgg	ataatgttca	tttctcggg	780
tacttgata	aagaaaaaat	cgatcattgt	tataatattt	cagatatagt	ttgttttccc	840
tctagggttag	aaacatgggg	attgccgttg	tctgaagcta	aagagcgagg	taagtgggta	900
ttagcatcag	atttcccatt	tactagagaa	actcttggt	gttatgaaaa	gaaagctttt	960
tttgattcta	ataacgatga	catgttagtt	aaacttatta	ttgacttcaa	aaaaggtaac	1020
ctcaaaaaag	atatctctga	tgcaaaattc	atttatcgta	atgaaaaatg	attagttggg	1080
tttgatgaac	tagttaattt	tattactgaa	gaacattga			1119

<210> 216
 <211> 591
 <212> DNA
 <213> E. Coli

<400> 216						
atgatcttaa	aactcgctaa	acgatatggt	ctctgtggtt	ttattcggct	tgtagagat	60
gtcttattga	ctcgtgtatt	ttaccggaac	tgtagaatta	ttcgatttcc	ctgctatatt	120
cgcaatgatg	gtagcattaa	ttttggtgaa	aatttcacaa	gtggagtcgg	tctcaggctg	180
gatgcatttg	gacgtggcgt	gatttttttt	tccgataatg	tgcaagttaa	cgactatggt	240
catatcgctt	caattgagag	cgttacgata	ggtcgggata	cgcttattgc	aagtaaagta	300
tttattaccg	atcataatca	cggttccctt	aagcactctg	atccaatgag	ttcgccaaat	360
ataacctccag	acatgcgcac	gttggaatct	tcagctgttg	taattggcca	gagggtttgg	420
ttgggtgaga	atgtgacggt	tttgccctga	acaattattg	gtaatggagt	cgtagtcggc	480
gccaatctcg	ttgttagagg	ttctattccc	gaaaatactg	tcattgcggg	agtaccagca	540
aaaatcataa	agaaatacaa	tcatgagacc	aaattatggg	aaaaagcata	g	591

<210> 217
 <211> 993
 <212> DNA
 <213> E. Coli

<400> 217						
atgtattttt	tgaatgattt	aaatttctct	agacgcgatg	ctggatttaa	agcaagaaaa	60
gatgcactgg	acattgcttc	agattatgaa	aacatttctg	ttgttaacat	tcctctatgg	120
gggtggagtag	tcagagagaat	tattagttct	gttaagctta	gtacatttct	ctgcggtctt	180
gaaaaataag	atgttttaat	tttcaatttc	cogatggcca	aaccattttg	gcatatattg	240
tcattctttc	accgccttct	aaaatttaga	atagtacctc	tgattcatga	tattgatgaa	300
ttaaagaggag	gagggggtag	tgattctgtg	cggttgcta	cctgtgatat	ggtcataagt	360
cacaatccac	aaatgacaaa	gtaccttagt	aaatatatgt	ctcaggataa	aatcaaaagac	420
ataaaaaatat	ttgattacct	cgtctcatct	gatgtggagc	atcgagatgt	tacggataag	480
caacgagggg	tcatatatgc	tggaacctt	tctaggcata	aatgttcttt	catatatact	540
gaaggatgcg	attttactct	ctttggtgtc	aactatgaaa	ataaagataa	tcctaaatat	600
cttggaagtt	ttgatgctca	atctccggaa	aagatttaacc	tcccaggcat	gcaatttgga	660
ctcatttggg	atggagattc	tgtcgaaacc	tgtagtggtg	cctttggcga	ctattttaaag	720
tttaataaacc	ctcataagac	atctctttat	ctttcaatgg	aacttccagt	atttatatgg	780
gataaagccg	cccttgccga	tttcattgta	gataatagaa	taggatatgc	agtgggatca	840
atcaaaagaaa	tgcaagagat	tggtgactcc	atgacaatag	aaacttataa	gcaaattagt	900
gagaatacaa	aaattatttc	tcagaaaatt	cgaacaggaa	gtactctcag	ggatgttctt	960
gaagaggtga	tcgatgatct	taaaactcgc	ttaa			993

<210> 218
 <211> 1167
 <212> DNA

<213> E. Coli

<400> 218

atgatctatc	ttgtaattag	tgtctttctc	attacagcat	ttatctgttt	atatcttaag	60
aaggatatat	tttatccagc	cgtatgcgtt	aatatcatct	tcgcactggg	cttattggga	120
tatgaaataa	cgtcagatat	atatgccttt	cagttaaatg	acgctacgtt	gatttttcta	180
ctttgcaatg	ttttgacatt	taccctgtca	tgtttattga	cggaaaagtgt	attagatcta	240
aatatcagaa	aagtcaataa	tgcattttat	agcataccat	cgaagaaagt	gcataatgta	300
ggcttggttag	ttatttcttt	ttcgatgata	tatatatgca	tgagggttaag	taactaccag	360
ttcgggacta	gcttacttag	ctatatgaat	ttgataagag	atgctgatgt	tgaagacaca	420
tcaagaaaatt	tctcagcata	catgcagcca	atcattctaa	ctacttttgc	tttattttatt	480
tggtctaaaa	aatttactaa	tacaaaaggta	agtaaaacat	ttactttact	tgtttttatt	540
gtattcatct	ttgcaattat	actgaatact	ggtaagcaaa	ttgtctttat	ggttatcatc	600
tcttatgcatt	tcattcgtagg	tgtaaataga	gtaaaacatt	atgtttatct	tattacagct	660
gtagggtgttc	tattctcctt	gtatatgctc	tttttacgtg	gactgcctgg	ggggatggca	720
tattatctat	ccatgtattt	ggtcagccct	ataatcgcgt	ttcaggaggt	ttattttcag	780
caagtatcta	actctgccag	ttctcatgtc	tttttggttt	ttgaaaaggct	gatggggcta	840
ttaacagggtg	gagtcctctat	gtcgttgcat	aaagaatttg	tgtgggtggg	tttgccaaca	900
aatgtttata	ctgctttttc	ggattatggt	tatatctccg	cggagctaa	ctatttgatg	960
atgggtattc	atggctgtat	ttcagggtgt	ttatggagat	tgtctcga	ttacatatct	1020
gtgaaaaatat	ttttattcata	ttttattttat	accttttctt	tcatttttta	tcataaaagc	1080
ttcatgacta	atattagcag	ttggatacaa	ataactcttt	gtatcatagt	attctctcaa	1140
tttcttaagg	cccagaaaat	aaagtga				1167

<210> 219

<211> 1104

<212> DNA

<213> E. Coli

<400> 219

atgtacgatt	atatcattgt	tggttctggt	ttgtttggtg	ccgtttgtgc	gaatgagtta	60
aaaaagctaa	acaaaaaagt	tttagtgatt	gagaaaaaga	atcatatcgg	tggaatgcg	120
tacacagagg	actgtgagg	tatccagatt	cataaatatg	gtgcacatat	tttccatacc	180
aatgataaat	atataatggga	ttacgttaat	gatttagtag	aatttaacg	ttttactaat	240
ttccactg	cgatttataa	agacaaaatta	ttcaaccttc	cttttaatat	gaatactttc	300
caccaaatgt	ggggagttaa	agatcctcaa	gaagctcaaa	atatcattaa	tgctcagaaa	360
aaaaagtatg	gtgacaagg	acctgaaaat	ttggaggagc	aggcgatttc	attagttggg	420
gaggacttat	accaagcatt	gataaagggt	tatacggaga	agcagtgagg	aagaagtgc	480
aaagaattgc	ctgcatttat	tattaagcga	atcccagtg	gatttacgtt	tgataacaat	540
tatttttccg	atcgctatca	aggtattccg	gtgggaggct	acactaagct	tattgaaaaa	600
atgcttgaag	gtgtggacgt	aaaattaggc	attgattttt	tgaaagacaa	agattctcta	660
gcgagtaaa	cccatagaat	catctacact	ggaccttgg	atcagtaact	cgactatagg	720
tttgagcgt	tagaatatcg	ctctttaaaa	tttgagacgg	aacgccatga	atttccaaac	780
ttccaaaggga	atgcagtaat	aaatttcact	gatgctaatt	taccatatac	cagaataatt	840
gagcataaac	attttgacta	tggttgagaca	aagcatacgg	ttgttacaaa	agaatatcca	900
ttagagtgg	aagttggcga	cgaaccttac	tatccagtta	atgataataa	aaacatggag	960
ctttttaaga	aatatagaga	gttagctagc	agagaagaca	aggttatatt	tggcgggctg	1020
ttggccgagt	ataaatatta	tgatatgcatt	caagtgatat	ctgccgctct	ttatcaagt	1080
aaaaatataa	tgagtacgga	ttaa				1104

<210> 220

<211> 1116

<212> DNA

<213> E. Coli

<400> 220

atgttcccaa	aaataatgaa	tgatgaaaac	tttttcaaaa	aagcggcggc	gcacggggag	60
gaacctcctt	taactcctca	aaacgaacat	cagcgggtccg	ggctgcgctt	cgccccgtcg	120
gtcagactac	cccgtgcggg	tgccctggct	ggcatgttct	taccgattgc	ttcaacgctg	180
gtttcacacc	cgcgcgggg	ctgggtggtg	ctgggtgttg	tcggctgggc	gttcgtctgg	240
ccgcatttag	cctggcagat	agcagcagg	gccgtcgatc	cgttagccg	ggaaatttat	300

aacttaaaaa	ccgatgcagt	attagcggga	atgtgggtag	gcgtaatggg	cgtaaactg	360
ctgccttcca	ccgcgatgtt	gatgattatg	tgtctgaatt	tgatgggggc	aggcgccccc	420
cgtctgtttg	tcgcgggtct	ggtgttgatg	gtggtttcct	gccttgtcac	cctcgagctg	480
acgggcatta	ccgtgtcggt	caatagtgcg	ccgctggaat	ggtggctctc	ccttccatt	540
attgtcattt	atcctctgct	gtttggctgg	gtcagctacc	agacggcaac	caaactggcg	600
gaacataaac	gcaggttgca	ggtcatgagt	acccgcgacg	gcatgacggg	cgtgtataac	660
cgacgtcatt	gggaaactat	gttacgcaat	gaatttgata	actgtcggcg	gcataatcgc	720
gatgcaacgt	tactgattat	cgatatcgac	catttcaaga	gcatcaacga	tacctggggc	780
catgatgtgg	gcgatgaagc	gattgtggcg	cttaccgcac	agttacaaat	taccctgcgc	840
ggtagcgaag	tgattggctg	gtttggcgcg	gatgagtttg	cagtaatcat	gtccggtagc	900
ccagctgaga	gcgccattac	cgccatgtta	cggtgtcatg	aagggtctaa	tacattacgt	960
ttgccgaata	cgccacaggt	aactttacgg	attagtgtgg	gggtgtcgcc	gctgaaccca	1020
caaatgagtc	actatcgtga	gtggttgaaa	tcggcagatt	tggcgcttta	caaagcaaa	1080
aaagccggac	gtaaccgcac	cgaagtggcg	gcctga			1116

<210> 221

<211> 1404

<212> DNA

<213> E. Coli

<400> 221

ttggatgtga	acgttgatca	gttcgatact	gaagctttcc	gtactgacaa	actggaactg	60
accagcggca	acatcgctga	ccataacggt	aacgtagtat	ctgggtgtgt	cgatatccat	120
agcagcgatt	acgttctgaa	cgctgatctg	gtgaacgacc	gtacctggga	tacttccaag	180
tctaactacg	gttacggtat	tgttgctatg	aactctgatg	gtcacctgac	tatcaacggt	240
aacggcgacg	tagacaacgg	tactgaactg	gataacagct	ctgtagacaa	tgttgttgct	300
gcaaccggta	actacaaagt	tcgtatcgac	aacgcaactg	gcgctggcgc	tatcgctgat	360
tacaaagata	aagaaattat	ctacgtaaac	gacgtcaaca	gcaacgcgac	cttctctgct	420
gctaacaagg	ctgacctggg	tgcatacacc	tatcaggctg	aacagcgcg	taacaccggt	480
gttctgcaac	agatggagct	gaccgactac	gctaaccatg	cgctgagcat	cccgtctcgc	540
aacaccaata	tctggaacct	ggaaccaagac	accgttggta	ctcgrctgac	caactctcgt	600
catggcctgg	ctgataacgg	cggcgcgatg	gtaagctact	tcggtgtgaa	cttcaacggc	660
gacaacggca	ccatcaacta	tgatcaggat	gttaacggca	tcattggtcgg	tgttgatacc	720
aaaattgacg	gtaacaacgc	taagtggatc	gtcgggtcgg	ctgcaggctt	cgctaaagggt	780
gacatgaatg	accgttctgg	tcaggtggat	caagacagcc	agactgccta	catctactct	840
tctgtctact	tcgcgaacaa	cgtctttggt	gatggtagct	tgagctactc	tcacttcaac	900
aacgacctgt	ctgcaacctg	gagcaacggt	acttacgttg	acggtagcac	caactccgac	960
gcttggggct	tcggtttgaa	agccgggtac	gacttcaaac	tgggtgatgc	tggttacgtg	1020
actccttacg	gcagcggttc	tggtctgttc	cagtctgggt	atgactacca	gctgagcaac	1080
gacatgaaag	ttgacgggtca	gtctttacgac	agcatgcgtt	atgaactggg	tgtagatgca	1140
ggttatacct	tcacctacag	cgaagatcag	gctctgactc	cgtacttcaa	actggcttac	1200
gtctacgacg	actctaacaa	cgataacgat	gtgaacggcg	attccatcga	taacgggtact	1260
gaagggtctg	cggtacgtgt	tggtctgggt	actcagttta	gcttcaccaa	gaacttcagc	1320
gcctataaccg	atgctaacta	cctcggtggt	ggtgacgtag	atcaagactg	gtccgcgaac	1380
gtgggtgtta	aatatacctg	gtaa				1404

<210> 222

<211> 669

<212> DNA

<213> E. Coli

<400> 222

atgcccgctca	aggatttgac	gggcattact	gcaaaggacg	cgcaaatgtt	atctgtagtt	60
aaacctcttc	aggaatttgg	taagctcgat	aaatgtttgt	ccagatacgg	tacgcgcttc	120
gagttttaata	atgaaaagca	agttatat	tccagtgatg	tcaataacga	agatactttc	180
gttatcttag	agggagttat	ctctctgcgt	agagaagaaa	acgtacttat	cggattatcc	240
cagggtcctt	atattatggg	gctggctgat	ggtttaatga	aaaacgatat	accatacaaa	300
ttaatatcag	aaggaaattg	tacgggatat	catctaccag	ccaaacaaac	cattacgctt	360
attgaacaaa	atcaactctg	gcgagacgct	ttttactggg	tagcctggca	aaatagaatt	420
ctggaattac	gcgacgtgca	gctcattggg	cataattcct	acgaacaaat	ccgcgcaaca	480
ttattatcaa	tgattgactg	gaatgaagaa	ttgcgatcac	gtattggtgt	gatgaattat	540

atccatcaac gtacacgcat atcgcggttct gtcgtcgag aagttctcgc tgccttgcgt 600
 aaaggcggct atatcgaaat gaataaaggc aaactggctg ctatcaaccg ttgccttca 660
 gagtattaa 669

<210> 223
 <211> 255
 <212> DNA
 <213> E. Coli

<400> 223
 atgaccgata aaatccgtac tctgcaaggc cgcgttgta gcgacaaaat ggagaaatcc 60
 attgttgttg ctatcgaaac ttttgtgaaa caccgatct acggtaaatt catcaagcgt 120
 acgaccaaac tgcacgtaca tgacgagaac aacgaatgcg gtatcggtga cgtggttgaa 180
 atccgcgaat gccgtccgct gtccaagact aaatcctgga cgctggttcg cgttgtagag 240
 aaagcgggttc tgtaa 255

<210> 224
 <211> 192
 <212> DNA
 <213> E. Coli

<400> 224
 atgaaagcaa aagagctgcg tgagaagagc gttgaagagc tgaacaccga gctgctgaac 60
 ctgctgcgtg agcagttcaa cctgcgtatg caggctgcaa gtggccagct gcaacagctct 120
 cacctgttga agcaagtgcg tcgcgatgct gcacgcgtta agactttact gaacgagaag 180
 gcgggtgcgt aa 192

<210> 225
 <211> 411
 <212> DNA
 <213> E. Coli

<400> 225
 atgttacaaac caaagcgtac aaaattccgt aaaaatgcaca aaggccgtaa ccgcgggtctg 60
 gcgcagggta cggatgttag ctccggcagc ttcgggtctga aagctgttgg ccgtgggtcgt 120
 ctgactgccc gtcagatcga agcagcagct cgtgctatga cccgtgcagt taagcgtcaa 180
 ggtaagatct ggatccgtgt gttcccggac aaaccgatca ctgaaaaagcc gctggcagtg 240
 cgtatgggta aaggtaaagg taacgtggag tattgggttg ccttgattca gccgggtaaa 300
 gtcctgtatg aaatggacgg tttccggaa gagctggccc gtgaagcatt caagctggca 360
 gcagcgaaac tgccgattaa aaccaccttt gtaactaaga cgggtgatgta a 411

<210> 226
 <211> 702
 <212> DNA
 <213> E. Coli

<400> 226
 atgggtcaga aagtacatcc taatgggtatt cgcctgggta ttgtaaaacc atggaactct 60
 acctggtttg cgaacaccaa agaattcgtc gacaacctgg acagcgattt taaagtacgt 120
 cagtacctga ctaaggaaact ggctaaagcg tccgtatctc gtatcgttat cgagcgtccg 180
 gctaagagca tccgtgtaac cattcacact gtcgcccccg gtatcgttat cgttaaaaaa 240
 ggtgaagacg tagaaaaact gcgtaaggtc gtagcggaca tcgctggcgt tcctgcacag 300
 atcaacatcg ccgaagttcg taagcctgaa ctggacgcaa aactggttgc tgacagcatc 360
 acttctcagc tggaaacgtcg cgttatgttc cgtcgtgcta tgaagcgtgc tgtacagaac 420
 gcaatgcgtc tgggcgctaa aggtattaaa gttgaagtta gcggccgtct gggcggcgcg 480
 gaaatcgcac gtaccgaatg gtaccgcgaa ggtcgcgtac cgtgcacac tctgcgtgct 540
 gacatcgact acaacacctc tgaagcgcac accacttacg gtgtaatcgg cgttaaaagt 600
 tggatcttca aaggcgagat cctgggtggt atggctgctg ttgaacaacc ggaaaaaccg 660
 gctgctcagc ctaaaaagca gcagcgtaaa ggccgtaaat aa 702

<210> 227

<211> 333
 <212> DNA
 <213> E. Coli

<400> 227
 atggaaacta tcgctaaaca tcgccatgct cgttcttctg ctcagaaggt tcgccttgtt 60
 gctgacctga ttccgcgtaa gaaagtgtcg caggctctgg atattttgac ctacaccaac 120
 aagaaagcgg ctgtactggt caagaaagt ctggaatctg ccattgctaa cgtcgaacac 180
 aacgatggcg ctgacattga cgtatctgaaa gttacgaaaa ttttcgtaga cgaaggcccc 240
 agcatgaagc gcattatgcc gcgtgcacaaa ggtcgtgcag atcgcaccc tgaagcgacc 300
 agccacatca ctgtggtgt gtccgatcgc tga 333

<210> 228
 <211> 279
 <212> DNA
 <213> E. Coli

<400> 228
 atgccacgtt ctctcaagaa aggtcctttt attgacctgc acttgctgaa gaaggtagag 60
 aaagcggtgg aaagcggaga caagaagccc ctgcgcactt ggtcccgtcg ttcaacgac 120
 tttcctaaca tgatcggttt gaccatcgct gtccataatg gtcgtcagca cgttccggta 180
 tttgtaaccg acgaaatggt tggtcacaaa ctgggtgaat tcgcaccgac tcgtacttat 240
 cgcggccacg ctgctgataa aaaagcgag agaaataa 279

<210> 229
 <211> 822
 <212> DNA
 <213> E. Coli

<400> 229
 atggcagttg ttaaatgtaa accgacatct ccgggtcgtc gccacgtagt taaagtgtt 60
 aaccctgagc tgcacaaggg caaacctttt gtcctgtgca tggaaaaaaa cagcaaatcc 120
 ggtggtcgta acaacaatgg ccgtatcacc actcgtcata tcggtggtgg ccacaagcag 180
 gcttaccgta ttgttgactt caaacgcaac aaagacggta tcccggcagt tgttgaacgt 240
 cttagtagac atccgaaccg ttccgcgaac atcgcgtggt tttctgtaca agacggtgaa 300
 cgcctgtaca tcctggcccc taaaggcctg aaagctggcg accagattca gtctggcggt 360
 gatgctgcaa tcaaacagg taacaccctg ccgatgcgca acatcccgtg tgggttctact 420
 gttcataacg tagaaatgaa accaggtaaa ggcggtcagc tggcacgttc cgctgggtact 480
 tacgttcaga tcgttgctcg tgatggtgct tatgtcacc tgcgtctgca tttctggtgaa 540
 atgctgtaag tagaagcaga ctgcctgca actctggcg aagttggcaa tgctgagcat 600
 atgctgctcg tttctgggtaa agcaggtgct gcacgtggcg gtggtgttcg tccgaccgtt 660
 cgcggtaccg cgatgaaccc ggtagaccac ccacatgggt gtggtgaagg tcgtaacttt 720
 ggtaagcacc cggttaactc gtggggcggt cagaccaaag gtaagaagac ccgcagcaac 780
 aagcgtactg ataaattcat cgtacgtcgc cgtagcaaat aa 822

<210> 230
 <211> 303
 <212> DNA
 <213> E. Coli

<400> 230
 atgattcgtg aagaacgtct gctgaagggt ctgcgtgcac cgcacgtttc tgaaaaagcg 60
 tctactgcga tggaaaaatc caacaccatc gtactcaaag ttgctaaaaga cgcgacccaa 120
 gcagaaatca aagctgctgt gcagaaactg tttgaagtcg aagtcgaagt cgttaacacc 180
 ctggtagtta aagggaaggt taaacgtcac ggacagcgta tcggtcgtcg tagcgactgg 240
 aaaaaagcgt acgtcacccc gaaagaagcg cagaatctgg acttcgttgg cggcgctgag 300
 taa 303

<210> 231
 <211> 630
 <212> DNA

<213> E. Coli

<400> 231

atgattgggt	tagtcggttaa	aaaagtgggt	atgaccgta	tcttcacaga	agacggcggt	60
tctatcccag	taaccgtaat	cgaagttgaa	gcaaaccgcg	ttactcaggt	taaagacctg	120
gctaaccgatg	gctaccgtgc	tattcaggtg	accaccggtg	ctaaaaaagc	taaccgtgtg	180
accaagcctg	aagctggcca	cttcgctaaa	gctggcgtag	aagctggccg	tggtctgtgg	240
gaattccgcc	tggtggaag	cgaagagttc	actgtaggtc	agagcattag	cggtgaactg	300
tttgctgacg	ttaaaaaagt	tgacgtaact	ggcacctcta	aaggtaaagg	tttcgcaggt	360
accgttaagc	gctggaaactt	ccgtaccag	gacgctactc	acggtaactc	cttgtctcac	420
cgcgttcg	gttctatcgg	tcagaaccag	actccgggca	aagtgttcaa	aggcaagaaa	480
atggcaggtc	agatgggtaa	cgaacgtgta	accgttcaga	gccttgacgt	agtacgcgtt	540
gacgctgagc	gcaacctgct	gctgggttaa	ggtgctgtcc	cggttgcaac	cggtagcgac	600
ctgatcgta	aaccagctgt	gaaggcgtaa				630

<210> 232

<211> 606

<212> DNA

<213> E. Coli

<400> 232

atggaattag	tattgaaaga	cgcgagagc	gcgctgactg	tttccgaaac	taccttcggt	60
cgtagattca	acgaagcgct	ggttcaccag	gttggtgttg	cttatgcagc	tggtgctcgt	120
cagggtactc	gtgctcagaa	gactcgtgct	gaagtaactg	gttccggtaa	aaaaccgtgg	180
cgccagaaaag	gcaccggccg	tgcgcggttct	ggttcratca	agagcccgat	ctggcggttct	240
gggtggcgta	cctttgtgct	tcgtccgcag	gaccacagtc	aaaaagttaa	caagaagatg	300
taccgcggcg	cgctgaaaaa	catcctgtcc	gaactgggtac	gtcaggatcg	tctgatcggt	360
gtcgagaaagt	tctctgtaga	agcgccgaaa	actaagctgc	tggtcacagaa	actgaaagac	420
atggctctgg	aagatgtgct	gatcatcacc	ggtgagctgg	acgaaaaacct	gttcctggct	480
gcgcgcaacc	tgacacaagg	tgacgtacgc	gatgcaactg	gtatcgaccc	ggttagcctg	540
atgccttcg	acaaagtcgt	aatgactgct	gatgctgtta	agcaagttga	ggagatgctg	600
gcata						606

<210> 233

<211> 312

<212> DNA

<213> E. Coli

<400> 233

atgcagaacc	aaagaatccg	tatccgcctg	aaagcggttg	atcatcgctc	gatcgatcaa	60
gcaaccgcgg	aaatcgctga	gactgccaag	cgactgggtg	cgaggtccg	tggtccgatc	120
ccgctgccga	cacgcaaaga	gcgcttcact	gttctgatct	ccccgcagct	caacaaagac	180
gcgcgcgatc	agtacgaaat	ccgtactcac	ttgcgtctgg	ttgacatcgt	tgagccaacc	240
gagaaaaccg	ttgatgctct	gatgcgtctg	gatctggctg	ccggtgtaga	cgtgcagatc	300
agcctgggtt	aa					312

<210> 234

<211> 357

<212> DNA

<213> E. Coli

<400> 234

atggctcgcg	taaaaagctgg	tggtattgca	cgtgcacgtc	acaagaaaat	tttgaacaa	60
gctaaaggct	actacggtgc	gcgttctcgc	gtataccgcg	ttgccttcca	ggctgttatc	120
aaagctggtc	agtatgctta	ccgtgaccgt	cgtcaacgta	agcgtcagtt	ccgtcaactg	180
tggtatgcgc	gtatcaacgc	agcagcacgt	cagaacggtg	tttcttacag	caaattcatc	240
aatggcctga	aaaaagcctc	tggtgaaatc	gaccgtaaga	tectggctga	tatcgagta	300
ttcgacaaaag	tagcgttcac	cgctctggtt	gaaaaagcga	aagcagctct	ggcataa	357

<210> 235

<211> 198

<212> DNA
<213> E. Coli

<400> 235

atgccaaaaa	ttaagaccgt	acgcgggtgct	gctaagcgct	tcaaaaaaac	cggtaaaggt	60
ggtttttaagc	acaagcacgc	taacctgcgt	cacattctga	ccaaaaaagc	gaccaaacgt	120
aaacgtcacc	tgcgctccgaa	agccatggtt	tccaaaggcg	atctgggcct	ggtaatcgcg	180
tgcttgccgt	acgcataa					198

<210> 236
<211> 543
<212> DNA
<213> E. Coli

<400> 236

attaaaggcg	gaaaacgagt	tcaaacggcg	cgccctaacc	gtatcaatgg	cgaaattcgc	60
gcccaggaag	ttcgcttaac	aggtctggaa	ggcgagcagc	ttggtattgt	gagctctgaga	120
gaagctctgg	agaaagcaga	agaagccgga	gtagacttag	tcgagatcag	ccctaacgcc	180
gagccgccc	tttgtcgat	aatggattac	ggcaaattcc	tctatgaaaa	gagcaagtct	240
tctaagggaac	agaagaaaaa	gcaaaaagtt	atccagggtta	aggaaattaa	attccgtcct	300
ggtaacagatg	aaggcgacta	tcaggtaaaa	ctccgcagcc	tgattcgctt	tctcgaaagag	360
gggtgataaag	ccaaaatcac	gctgctgttc	cgcggtcgtg	agatggcgca	ccagcaaatac	420
ggatcggaag	tgcttaatcg	cgtgaaagac	gatttgcaag	aactggcagc	ggtcgaatcc	480
ttcccaacga	agatcgaaag	ccgccagatg	atcatggtgc	tcgctcctaa	gaagaaacag	540
taa						543

<210> 237
<211> 1929
<212> DNA
<213> E. Coli

<400> 237

atgcctgttta	taactcttcc	tgatggcagc	caacgccatt	acgatcacgc	tgtaagcccc	60
atggatgttg	cgctggacat	tggtccaggt	ctggcgaaaag	cctgtatcgc	agggcgcggtt	120
aatggcgaaac	tggttgatgc	ttgcgatctg	attgaaaacg	acgcacaact	gtcgatcatt	180
accgccaaaag	acgaagaagg	tctggagatc	attcgtcact	cctgtgcgca	cctgttaggg	240
cacgcgatta	aacaactttg	gcgcataacc	aaaatggcaa	tcggcccgggt	tattgacaac	300
ggtttttatt	acgacgttga	tcctgaccgc	acgttaaccc	aggaagatgt	cgaagcactc	360
gagaagcgga	tgcatgagct	tgctgagaaa	aactacgacg	tcattaagaa	gaaagtcagc	420
tggcacgaag	cgctgaaaac	tttcgccaac	cgtggggaga	gctacaaaag	ctccattctt	480
gacgaaaaca	tcgcccataga	tgacaagcca	ggtctgtact	tccatgaaga	atatgtcgat	540
atgtgcccg	gtccgcacgt	accgaacatg	cgtttctgcc	atcatttcaa	actaatgaaa	600
acggcagggg	cttactggcg	tggcgacagc	aacaacaaaa	tgctgcaacg	tatttacggt	660
acggcggtggg	cagacaaaaa	agcacttaac	gcttacctgc	agcgccctgga	agaagccgcg	720
aaacgcgacc	accgtaaaat	cggtaaaacg	ctcgacctgt	accatataca	ggaagaagcg	780
ccgggtatgg	tattctggca	caacgacggc	tggaacctct	tccgtgaact	ggaagtgttt	840
gttcgttcta	aactgaaaag	gtaccagtat	caggaagtta	aagggtccgtt	catgatggac	900
cgtgtcctgt	gggaaaaaac	cggtcactgg	gacaactaca	aagatgcaat	gttcaccaca	960
tcttctgaga	accgtgaata	ctgcattaa	ccgatgaact	gcccgggtca	cgtacaaatt	1020
ttcaaccagg	ggctgaagtc	ttatcgcgat	ctgccgctgc	gtatggccga	gtttggtagc	1080
tgccaccgta	acgagccgtc	agggttcgtg	catggcctga	tgccgctg	tggtattacc	1140
caggatgacg	cgcatatctt	ctgtactgaa	gaacaaatc	gcgatgaagt	taacggatgt	1200
atccgttttag	tctatgatat	gtacagcact	tttggtctcg	agaagatcgt	cgtcaaaactc	1260
tccactcgtc	ctgaaaaacg	tattggcagc	gacgaaatgt	gggatcgtgc	tgaggcgagc	1320
ctggcggttg	cgctggaaga	aaacaacatc	ccgtttgaat	atcaactggg	tgaagcgct	1380
ttctacggtc	cgaaaattga	atttaccctg	tatgactgcc	tcgatcgtgc	atggcagtc	1440
ggtaacagtac	agctggactt	ctctttgcg	tctcgtctga	gcgcttctta	tgtaggcgaa	1500
gacaatgaac	gtaaaagtacc	ggtaaatgatt	caccgcgcaa	ttctggggtc	gatggaaact	1560
ttcatcggtta	tcctgaccga	agagttcgct	ggtttcttcc	cgacctgggt	tcgcccgggt	1620
caggttggtta	tcatgaatat	taccgattca	cagttctgaat	acgttaacga	attgacgcaa	1680
aaactatcaa	atgcgggcat	tcgtgttaaa	gcagacttga	gaaatgagaa	gattggcttt	1740

aaaaatccgcg	agcacacttt	gcgtcgcgtc	ccatatatgc	tggctctgtg	tgataaagag	1800
gtggaatcag	gcaaagtgc	cggtcgcacc	cgccgtggta	aagacctggg	aagcatggac	1860
gtaaatgaag	tgatcgagaa	gctgcaacaa	gagattcgca	gccgcagctc	taaacattg	1920
gaggaataa						1929

<210> 238
 <211> 1353
 <212> DNA
 <213> E. Coli

<400> 238

atgactaaac	actatgatta	catcgccatc	ggcggcgcca	gcggcggtat	cgccctccatc	60
aaccgcgcgg	ctatgtacgg	ccagaaatgt	gcgctgattg	aagccaaaga	gctgggcggc	120
acctgcgtaa	atgttggctg	tgtgccgaaa	aaagtgatgt	ggcacgcggc	gcaaatccgt	180
gaagcgatcc	atatgtacgg	cccggattat	ggttttgata	ccactatcaa	taaattcaac	240
tgggaaacgt	tgatcgccag	ccgtaccgcc	tatatcgacc	gtattcatac	ttcctatgaa	300
aacgtgctcg	gtaaaaataa	cgttgatgta	atcaaaggct	tgcccgcgtt	cgttgatgcc	360
aaaacgctgg	aggtaaacgg	cgaaaccatc	acggccgcatc	atattctgat	cgccacaggc	420
ggtcgtccga	gccaccgcga	tattccgggc	gtggaatacg	gtattgattc	tgatggcttc	480
ttcgcccttc	ctgctttgcc	agagcgcgtg	gcggttqttg	gcgcgggtta	catcgccgtt	540
gagctggcgg	gcgtgattaa	cgccctcggc	gcgaaaacgc	atctgtttgt	gcgtaaacat	600
gcgccctgct	gcagcttcga	cccgatgatt	tccgaaacgc	tggtcgaaat	gatgaacgcc	660
gaaggcccg	agctgcacac	caacgcctac	ccgaaagcgg	tagtgaaaaa	taccgatggt	720
agcctgacgc	tggaagctgga	agatggctcg	agtgaacgg	tggtttgcct	gatttggggc	780
attggtcgcg	agcctgcca	tgacaacatc	aacctggaag	ccgctggcgt	taaaactaac	840
gaaaaaggct	atatcgctgt	cgataaatat	caaaacacca	atattgaagg	tatttacgcg	900
gtgggcgata	acacgggtgc	agtggagctg	acaccgggtg	cagttgcagc	gggtcgccgt	960
ctctctgaac	gcctgtttaa	taacaagcgg	gatgagcatc	tggtattacg	caacattccg	1020
accgtggtct	tcagccatcc	gccgattggt	actgttggtt	taacggaacc	gcaggcgccg	1080
gagcagtatg	gcgacgatca	ggtgaaagtg	tataaatcct	ctttcaccgc	gatgtatacc	1140
gccgtcacca	ctcaccgcca	gccgtgccgc	atgaagctgg	tgtgcgttgg	atcggaagag	1200
aaqattgtcg	gtattcacgg	cattggcttt	ggtatggacg	aaatgttgca	gggcttcgcg	1260
gtggcgctga	agatgggggc	aaccaaaaaa	gacttcgaca	ataccgtcgc	cattcaccca	1320
acggcgcgag	aagagttcgt	gacaatgcgt	taa			1353

<210> 239
 <211> 2904
 <212> DNA
 <213> E. Coli

<400> 239

aaagttaagc	ctcacggttc	attagtagcg	gttagctcaa	cgcatcgctg	cgcttacaca	60
cccgccctat	caacgtcgtc	gtcttcaacg	ttccttcagg	acccttaaa	ggtcagggag	120
aactcatctc	ggggcaagtt	tcgtgcttag	atgctttcag	cacttatctc	ttccgcattt	180
agctaccggg	cagtgccatt	ggcatgacaa	cccgaacacc	agtgatgcgt	ccactccggg	240
cctctcgtac	taggagcagc	cccctcagt	tctccagcgc	ccacggcaga	tagggaccga	300
actgtctcac	gacgttctaa	acccagctcg	cgtaccactt	taaatggcga	acagccatac	360
ccttggggacc	tacttcagcc	ccaggatgtg	atgagccgac	atcgagggtc	caaacaccgc	420
cgctgatatg	aactcttggg	cggtatcagc	ctgttatccc	cggagtagct	tttatccgtt	480
gagcgatggc	ccttccattc	agaaccaccg	gatcactatg	acctgcttcc	gcacctgctc	540
gcgccgtcac	gctcgagtc	aagctggctt	atgccattgc	actaacctcc	tgatgtccga	600
ccaggattag	ccaaccttcg	tgctcctccg	ttactcttta	ggaggagacc	gcccagtcga	660
aactacccac	cagacactgt	ccgcaacccg	gattacgggt	caacgttaga	acatcaaaaca	720
ttaaagggtg	gtatttcaag	gtcggtccca	tgacagactg	cgtccacact	tcaaagcctc	780
ccacctatcc	tacacatcaa	ggctcaatgt	tcagtgtcaa	gctatagtaa	aggttcacgg	840
ggtctttccg	tcttggccgg	ggtacactgc	atcttcacag	cgagttcaat	ttcactgagt	900
ctcgggtgga	gacagcctgg	ccatcattac	gccattcgtg	caggtcggaa	cttaccggac	960
aaggaatttc	gctaccttag	gaccgttata	gttacggccg	ccgtttaccg	gggcttcgat	1020
caagagcttc	gcttgcgcta	accccatcaa	ttaaccttec	ggcaccgggc	aggcgctaca	1080
ccgtatacgt	ccactttcgt	gtttgcacag	tgctgtgttt	ttataaaaca	gttcagacca	1140
gctggtatct	tcgactgatt	tcagctccat	ccgcgaggga	cctcacctac	atatcagcgt	1200

```

gccttctccc gaagttacgg caccattttg cctagtctct tcacccgagt tctctcaagc 1260
gccttggtat tctctacctg accacctgtg tcggtttggg gtacgatttg atgttacctg 1320
atgcttagag gcttttccctg gaagcagggc atttggtgct tcagcaccgt agtgccctcgt 1380
catcacgctt cagccttgat tttccggatt tgcctggaaa accagcctac acgcttaaac 1440
cgggacaacc gtcgcccggc caacatagcc ttctccgtcc ccccttcgca gtaacaccaa 1500
gtacaggaaat attaacctgt ttcccatcga ctacgccttt cggcctcggc ttaggggtcg 1560
actcaccctg ccccgattaa cgttgacag gaacccttgg tcttccggcg agcgggcttt 1620
tcaccgctt tctcgttact tatgtcagca ttcgcacttc tgatacctcc agcatgcctc 1680
acagcacacc ttcgaggctt tacagaacgc tccctacccc aacaacgcat aagcgtcgtc 1740
gocgcagctt cgggtgcatg tttagccccg ttacatcttc cgcgcaggcc gactcgacca 1800
gtgagctatt acgctttctt taaatgatgg ctgcttctaa gccaacatcc tggctgtctg 1860
ggccttccca catcgtttcc cacttaacca tgactttggg accttagctg gcggtctggg 1920
ttgtttccct cttcacgacg gacgttagca cccgccgtgt gtctcccggt ataactttct 1980
ccggtattcg cagtttgcat cgggttggtg agtcgggatg accccttgc cgaacacagt 2040
ctctaccccc ggagatgaat tcacgaggcg ctacctaaat agctttcggg gagaaccagc 2100
tatctcccggt tttgattggc ctttcacccc cagccacaag tcacccgcta atttttcaac 2160
attagtcggt tcggtcctcc agttagtgtt acccaacctt caacctgccc atggctagat 2220
caccgggttt cgggtctata ccctgcaact taacgcccag ttaagactcg gtttcccttc 2280
ggctccctta ttcggttaac cttgctacag aatataagtc gctgacctat tatacaaaag 2340
gtacgcagtc acacgcctaa gcgtgctccc actgcttgta cgtacacggt ttcaggttct 2400
ttttcactcc cctcgccggg gttcttttct cctttccctc acggtactgg ttcactatcg 2460
gtcagtcagg agtatttagc cttggaggat ggtcccccca tattcagaca ggataccacg 2520
tgtcccgccc tactcatcga gctcacagca tgtgcatttt tgtgtacggg gctgtcacc 2580
tgtatcgcg ccttttccag acgcttccac taacacacac actgattcag gctctgggct 2640
gctccccgtt cgtcgcgcgc tactggggga atctcggtt atttcttttc ctcggggtac 2700
ttagatgttt cagttccccc ggttcgcctc attaacctat ggattcagtt aatgatagtg 2760
tgtcgaaaaca cactgggttt ccccatcggg aaatcgccgg ttataacggt tcataacc 2820
ttaccgacgc ttatcgcgaga ttacgacgtc cttcatcgcc tctgactgcc agggcatcca 2880
ccgtgtacgc ttagtcgctt aacc 2904

```

<210> 240
 <211> 120
 <212> DNA
 <213> E. Coli

```

<400> 240
atgcctggca gttccctact ctgcgatggg gagaccccac actaccatcg gcgctacggc 60
gtttcacttc tgagttcggc atggggtcag gtgggaccac cgcgctacgg cgcgacggca 120

```

<210> 241
 <211> 76
 <212> DNA
 <213> E. Coli

```

<400> 241
gtccctttcg tctagaggcc caggacaccg ccctttcacg gcggtaacag gggttcgaat 60
cccctagggg acgcca 76

```

<210> 242
 <211> 1549
 <212> DNA
 <213> E. Coli

```

<400> 242
aaattgaaga gtttgatcat ggctcagatt gaacgctggc ggaggcccta acacatgcaa 60
gtcgaacggt aacagggaag agcttgctgc ttgcgtgacg agtgccggac gggtagtaaa 120
tgtctgggaa gctgcctgat ggagggggat aactactgga aacggtagct aataccgcat 180
aatgtcgcaa gaccaaagag ggggaccttc gggcctcttg ccacgtagt tgcccagatg 240
ggattagctt gttggtgggg taacggctca ccaaggcgac gatccctagc tggctgaga 300
ggatgaccag ccacactgga actgagacac ggtccagact cctacgggag gcagcagtg 360
ggaatattgc acaatggggc caagcctgat gcagccatgc cgcgtgtatg aagaaggcct 420

```

```

tcgggttgta aagtactttc agcggggagg aaggagtaa agttaatacc tttgctcatt 480
gacgttaccg gcagaagaag caccggctaa ctccgtgccg gcagccgagg taatacggag 540
gggtgcaagcg ttaacgga ttaactggcg taaagcgac gcagcgagg tgggtaagtc 600
agatgtgaaa tccccgggct caacctggga actgcatctg atactggcaa gcttgagtct 660
cgtagagggg ggtagaattc caggtgtagc ggtgaaatgc gtagagatct ggaggaatac 720
cggtggcgaa ggcggccccc tggacgaaga ctgacgctca ggtgcgaaag cgtggggagc 780
aaacaggatt agataccctg gtagtccacg ccgtaaacga tgtcgacttg gaggttggtc 840
ccttgaggcg tggcttcgg agctaacgcg ttaagtcgac cgcctgggga gtacggccgc 900
aaggttaaaa ctcaaatgaa ttgacggggg cccgcacaag cgggtggagca tgtggtttaa 960
ttcgatgcaa cgcgaagaac cttacctggt cttgacatcc acggaagttt tcagagatga 1020
gaatgtgcct tcgggaaccg tgagacaggt gctgcatggc tgctgctcagc tcgtgttgtg 1080
aaatgttggg ttaagtcccg caacgagcgc aacccttacc cttgtgtgcc agcgggtccg 1140
ccgggaactc aaaggagact gccagtata aactggagga aggtggggat gacgtcaagt 1200
catcatggcc cttacgacca gggctacaca cgtgctacaa tggcgcatc aaagagaagc 1260
gacctcgcca gagcaagcgg acctcataaa gtgcgtcgta gtccggattg gactctgcaa 1320
ctcgactcca tgaagtcgga atcgctagta atcggtggatc agaatgccac ggtgaatacg 1380
ttccggggcc ttgtacacac cgcccgctcac accatgggag tgggttgcaa aagaagtagg 1440
tagcttaacc ttggggaggg cgcttaccac tttgtgattc atgactgggg tgaagtcgta 1500
acaaggtaac cgtaggggaa cctgcggttg gatcacctcc ttaccttaa 1549

```

<210> 243

<211> 221

<212> PRT

<213> E. Coli

<400> 243

```

Met Asn Val Phe Ser Gln Thr Gln Arg Tyr Lys Ala Leu Phe Trp Leu
1 5 10 15
Ser Leu Phe His Leu Leu Val Ile Thr Ser Ser Asn Tyr Leu Val Gln
20 25 30
Leu Pro Val Ser Ile Leu Gly Phe His Thr Thr Trp Gly Ala Phe Ser
35 40 45
Phe Pro Phe Ile Phe Leu Ala Thr Asp Leu Thr Val Arg Ile Phe Gly
50 55 60
Ala Pro Leu Ala Arg Arg Ile Ile Phe Ala Val Met Ile Pro Ala Leu
65 70 75 80
Leu Ile Ser Tyr Val Ile Ser Ser Leu Phe Tyr Met Gly Ser Trp Gln
85 90 95
Gly Phe Gly Ala Leu Ala His Phe Asn Leu Phe Val Ala Arg Ile Ala
100 105 110
Thr Ala Ser Phe Met Ala Tyr Ala Leu Gly Gln Ile Leu Asp Val His
115 120 125
Val Phe Asn Arg Leu Arg Gln Ser Arg Arg Trp Trp Leu Ala Pro Thr
130 135 140
Ala Ser Thr Leu Phe Gly Asn Val Ser Asp Thr Leu Ala Phe Phe Phe
145 150 155 160
Ile Ala Phe Trp Arg Ser Pro Asp Ala Phe Met Ala Glu His Trp Met
165 170 175
Glu Ile Ala Leu Val Asp Tyr Cys Phe Lys Val Leu Ile Ser Ile Val
180 185 190
Phe Phe Leu Pro Met Tyr Gly Val Leu Leu Asn Met Leu Leu Lys Arg
195 200 205
Leu Ala Asp Lys Ser Glu Ile Asn Ala Leu Gln Ala Ser
210 215 220

```

<210> 244

<211> 203

<212> PRT

<213> E. Coli

<400> 244

```

Met Ile Arg Trp Met Asn Glu Pro Leu Trp Pro Phe Ile Glu Arg Lys
 1           5           10           15
Lys Ser Met Arg Asn Leu Val Lys Tyr Val Gly Ile Gly Leu Leu Val
 20           25           30
Met Gly Leu Ala Ala Cys Asp Asp Lys Asp Thr Asn Ala Thr Ala Gln
 35           40           45
Gly Ser Val Ala Glu Ser Asn Ala Thr Gly Asn Pro Val Asn Leu Leu
 50           55           60
Asp Gly Lys Leu Ser Phe Ser Leu Pro Ala Asp Met Thr Asp Gln Ser
 65           70           75           80
Gly Lys Leu Gly Thr Gln Ala Asn Asn Met His Val Trp Ser Asp Ala
 85           90           95
Thr Gly Gln Lys Ala Val Ile Val Ile Met Gly Asp Asp Pro Lys Glu
100           105           110
Asp Leu Ala Val Leu Ala Lys Arg Leu Glu Asp Gln Gln Arg Ser Arg
115           120           125
Asp Pro Gln Leu Gln Val Val Thr Asn Lys Ala Ile Glu Leu Lys Gly
130           135           140
His Lys Met Gln Gln Leu Asp Ser Ile Ile Ser Ala Lys Gly Gln Thr
145           150           155           160
Ala Tyr Ser Ser Val Ile Leu Gly Asn Val Gly Asn Gln Leu Leu Thr
165           170           175
Met Gln Ile Thr Leu Pro Ala Asp Asp Gln Gln Lys Ala Gln Thr Thr
180           185           190
Ala Glu Asn Ile Ile Asn Thr Leu Val Ile Gln
195           200

```

<210> 245

<211> 324

<212> PRT

<213> E. Coli

<400> 245

```

Met Ala Asn Met Phe Ala Leu Ile Leu Val Ile Ala Thr Leu Val Thr
 1           5           10           15
Gly Ile Leu Trp Cys Val Asp Lys Phe Phe Ala Pro Lys Arg Arg
 20           25           30
Glu Arg Gln Ala Ala Ala Gln Ala Ala Ala Gly Asp Ser Leu Asp Lys
 35           40           45
Ala Thr Leu Lys Lys Val Ala Pro Lys Pro Gly Trp Leu Glu Thr Gly
 50           55           60
Ala Ser Val Phe Pro Val Leu Ala Ile Val Leu Ile Val Arg Ser Phe
 65           70           75           80
Ile Tyr Glu Pro Phe Gln Ile Pro Ser Gly Ser Met Met Pro Thr Leu
 85           90           95
Leu Ile Gly Asp Phe Ile Leu Val Glu Lys Phe Ala Tyr Gly Ile Lys
100           105           110
Asp Pro Ile Tyr Gln Lys Thr Leu Ile Glu Thr Gly His Pro Lys Arg
115           120           125
Gly Asp Ile Val Val Phe Lys Tyr Pro Glu Asp Pro Lys Leu Asp Tyr
130           135           140
Ile Lys Arg Ala Val Gly Leu Pro Gly Asp Lys Val Thr Tyr Asp Pro
145           150           155           160
Val Ser Lys Glu Leu Thr Ile Gln Pro Gly Cys Ser Ser Gly Gln Ala
165           170           175
Cys Glu Asn Ala Leu Pro Val Thr Tyr Ser Asn Val Glu Pro Ser Asp
180           185           190
Phe Val Gln Thr Phe Ser Arg Arg Asn Gly Gly Glu Ala Thr Ser Gly

```

[illegible]

```
<210> 246
<211> 586
<212> PRT
<213> E. Coli
```

<400> 246																
Met	Thr	Ile	Thr	Lys	Leu	Ala	Trp	Arg	Asp	Leu	Val	Pro	Asp	Thr	Asp	
1				5					10					15		
Ser	Tyr	Gln	Glu	Ile	Phe	Ala	Gln	Pro	His	Leu	Ile	Asp	Glu	Asn	Asp	
			20					25					30			
Pro	Leu	Phe	Ser	Asp	Thr	Gln	Pro	Arg	Leu	Gln	Phe	Ala	Leu	Glu	Gln	
		35					40					45				
Leu	Leu	His	Thr	Arg	Ala	Ser	Ser	Ser	Phe	Met	Leu	Ala	Lys	Ala	Pro	
	50					55				60						
Glu	Glu	Ser	Glu	Tyr	Leu	Asn	Leu	Ile	Ala	Asn	Ala	Ala	Arg	Thr	Leu	
65					70					75					80	
Gln	Ser	Asp	Ala	Gly	Gln	Leu	Val	Gly	Gly	His	Tyr	Glu	Val	Ser	Gly	
				85					90					95		
His	Ser	Ile	Arg	Leu	Arg	His	Ala	Val	Ser	Ala	Asp	Asp	Asn	Phe	Ala	
			100					105					110			
Thr	Leu	Thr	Gln	Val	Val	Ala	Ala	Asp	Trp	Val	Glu	Ala	Glu	Gln	Leu	
		115					120					125				
Phe	Gly	Cys	Leu	Arg	Gln	Phe	Asn	Gly	Asp	Ile	Thr	Leu	Gln	Pro	Gly	
	130					135					140					
Leu	Val	His	Gln	Ala	Asn	Gly	Gly	Ile	Leu	Ile	Ile	Ser	Leu	Arg	Thr	
145					150					155					160	
Leu	Leu	Ala	Gln	Pro	Leu	Leu	Trp	Met	Arg	Leu	Lys	Asn	Ile	Val	Asn	
			165						170					175		
Arg	Glu	Arg	Phe	Asp	Trp	Val	Ala	Phe	Asp	Glu	Ser	Arg	Pro	Leu	Pro	
			180					185					190			
Val	Ser	Val	Pro	Ser	Met	Pro	Leu	Lys	Leu	Lys	Val	Ile	Leu	Val	Gly	
		195					200					205				
Glu	Arg	Glu	Ser	Leu	Ala	Asp	Phe	Gln	Glu	Met	Glu	Pro	Glu	Leu	Ser	
	210					215					220					
Glu	Gln	Ala	Ile	Tyr	Ser	Glu	Phe	Glu	Asp	Thr	Leu	Gln	Ile	Val	Asp	
				230					235					240		
Ala	Glu	Ser	Val	Thr	Gln	Trp	Cys	Arg	Trp	Val	Thr	Phe	Thr	Ala	Arg	
			245						250					255		
His	Asn	His	Leu	Pro	Ala	Pro	Gly	Ala	Asp	Ala	Trp	Pro	Ile	Leu	Ile	
			260					265					270			
Arg	Glu	Ala	Ala	Arg	Tyr	Thr	Gly	Glu	Gln	Glu	Thr	Leu	Pro	Leu	Ser	

```

      275      280      285
Pro Gln Trp Ile Leu Arg Gln Cys Lys Glu Val Ala Ser Leu Cys Asp
290      295      300
Gly Asp Thr Phe Ser Gly Glu Gln Leu Asn Leu Met Leu Gln Gln Arg
305      310      315      320
Glu Trp Arg Glu Gly Phe Leu Ala Glu Arg Met Gln Asp Glu Ile Leu
      325      330      335
Gln Glu Gln Ile Leu Ile Glu Thr Glu Gly Glu Arg Ile Gly Gln Ile
      340      345      350
Asn Ala Leu Ser Val Ile Glu Phe Pro Gly His Pro Arg Ala Phe Gly
355      360      365
Glu Pro Ser Arg Ile Ser Cys Val Val His Ile Gly Asp Gly Glu Phe
370      375      380
Thr Asp Ile Glu Arg Lys Ala Glu Leu Gly Gly Asn Ile His Ala Lys
385      390      395      400
Gly Met Met Ile Met Gln Ala Phe Leu Met Ser Glu Leu Gln Leu Glu
      405      410      415
Gln Gln Ile Pro Phe Ser Ala Ser Leu Thr Phe Glu Gln Ser Tyr Ser
      420      425      430
Glu Val Asp Gly Asp Ser Ala Ser Met Ala Glu Leu Cys Ala Leu Ile
435      440      445
Ser Ala Leu Ala Asp Val Pro Val Asn Gln Ser Ile Ala Ile Thr Gly
450      455      460
Ser Val Asp Gln Phe Gly Arg Ala Gln Pro Val Gly Gly Leu Asn Glu
465      470      475      480
Lys Ile Glu Gly Phe Phe Ala Ile Cys Gln Gln Arg Glu Leu Thr Gly
      485      490      495
Lys Gln Gly Val Ile Ile Pro Thr Ala Asn Val Arg His Leu Ser Leu
500      505      510
His Ser Glu Leu Val Lys Ala Val Glu Glu Gly Lys Phe Thr Ile Trp
515      520      525
Ala Val Asp Asp Val Thr Asp Ala Leu Pro Leu Leu Leu Asn Leu Val
530      535      540
Trp Asp Gly Glu Gly Gln Thr Thr Leu Met Gln Thr Ile Gln Glu Arg
545      550      555      560
Ile Ala Gln Ala Ser Gln Gln Glu Gly Arg His Arg Phe Pro Trp Pro
565      570      575
Leu Arg Trp Leu Asn Trp Phe Ile Pro Asn
580      585

```

<210> 247
 <211> 394
 <212> PRT
 <213> E. Coli

```

      <400> 247
Met Ser Lys Glu Lys Phe Glu Arg Thr Lys Pro His Val Asn Val Gly
1      5      10      15
Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
20      25      30
Thr Thr Val Leu Ala Lys Thr Tyr Gly Gly Ala Ala Arg Ala Phe Asp
35      40      45
Gln Ile Asp Asn Ala Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
50      55      60
Thr Ser His Val Glu Tyr Asp Thr Pro Thr Arg His Tyr Ala His Val
65      70      75      80
Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
85      90      95
Ala Gln Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro
100      105      110

```

```

Met Pro Gln Thr Arg Glu His Ile Leu Leu Gly Arg Gln Val Gly Val
  115      120      125
Pro Tyr Ile Ile Val Phe Leu Asn Lys Cys Asp Met Val Asp Asp Glu
  130      135      140
Glu Leu Leu Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ser Gln
  145      150      155      160
Tyr Asp Phe Pro Gly Asp Asp Thr Pro Ile Val Arg Gly Ser Ala Leu
  165      170      175
Lys Ala Leu Glu Gly Asp Ala Glu Trp Glu Ala Lys Ile Leu Glu Leu
  180      185      190
Ala Gly Phe Leu Asp Ser Tyr Ile Pro Glu Pro Glu Arg Ala Ile Asp
  195      200      205
Lys Pro Phe Leu Leu Pro Ile Glu Asp Val Phe Ser Ile Ser Gly Arg
  210      215      220
Gly Thr Val Val Thr Gly Arg Val Glu Arg Gly Ile Ile Lys Val Gly
  225      230      235      240
Glu Glu Val Glu Ile Val Gly Ile Lys Glu Thr Gln Lys Ser Thr Cys
  245      250      255
Thr Gly Val Glu Met Phe Arg Lys Leu Leu Asp Glu Gly Arg Ala Gly
  260      265      270
Glu Asn Val Gly Val Leu Leu Arg Gly Ile Lys Arg Glu Glu Ile Glu
  275      280      285
Arg Gly Gln Val Leu Ala Lys Pro Gly Thr Ile Lys Pro His Thr Lys
  290      295      300
Phe Glu Ser Glu Val Tyr Ile Leu Ser Lys Asp Glu Gly Gly Arg His
  305      310      315      320
Thr Pro Phe Phe Lys Gly Tyr Arg Pro Gln Phe Tyr Phe Arg Thr Thr
  325      330      335
Asp Val Thr Gly Thr Ile Glu Leu Pro Glu Gly Val Glu Met Val Met
  340      345      350
Pro Gly Asp Asn Ile Lys Met Val Val Thr Leu Ile His Pro Ile Ala
  355      360      365
Met Asp Asp Gly Leu Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Val
  370      375      380
Gly Ala Gly Val Val Ala Lys Val Leu Gly
  385      390

```

<210> 248
 <211> 704
 <212> PRT
 <213> E. Coli

```

<400> 248
Met Ala Arg Thr Thr Pro Ile Ala Arg Tyr Arg Asn Ile Gly Ile Ser
  1      5      10      15
Ala His Ile Asp Ala Gly Lys Thr Thr Thr Thr Glu Arg Ile Leu Phe
  20      25      30
Tyr Thr Gly Val Asn His Lys Ile Gly Glu Val His Asp Gly Ala Ala
  35      40      45
Thr Met Asp Trp Met Glu Gln Glu Gln Arg Gly Ile Thr Ile Thr
  50      55      60
Ser Ala Ala Thr Thr Ala Phe Trp Ser Gly Met Ala Lys Gln Tyr Glu
  65      70      75      80
Pro His Arg Ile Asn Ile Ile Asp Thr Pro Gly His Val Asp Phe Thr
  85      90      95
Ile Glu Val Glu Arg Ser Met Arg Val Leu Asp Gly Ala Val Met Val
  100      105      110
Tyr Cys Ala Val Gly Gly Val Gln Pro Gln Ser Glu Thr Val Trp Arg
  115      120      125

```

Gln Ala Asn Lys Tyr Lys Val Pro Arg Ile Ala Phe Val Asn Lys Met
 130 135 140
 Asp Arg Met Gly Ala Asn Phe Leu Lys Val Val Asn Gln Ile Lys Thr
 145 150 155 160
 Arg Leu Gly Ala Asn Pro Val Pro Leu Gln Leu Ala Ile Gly Ala Glu
 165 170 175
 Glu His Phe Thr Gly Val Val Asp Leu Val Lys Met Lys Ala Ile Asn
 180 185 190
 Trp Asn Asp Ala Asp Gln Gly Val Thr Phe Glu Tyr Glu Asp Ile Pro
 195 200 205
 Ala Asp Met Val Glu Leu Ala Asn Glu Trp His Gln Asn Leu Ile Glu
 210 215 220
 Ser Ala Ala Glu Ala Ser Glu Glu Leu Met Glu Lys Tyr Leu Gly Gly
 225 230 235 240
 Glu Glu Leu Thr Glu Ala Glu Ile Lys Gly Ala Leu Arg Gln Arg Val
 245 250 255
 Leu Asn Asn Glu Ile Ile Leu Val Thr Cys Gly Ser Ala Phe Lys Asn
 260 265 270
 Lys Gly Val Gln Ala Met Leu Asp Ala Val Ile Asp Tyr Leu Pro Ser
 275 280 285
 Pro Val Asp Val Pro Ala Ile Asn Gly Ile Leu Asp Asp Gly Lys Asp
 290 295 300
 Thr Pro Ala Glu Arg His Ala Ser Asp Asp Glu Pro Phe Ser Ala Leu
 305 310 315 320
 Ala Phe Lys Ile Ala Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe
 325 330 335
 Arg Val Tyr Ser Gly Val Val Asn Ser Gly Asp Thr Val Leu Asn Ser
 340 345 350
 Val Lys Ala Ala Arg Glu Arg Phe Gly Arg Ile Val Gln Met His Ala
 355 360 365
 Asn Lys Arg Glu Glu Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala
 370 375 380
 Ala Ile Gly Leu Lys Asp Val Thr Thr Gly Asp Thr Leu Cys Asp Pro
 385 390 395 400
 Asp Ala Pro Ile Ile Leu Glu Arg Met Glu Phe Pro Glu Pro Val Ile
 405 410 415
 Ser Ile Ala Val Glu Pro Lys Thr Lys Ala Asp Gln Glu Lys Met Gly
 420 425 430
 Leu Ala Leu Gly Arg Leu Ala Lys Glu Asp Pro Ser Phe Arg Val Trp
 435 440 445
 Thr Asp Glu Glu Ser Asn Gln Thr Ile Ile Ala Gly Met Gly Glu Leu
 450 455 460
 His Leu Asp Ile Ile Val Asp Arg Met Lys Arg Glu Phe Asn Val Glu
 465 470 475 480
 Ala Asn Val Gly Lys Pro Gln Val Ala Tyr Arg Glu Thr Ile Arg Gln
 485 490 495
 Lys Val Thr Asp Val Glu Gly Lys His Ala Lys Gln Ser Gly Gly Arg
 500 505 510
 Gly Gln Tyr Gly His Val Val Ile Asp Met Tyr Pro Leu Glu Pro Gly
 515 520 525
 Ser Asn Pro Lys Gly Tyr Glu Phe Ile Asn Asp Ile Lys Gly Gly Val
 530 535 540
 Ile Pro Gly Glu Tyr Ile Pro Ala Val Asp Lys Gly Ile Gln Glu Gln
 545 550 555 560
 Leu Lys Ala Gly Pro Leu Ala Gly Tyr Pro Val Val Asp Met Gly Ile
 565 570 575
 Arg Leu His Phe Gly Ser Tyr His Asp Val Asp Ser Ser Glu Leu Ala
 580 585 590
 Phe Lys Leu Ala Ala Ser Ile Ala Phe Lys Glu Gly Phe Lys Lys Ala
 595 600 605
 Lys Pro Val Leu Leu Glu Pro Ile Met Lys Val Glu Val Glu Thr Pro

610		615		620
Glu Glu Asn Thr Gly Asp Val Ile Gly Asp Leu Ser Arg Arg Arg Gly				
625		630		635
Met Leu Lys Gly Gln Glu Ser Glu Val Thr Gly Val Lys Ile His Ala				
	645		650	655
Glu Val Pro Leu Ser Glu Met Phe Gly Tyr Ala Thr Gln Leu Arg Ser				
	660		665	670
Leu Thr Lys Gly Arg Ala Ser Tyr Thr Met Glu Phe Leu Lys Tyr Asp				
	675		680	685
Glu Ala Pro Ser Asn Val Ala Gln Ala Val Ile Glu Ala Arg Gly Lys				
690		695		700

<210> 249
 <211> 179
 <212> PRT
 <213> E. Coli

<400> 249
Met Pro Arg Arg Val Ile Gly Gln Arg Lys Ile Leu Pro Asp Pro
1 5 10 15
Lys Phe Gly Ser Glu Leu Leu Ala Lys Phe Val Asn Ile Leu Met Val
20 25 30
Asp Gly Lys Lys Ser Thr Ala Glu Ser Ile Val Tyr Ser Ala Leu Glu
35 40 45
Thr Leu Ala Gln Arg Ser Gly Lys Ser Glu Leu Glu Ala Phe Glu Val
50 55 60
Ala Leu Glu Asn Val Arg Pro Thr Val Glu Val Lys Ser Arg Arg Val
65 70 75 80
Gly Gly Ser Thr Tyr Gln Val Pro Val Glu Val Arg Pro Val Arg Arg
85 90 95
Asn Ala Leu Ala Met Arg Trp Ile Val Glu Ala Ala Arg Lys Arg Gly
100 105 110
Asp Lys Ser Met Ala Leu Arg Leu Ala Asn Glu Leu Ser Asp Ala Ala
115 120 125
Glu Asn Lys Gly Thr Ala Val Lys Lys Arg Glu Asp Val His Arg Met
130 135 140
Ala Glu Ala Asn Lys Ala Phe Ala His Tyr Arg Trp Leu Ser Leu Arg
145 150 155 160
Ser Phe Ser His Gln Ala Gly Ala Ser Ser Lys Gln Pro Ala Leu Gly
165 170 175
Tyr Leu Asn

<210> 250
 <211> 124
 <212> PRT
 <213> E. Coli

<400> 250
Met Ala Thr Val Asn Gln Leu Val Arg Lys Pro Arg Ala Arg Lys Val
1 5 10 15
Ala Lys Ser Asn Val Pro Ala Leu Glu Ala Cys Pro Gln Lys Arg Gly
20 25 30
Val Cys Thr Arg Val Tyr Thr Thr Pro Lys Lys Pro Asn Ser Ala
35 40 45
Leu Arg Lys Val Cys Arg Val Arg Leu Thr Asn Gly Phe Glu Val Thr
50 55 60
Ser Tyr Ile Gly Gly Glu Gly His Asn Leu Gln Glu His Ser Val Ile
65 70 75 80

Leu Ile Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr His
 85 90 95
 Thr Val Arg Gly Ala Leu Asp Cys Ser Gly Val Lys Asp Arg Lys Gln
 100 105 110
 Ala Arg Ser Lys Tyr Gly Val Lys Arg Pro Lys Ala
 115 120

<210> 251
 <211> 165
 <212> PRT
 <213> E. Coli

<400> 251
 Met Ala Leu Asn Leu Gln Asp Lys Gln Ala Ile Val Ala Glu Val Ser
 1 5 10 15
 Glu Val Ala Lys Gly Ala Leu Ser Ala Val Val Ala Asp Ser Arg Gly
 20 25 30
 Val Thr Val Asp Lys Met Thr Glu Leu Arg Lys Ala Gly Arg Glu Ala
 35 40 45
 Gly Val Tyr Met Arg Val Val Arg Asn Thr Leu Leu Arg Arg Ala Val
 50 55 60
 Glu Gly Thr Pro Phe Glu Cys Leu Lys Asp Ala Phe Val Gly Pro Thr
 65 70 75 80
 Leu Ile Ala Tyr Ser Met Glu His Pro Gly Ala Ala Ala Arg Leu Phe
 85 90 95
 Lys Glu Phe Ala Lys Ala Asn Ala Lys Phe Glu Val Lys Ala Ala Ala
 100 105 110
 Phe Glu Gly Glu Leu Ile Pro Ala Ser Gln Ile Asp Arg Leu Ala Thr
 115 120 125
 Leu Pro Thr Tyr Glu Glu Ala Ile Ala Arg Leu Met Ala Thr Met Lys
 130 135 140
 Glu Ala Ser Ala Gly Lys Leu Val Arg Thr Leu Ala Ala Val Arg Asp
 145 150 155 160
 Ala Lys Glu Ala Ala
 165

<210> 252
 <211> 121
 <212> PRT
 <213> E. Coli

<400> 252
 Met Ser Ile Thr Lys Asp Gln Ile Ile Glu Ala Val Ala Ala Met Ser
 1 5 10 15
 Val Met Asp Val Val Glu Leu Ile Ser Ala Met Glu Glu Lys Phe Gly
 20 25 30
 Val Ser Ala Ala Ala Val Ala Val Ala Ala Gly Pro Val Glu Ala
 35 40 45
 Ala Glu Glu Lys Thr Glu Phe Asp Val Ile Leu Lys Ala Ala Gly Ala
 50 55 60
 Asn Lys Val Ala Val Ile Lys Ala Val Arg Gly Ala Thr Gly Leu Gly
 65 70 75 80
 Leu Lys Glu Ala Lys Asp Leu Val Glu Ser Ala Pro Ala Ala Leu Lys
 85 90 95
 Glu Gly Val Ser Lys Asp Asp Ala Glu Ala Leu Lys Lys Ala Leu Glu
 100 105 110
 Glu Ala Gly Ala Glu Val Glu Val Lys
 115 120

<210> 253
 <211> 714
 <212> PRT
 <213> E. Coli

<400> 253
 Met Ser Arg Ile Ile Met Leu Ile Pro Thr Gly Thr Ser Val Gly Leu
 1 5 10 15
 Thr Ser Val Ser Leu Gly Val Ile Arg Ala Met Glu Arg Lys Gly Val
 20 25 30
 Arg Leu Ser Val Phe Lys Pro Ile Ala Gln Pro Arg Thr Gly Gly Asp
 35 40 45
 Ala Pro Asp Gln Thr Thr Thr Ile Val Arg Ala Asn Ser Ser Thr Thr
 50 55 60
 Thr Ala Ala Glu Pro Leu Lys Met Ser Tyr Val Glu Gly Leu Leu Ser
 65 70 75 80
 Ser Asn Gln Lys Asp Val Leu Met Glu Glu Ile Val Ala Asn Tyr His
 85 90 95
 Ala Asn Thr Lys Asp Ala Glu Val Val Leu Val Glu Gly Leu Val Pro
 100 105 110
 Thr Arg Lys His Gln Phe Ala Gln Ser Leu Asn Tyr Glu Ile Ala Lys
 115 120 125
 Thr Leu Asn Ala Glu Ile Val Phe Val Met Ser Gln Gly Thr Asp Thr
 130 135 140
 Pro Glu Gln Leu Lys Glu Arg Ile Glu Leu Thr Arg Asn Ser Phe Gly
 145 150 155 160
 Gly Ala Lys Asn Thr Asn Ile Thr Gly Val Ile Val Asn Lys Leu Asn
 165 170 175
 Ala Pro Val Asp Glu Gln Gly Arg Thr Arg Pro Asp Leu Ser Glu Ile
 180 185 190
 Phe Asp Asp Ser Ser Lys Ala Lys Val Asn Asn Val Asp Pro Ala Lys
 195 200 205
 Leu Gln Glu Ser Ser Pro Leu Pro Val Leu Gly Ala Val Pro Trp Ser
 210 215 220
 Phe Asp Leu Ile Ala Thr Arg Ala Ile Asp Met Ala Arg His Leu Asn
 225 230 235 240
 Ala Thr Ile Ile Asn Glu Gly Asp Ile Asn Thr Arg Arg Val Lys Ser
 245 250 255
 Val Thr Phe Cys Ala Arg Ser Ile Pro His Met Leu Glu His Phe Arg
 260 265 270
 Ala Gly Ser Leu Leu Val Thr Ser Ala Asp Arg Pro Asp Val Leu Val
 275 280 285
 Ala Ala Cys Leu Ala Ala Met Asn Gly Val Glu Ile Gly Ala Leu Leu
 290 295 300
 Leu Thr Gly Gly Tyr Glu Met Asp Ala Arg Ile Ser Lys Leu Cys Glu
 305 310 315 320
 Arg Ala Phe Ala Thr Gly Leu Pro Val Phe Met Val Asn Thr Asn Thr
 325 330 335
 Trp Gln Thr Ser Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val
 340 345 350
 Asp Asp His Glu Arg Ile Glu Lys Val Gln Glu Tyr Val Ala Asn Tyr
 355 360 365
 Ile Asn Ala Asp Trp Ile Glu Ser Leu Thr Ala Thr Ser Glu Arg Ser
 370 375 380
 Arg Arg Leu Ser Pro Pro Ala Phe Arg Tyr Gln Leu Thr Glu Leu Ala
 385 390 395 400
 Arg Lys Ala Gly Lys Arg Ile Val Leu Pro Glu Gly Asp Glu Pro Arg
 405 410 415
 Thr Val Lys Ala Ala Ile Cys Ala Glu Arg Gly Ile Ala Thr Cys
 420 425 430

Val Leu Leu Gly Asn Pro Ala Glu Ile Asn Arg Val Ala Ala Ser Gln
 435 440 445
 Gly Val Glu Leu Gly Ala Gly Ile Glu Ile Val Asp Pro Glu Val Val
 450 455 460
 Arg Glu Ser Tyr Val Gly Arg Leu Val Glu Leu Arg Lys Asn Lys Gly
 465 470 475 480
 Met Thr Glu Thr Val Ala Arg Glu Gln Leu Glu Asp Asn Val Val Leu
 485 490 495
 Gly Thr Leu Met Leu Glu Gln Asp Glu Val Asp Gly Leu Val Ser Gly
 500 505 510
 Ala Val His Thr Thr Ala Asn Thr Ile Arg Pro Pro Leu Gln Leu Ile
 515 520 525
 Lys Thr Ala Pro Gly Ser Ser Leu Val Ser Ser Val Phe Phe Met Leu
 530 535 540
 Leu Pro Glu Gln Val Tyr Val Tyr Gly Asp Cys Ala Ile Asn Pro Asp
 545 550 555 560
 Pro Thr Ala Glu Gln Leu Ala Glu Ile Ala Ile Gln Ser Ala Asp Ser
 565 570 575
 Ala Ala Ala Phe Gly Ile Glu Pro Arg Val Ala Met Leu Ser Tyr Ser
 580 585 590
 Thr Gly Thr Ser Gly Ala Gly Ser Asp Val Glu Lys Val Arg Glu Ala
 595 600 605
 Thr Arg Leu Ala Gln Glu Lys Arg Pro Asp Leu Met Ile Asp Gly Pro
 610 615 620
 Leu Gln Tyr Asp Ala Ala Val Met Ala Asp Val Ala Lys Ser Lys Ala
 625 630 635 640
 Pro Asn Ser Pro Val Ala Gly Arg Ala Thr Val Phe Ile Phe Pro Asp
 645 650 655
 Leu Asn Thr Gly Asn Thr Thr Tyr Lys Ala Val Gln Arg Ser Ala Asp
 660 665 670
 Leu Ile Ser Ile Gly Pro Met Leu Gln Gly Met Arg Lys Pro Val Asn
 675 680 685
 Asp Leu Ser Arg Gly Ala Leu Val Asp Asp Ile Val Tyr Thr Ile Ala
 690 695 700
 Leu Thr Ala Ile Gln Ser Ala Gln Gln Gln
 705 710

<210> 254
 <211> 588
 <212> PRT
 <213> E. Coli

<400> 254
 Met Asn Asn Ser Ile Asn His Lys Phe His His Ile Ser Arg Ala Glu
 1 5 10 15
 Tyr Gln Glu Leu Leu Ala Val Ser Arg Gly Asp Ala Val Ala Asp Tyr
 20 25 30
 Ile Ile Asp Asn Val Ser Ile Leu Asp Leu Ile Asn Gly Gly Glu Ile
 35 40 45
 Ser Gly Pro Ile Val Ile Lys Gly Arg Tyr Ile Ala Gly Val Gly Ala
 50 55 60
 Glu Tyr Thr Asp Ala Pro Ala Leu Gln Arg Ile Asp Ala Arg Gly Ala
 65 70 75 80
 Thr Ala Val Pro Gly Phe Ile Asp Ala His Leu His Ile Glu Ser Ser
 85 90 95
 Met Met Thr Pro Val Thr Phe Glu Thr Ala Thr Leu Pro Arg Gly Leu
 100 105 110
 Thr Thr Val Ile Cys Asp Pro His Glu Ile Val Asn Val Met Gly Glu
 115 120 125
 Ala Gly Phe Ala Trp Phe Ala Arg Cys Ala Glu Gln Ala Arg Gln Asn

130	135	140
Gln Tyr Leu Gln Val Ser Ser Cys Val Pro Ala Leu Glu Gly Cys Asp		
145	150	155
Val Asn Gly Ala Ser Phe Thr Leu Glu Gln Met Leu Ala Trp Arg Asp		160
	165	170
His Pro Gln Val Thr Gly Leu Ala Glu Met Met Asp Tyr Pro Gly Val		175
	180	185
Ile Ser Gly Gln Asn Ala Leu Leu Asp Lys Leu Asp Ala Phe Arg His		190
	195	200
Leu Thr Leu Asp Gly His Cys Pro Gly Leu Gly Gly Lys Glu Leu Asn		205
	210	215
Ala Tyr Ile Thr Ala Gly Ile Glu Asn Cys His Glu Ser Tyr Gln Leu		220
	225	230
Glu Glu Gly Arg Arg Lys Leu Gln Leu Gly Met Ser Leu Met Ile Arg		235
	245	250
Glu Gly Ser Ala Ala Arg Asn Leu Asn Ala Leu Ala Pro Leu Ile Asn		255
	260	265
Glu Phe Asn Ser Pro Gln Cys Met Leu Cys Thr Asp Asp Arg Asn Pro		270
	275	280
Trp Glu Ile Ala His Glu Gly His Ile Asp Ala Leu Ile Arg Arg Leu		285
	290	295
Ile Glu Gln His Asn Val Pro Leu His Val Ala Tyr Arg Val Ala Ser		300
	305	310
Trp Ser Thr Ala Arg His Phe Gly Leu Asn His Leu Gly Leu Leu Ala		315
	325	330
Pro Gly Lys Gln Ala Asp Ile Val Leu Leu Ser Asp Ala Arg Lys Val		335
	340	345
Thr Val Gln Gln Val Leu Val Lys Gly Glu Pro Ile Asp Ala Gln Thr		350
	355	360
Leu Gln Ala Glu Glu Ser Ala Arg Leu Ala Gln Ser Ala Pro Pro Tyr		365
	370	375
Gly Asn Thr Ile Ala Arg Gln Pro Val Ser Ala Ser Asp Phe Ala Leu		380
	385	390
Gln Phe Thr Pro Gly Lys Arg Tyr Arg Val Ile Asp Val Ile His Asn		395
	405	410
Glu Leu Ile Thr His Ser His Ser Ser Val Tyr Ser Glu Asn Gly Phe		415
	420	425
Asp Arg Asp Asp Val Ser Phe Ile Ala Val Leu Glu Arg Tyr Gly Gln		430
	435	440
Arg Leu Ala Pro Ala Cys Gly Leu Leu Gly Gly Phe Gly Leu Asn Glu		445
	450	455
Gly Ala Leu Ala Ala Thr Val Ser His Asp Ser His Asn Ile Val Val		460
	465	470
Ile Gly Arg Ser Ala Glu Glu Met Ala Leu Ala Val Asn Gln Val Ile		475
	485	490
Gln Asp Gly Gly Leu Cys Val Val Arg Asn Gly Gln Val Gln Ser		495
	500	505
His Leu Pro Leu Pro Ile Ala Gly Leu Met Ser Thr Asp Thr Ala Gln		510
	515	520
Ser Leu Ala Glu Gln Ile Asp Ala Leu Lys Ala Ala Ala Arg Glu Cys		525
	530	535
Gly Pro Leu Pro Asp Glu Pro Phe Ile Gln Met Ala Phe Leu Ser Leu		540
	545	550
Pro Val Ile Pro Ala Leu Lys Leu Thr Ser Gln Gly Leu Phe Asp Gly		555
	565	570
Glu Lys Phe Ala Phe Thr Thr Leu Glu Val Thr Glu		575
	580	585

<210> 255

<211> 408

<212> PRT

<213> E. Coli

<400> 255

```

Met Ala Tyr Cys Asn Pro Gly Leu Glu Ser Arg Pro Asn Lys Arg Asn
 1          5          10          15
Ala Leu Arg Arg His Val Val Thr Gly Ile Gly Met Lys Ile Val Ile
 20          25          30
Ala Pro Asp Ser Tyr Lys Glu Ser Leu Ser Ala Ser Glu Val Ala Gln
 35          40          45
Ala Ile Glu Lys Gly Phe Arg Gly Ile Phe Pro Asp Ala Gln Tyr Val
 50          55          60
Ser Val Pro Val Ala Asp Gly Gly Glu Gly Thr Val Glu Ala Met Ile
 65          70          75          80
Ala Ala Thr Gln Gly Ala Glu Arg His Ala Trp Val Thr Gly Pro Leu
 85          90          95
Gly Glu Lys Val Asn Ala Ser Trp Gly Ile Ser Gly Asp Gly Lys Thr
100          105          110
Ala Phe Ile Glu Met Ala Ala Ala Ser Gly Leu Glu Leu Val Pro Ala
115          120          125
Glu Lys Arg Asp Pro Leu Val Thr Thr Ser Arg Gly Thr Gly Glu Leu
130          135          140
Ile Leu Gln Ala Leu Glu Ser Gly Ala Thr Asn Ile Ile Ile Gly Ile
145          150          155          160
Gly Gly Ser Ala Thr Asn Asp Gly Gly Ala Gly Met Val Gln Ala Leu
165          170          175
Gly Ala Lys Leu Cys Asp Ala Asn Gly Asn Glu Ile Gly Phe Gly Gly
180          185          190
Gly Ser Leu Asn Thr Leu Asn Asp Ile Asp Ile Ser Gly Leu Asp Pro
195          200          205
Arg Leu Lys Asp Cys Val Ile Arg Val Ala Cys Asp Val Thr Asn Pro
210          215          220
Leu Val Gly Asp Asn Gly Ala Ser Arg Ile Phe Gly Pro Gln Lys Gly
225          230          235          240
Ala Ser Glu Ala Met Ile Val Glu Leu Asp Asn Asn Leu Ser His Tyr
245          250          255
Ala Glu Val Ile Lys Lys Ala Leu His Val Asp Val Lys Asp Val Pro
260          265          270
Gly Ala Gly Ala Ala Gly Gly Met Gly Ala Ala Leu Met Ala Phe Leu
275          280          285
Gly Ala Glu Leu Lys Ser Gly Ile Glu Ile Val Thr Thr Ala Leu Asn
290          295          300
Leu Glu Glu His Ile His Asp Cys Thr Leu Val Ile Thr Gly Glu Gly
305          310          315          320
Arg Ile Asp Ser Gln Ser Ile His Gly Lys Val Pro Ile Gly Val Ala
325          330          335
Asn Val Ala Lys Lys Tyr His Lys Pro Val Ile Gly Ile Ala Gly Ser
340          345          350
Leu Thr Asp Asp Val Gly Val Val His Gln His Gly Ile Asp Ala Val
355          360          365
Phe Ser Val Leu Thr Ser Ile Gly Thr Leu Asp Glu Ala Phe Arg Gly
370          375          380
Ala Tyr Asp Asn Ile Cys Arg Ala Ser Arg Asn Ile Ala Ala Thr Leu
385          390          395          400
Ala Ile Gly Met Arg Asn Ala Gly
405

```

<210> 256

<211> 299

<212> PRT

<213> E. Coli

<400> 256

```

Met Ile Asp Met Thr Met Lys Val Gly Phe Ile Gly Leu Gly Ile Met
 1           5           10          15
Gly Lys Pro Met Ser Lys Asn Leu Leu Lys Ala Gly Tyr Ser Leu Val
 20          25          30
Val Ala Asp Arg Asn Pro Glu Ala Ile Ala Asp Val Ile Ala Ala Gly
 35          40          45
Ala Glu Thr Ala Ser Thr Ala Lys Ala Ile Ala Glu Gln Cys Asp Val
 50          55          60
Ile Ile Thr Met Leu Pro Asn Ser Pro His Val Lys Glu Val Ala Leu
 65          70          75          80
Gly Glu Asn Gly Ile Ile Glu Gly Ala Lys Pro Gly Thr Val Leu Ile
 85          90          95
Asp Met Ser Ser Ile Ala Pro Leu Ala Ser Arg Glu Ile Ser Glu Ala
100         105         110
Leu Lys Ala Lys Gly Ile Asp Met Leu Asp Ala Pro Val Ser Gly Gly
115         120         125
Glu Pro Lys Ala Ile Asp Gly Thr Leu Ser Val Met Val Gly Gly Asp
130         135         140
Lys Ala Ile Phe Asp Lys Tyr Tyr Asp Leu Met Lys Ala Met Ala Gly
145         150         155         160
Ser Val Val His Thr Gly Glu Ile Gly Ala Gly Asn Val Thr Lys Leu
165         170         175
Ala Asn Gln Val Ile Val Ala Leu Asn Ile Ala Ala Met Ser Glu Ala
180         185         190
Leu Thr Leu Ala Thr Lys Ala Gly Val Asn Pro Asp Leu Val Tyr Gln
195         200         205
Ala Ile Arg Gly Gly Leu Ala Gly Ser Thr Val Leu Asp Ala Lys Ala
210         215         220
Pro Met Val Met Asp Arg Asn Phe Lys Pro Gly Phe Arg Ile Asp Leu
225         230         235         240
His Ile Lys Asp Leu Ala Asn Ala Leu Asp Thr Ser His Gly Val Gly
245         250         255
Ala Gln Leu Pro Leu Thr Ala Ala Val Met Glu Met Met Gln Ala Leu
260         265         270
Arg Ala Asp Gly Leu Gly Thr Ala Asp His Ser Ala Leu Ala Cys Tyr
275         280         285
Tyr Glu Lys Leu Ala Lys Val Glu Val Thr Arg
290         295

```

<210> 257

<211> 256

<212> PRT

<213> E. Coli

<400> 257

```

Met Asn Asn Asp Val Phe Pro Asn Lys Phe Lys Ala Ala Leu Ala Ala
 1           5           10          15
Lys Gln Val Gln Ile Gly Cys Trp Ser Ala Leu Ser Asn Pro Ile Ser
 20          25          30
Thr Glu Val Leu Gly Leu Ala Gly Phe Asp Trp Leu Val Leu Asp Gly
 35          40          45
Glu His Ala Pro Asn Asp Ile Ser Thr Phe Ile Pro Gln Leu Met Ala
 50          55          60
Leu Lys Gly Ser Ala Ser Ala Pro Val Val Arg Val Pro Thr Asn Glu
 65          70          75          80
Pro Val Ile Ile Lys Arg Leu Leu Asp Ile Gly Phe Tyr Asn Phe Leu

```

				85					90				95				
Ile	Pro	Phe	Val	Glu	Thr	Lys	Glu	Glu	Ala	Glu	Leu	Ala	Val	Ala	Ser		
			100						105				110				
Thr	Arg	Tyr	Pro	Pro	Glu	Gly	Ile	Arg	Gly	Val	Ser	Val	Ser	His	Arg		
		115					120					125					
Ala	Asn	Met	Phe	Gly	Thr	Val	Ala	Asp	Tyr	Phe	Ala	Gln	Ser	Asn	Lys		
	130					135					140						
Asn	Ile	Thr	Ile	Leu	Val	Gln	Ile	Glu	Ser	Gln	Gln	Gly	Val	Asp	Asn		
145					150					155					160		
Val	Asp	Ala	Ile	Ala	Ala	Thr	Glu	Gly	Val	Asp	Gly	Ile	Phe	Val	Gly		
			165						170					175			
Pro	Ser	Asp	Leu	Ala	Ala	Ala	Leu	Gly	His	Leu	Gly	Asn	Ala	Ser	His		
		180							185				190				
Pro	Asp	Val	Gln	Lys	Ala	Ile	Gln	His	Ile	Phe	Asn	Arg	Ala	Ser	Ala		
	195					200					205						
His	Gly	Lys	Pro	Ser	Gly	Ile	Leu	Ala	Pro	Val	Glu	Ala	Asp	Ala	Arg		
	210				215					220							
Arg	Tyr	Leu	Glu	Trp	Gly	Ala	Thr	Phe	Val	Ala	Val	Gly	Ser	Asp	Leu		
225					230					235					240		
Gly	Val	Phe	Arg	Ser	Ala	Thr	Gln	Lys	Leu	Ala	Asp	Thr	Phe	Lys	Lys		
			245						250					255			

<210> 258

<211> 444

<212> PRT

<213> E. Coli

<400> 258

Met	Ile	Leu	Asp	Thr	Val	Asp	Glu	Lys	Lys	Lys	Gly	Val	His	Thr	Arg		
1				5					10					15			
Tyr	Leu	Ile	Leu	Leu	Ile	Ile	Phe	Ile	Val	Thr	Ala	Val	Asn	Tyr	Ala		
			20					25					30				
Asp	Arg	Ala	Thr	Leu	Ser	Ile	Ala	Gly	Thr	Glu	Val	Ala	Lys	Glu	Leu		
		35				40						45					
Gln	Leu	Ser	Ala	Val	Ser	Met	Gln	Ile	Pro	Gly	Gly	Trp	Leu	Leu	Asp	Lys	Phe
	50					55					60						
Ala	Tyr	Leu	Leu	Met	Gln	Ile	Pro	Gly	Gly	Trp	Leu	Leu	Asp	Lys	Phe		
65				70					75					80			
Gly	Ser	Lys	Lys	Val	Tyr	Thr	Tyr	Ser	Leu	Phe	Phe	Trp	Ser	Leu	Phe		
			85					90					95				
Thr	Phe	Leu	Gln	Gly	Phe	Val	Asp	Met	Phe	Pro	Leu	Ala	Trp	Ala	Gly		
		100						105					110				
Ile	Ser	Met	Phe	Phe	Met	Arg	Phe	Met	Leu	Gly	Phe	Ser	Glu	Ala	Pro		
	115					120						125					
Ser	Phe	Pro	Ala	Asn	Ala	Arg	Ile	Val	Ala	Ala	Trp	Phe	Pro	Thr	Lys		
	130				135						140						
Glu	Arg	Gly	Thr	Ala	Ser	Ala	Ile	Phe	Asn	Ser	Ala	Gln	Tyr	Phe	Ser		
145				150					155					160			
Leu	Ala	Leu	Phe	Ser	Pro	Leu	Leu	Gly	Trp	Leu	Thr	Phe	Ala	Trp	Gly		
			165						170					175			
Trp	Glu	His	Val	Phe	Thr	Val	Met	Gly	Val	Ile	Gly	Phe	Val	Leu	Thr		
		180					185					190					
Ala	Leu	Trp	Ile	Lys	Leu	Ile	His	Asn	Pro	Thr	Asp	His	Pro	Arg	Met		
	195					200					205						
Ser	Ala	Glu	Glu	Leu	Lys	Phe	Ile	Ser	Glu	Asn	Gly	Ala	Val	Val	Asp		
	210				215					220							
Met	Asp	His	Lys	Lys	Pro	Gly	Ser	Ala	Ala	Ala	Ser	Gly	Pro	Lys	Leu		
225				230					235					240			
His	Tyr	Ile	Lys	Gln	Leu	Leu	Ser	Asn	Arg	Met	Met	Leu	Gly	Val	Phe		
			245					250					255				

Phe Gly Gln Tyr Phe Ile Asn Thr Ile Thr Trp Phe Phe Leu Thr Trp
 260 265 270
 Phe Pro Ile Tyr Leu Val Gln Glu Lys Gly Met Ser Ile Leu Lys Val
 275 280 285
 Gly Leu Val Ala Ser Ile Pro Ala Leu Cys Gly Phe Ala Gly Gly Val
 290 295 300
 Leu Gly Gly Val Phe Ser Asp Tyr Leu Ile Lys Arg Gly Leu Ser Leu
 305 310 315 320
 Thr Leu Ala Arg Lys Leu Pro Ile Val Leu Gly Met Leu Leu Ala Ser
 325 330 335
 Thr Ile Ile Leu Cys Asn Tyr Thr Asn Asn Thr Thr Leu Val Val Met
 340 345 350
 Leu Met Ala Leu Ala Phe Phe Gly Lys Gly Phe Gly Ala Leu Gly Trp
 355 360 365
 Pro Val Ile Ser Asp Thr Ala Pro Lys Glu Ile Val Gly Leu Cys Gly
 370 375 380
 Gly Val Phe Asn Val Phe Gly Asn Val Ala Ser Ile Val Thr Pro Leu
 385 390 395 400
 Val Ile Gly Tyr Leu Val Ser Glu Leu His Ser Phe Asn Ala Ala Leu
 405 410 415
 Val Phe Val Gly Cys Ser Ala Leu Met Ala Met Val Cys Tyr Leu Phe
 420 425 430
 Val Val Gly Asp Ile Lys Arg Met Glu Leu Gln Lys
 435 440

<210> 259
 <211> 511
 <212> PRT
 <213> E. Coli

<400> 259
 Met Gln Thr Ser Asp Thr Arg Ala Leu Pro Leu Leu Cys Ala Arg Ser
 1 5 10 15
 Val Tyr Lys Gln Tyr Ser Gly Val Asn Val Leu Lys Gly Ile Asp Phe
 20 25 30
 Thr Leu His Gln Gly Glu Val His Ala Leu Leu Gly Gly Asn Gly Ala
 35 40 45
 Gly Lys Ser Thr Leu Met Lys Ile Ile Ala Gly Ile Thr Pro Ala Asp
 50 55 60
 Ser Gly Thr Leu Glu Ile Glu Gly Asn Asn Tyr Val Arg Leu Thr Pro
 65 70 75 80
 Val His Ala His Gln Leu Gly Ile Tyr Leu Val Pro Gln Glu Pro Leu
 85 90 95
 Leu Phe Pro Ser Leu Ser Ile Lys Glu Asn Ile Leu Phe Gly Leu Ala
 100 105 110
 Lys Lys Gln Leu Ser Met Gln Lys Met Lys Asn Leu Leu Ala Ala Leu
 115 120 125
 Gly Cys Gln Phe Asp Leu His Ser Leu Ala Gly Ser Leu Asp Val Ala
 130 135 140
 Asp Arg Gln Met Val Glu Ile Leu Arg Gly Leu Met Arg Asp Ser Arg
 145 150 155 160
 Ile Leu Ile Leu Asp Glu Pro Thr Ala Ser Leu Thr Pro Ala Glu Thr
 165 170 175
 Glu Arg Leu Phe Ser Arg Leu Gln Glu Leu Leu Ala Thr Gly Val Gly
 180 185 190
 Ile Val Phe Ile Ser His Lys Leu Pro Glu Ile Arg Gln Ile Ala Asp
 195 200 205
 Arg Ile Ser Val Met Arg Asp Gly Thr Ile Ala Leu Ser Gly Lys Thr
 210 215 220
 Ser Glu Leu Ser Thr Asp Asp Ile Ile Gln Ala Ile Thr Pro Ala Val

225 230 235 240
 Arg Glu Lys Ser Leu Ser Ala Ser Gln Lys Leu Trp Leu Glu Leu Pro
 245 250 255
 Gly Asn Arg Pro Gln His Ala Ala Gly Thr Pro Val Leu Thr Leu Glu
 260 265 270
 Asn Leu Thr Gly Glu Gly Phe Arg Asn Val Ser Leu Thr Leu Asn Ala
 275 280 285
 Gly Glu Ile Leu Gly Leu Ala Gly Leu Val Gly Ala Gly Arg Thr Glu
 290 295 300
 Leu Ala Glu Thr Leu Tyr Gly Leu Arg Thr Leu Arg Gly Gly Arg Ile
 305 310 315 320
 Met Leu Asn Gly Lys Glu Ile Asn Lys Leu Ser Thr Gly Glu Arg Leu
 325 330 335
 Leu Arg Gly Leu Val Tyr Leu Pro Glu Asp Arg Gln Ser Ser Gly Leu
 340 345 350
 Asn Leu Asp Ala Ser Leu Ala Trp Asn Val Cys Ala Leu Thr His Asn
 355 360 365
 Leu Arg Gly Phe Trp Ala Lys Thr Ala Lys Asp Asn Ala Thr Leu Glu
 370 375 380
 Arg Tyr Arg Arg Ala Leu Asn Ile Lys Phe Asn Gln Pro Glu Gln Ala
 385 390 395 400
 Ala Arg Thr Leu Ser Gly Gly Asn Gln Gln Lys Ile Leu Ile Ala Lys
 405 410 415
 Cys Leu Glu Ala Ser Pro Gln Val Leu Ile Val Asp Glu Pro Thr Arg
 420 425 430
 Gly Val Asp Val Ser Ala Arg Asn Asp Ile Tyr Gln Leu Leu Arg Ser
 435 440 445
 Ile Ala Ala Gln Asn Val Ala Val Leu Leu Ile Ser Ser Asp Leu Glu
 450 455 460
 Glu Ile Glu Leu Met Ala Asp Arg Val Tyr Val Met His Gln Gly Glu
 465 470 475 480
 Ile Thr His Ser Ala Leu Thr Glu Arg Asp Ile Asn Val Glu Thr Ile
 485 490 495
 Met Arg Val Ala Phe Gly Asp Ser Gln Arg Gln Glu Ala Ser Cys
 500 505 510

<210> 260
 <211> 342
 <212> PRT
 <213> E. Coli

<400> 260
 Met Leu Lys Phe Ile Gln Asn Asn Arg Glu Ile Thr Ala Leu Leu Ala
 1 5 10 15
 Val Val Leu Leu Phe Val Leu Pro Gly Phe Leu Asp Arg Gln Tyr Leu
 20 25 30
 Ser Val Gln Thr Leu Thr Met Val Tyr Ser Ser Ala Gln Ile Leu Ile
 35 40 45
 Leu Leu Ala Met Gly Ala Thr Leu Val Met Leu Thr Arg Asn Ile Asp
 50 55 60
 Val Ser Val Gly Ser Ile Thr Gly Met Cys Ala Val Leu Leu Gly Met
 65 70 75 80
 Leu Leu Asn Ala Gly Tyr Ser Leu Pro Val Ala Cys Val Ala Thr Leu
 85 90 95
 Leu Leu Gly Leu Leu Ala Gly Phe Phe Asn Gly Val Leu Val Ala Trp
 100 105 110
 Leu Lys Ile Pro Ala Ile Val Ala Thr Leu Gly Thr Leu Gly Leu Tyr
 115 120 125
 Arg Gly Ile Met Leu Leu Trp Thr Gly Gly Lys Trp Ile Glu Gly Leu
 130 135 140

Pro Ala Glu Leu Lys Gln Leu Ser Ala Pro Leu Leu Leu Gly Val Ser
 145 150 155 160
 Ala Ile Gly Trp Leu Thr Ile Ile Leu Val Ala Phe Met Ala Trp Leu
 165 170 175
 Leu Ala Lys Thr Ala Phe Gly Arg Ser Phe Tyr Ala Thr Gly Asp Asn
 180 185 190
 Leu Gln Gly Ala Arg Gln Leu Gly Val Arg Thr Glu Ala Ile Arg Ile
 195 200 205
 Val Ala Phe Ser Leu Asn Gly Cys Met Ala Ala Leu Ala Gly Ile Val
 210 215 220
 Phe Ala Ser Gln Ile Gly Phe Ile Pro Asn Gln Thr Gly Thr Gly Leu
 225 230 235 240
 Glu Met Lys Ala Ile Ala Ala Cys Val Leu Gly Gly Ile Ser Leu Leu
 245 250 255
 Gly Gly Ser Gly Ala Ile Ile Gly Ala Val Leu Gly Ala Trp Phe Leu
 260 265 270
 Thr Gln Ile Asp Ser Val Leu Val Leu Arg Ile Pro Ala Trp Trp
 275 280 285
 Asn Asp Phe Ile Ala Gly Leu Val Leu Leu Ala Val Leu Val Phe Asp
 290 295 300
 Gly Arg Leu Arg Cys Ala Leu Glu Arg Asn Leu Arg Arg Gln Lys Tyr
 305 310 315 320
 Ala Arg Phe Met Thr Pro Pro Pro Ser Val Lys Pro Ala Ser Ser Gly
 325 330 335
 Lys Lys Arg Glu Ala Ala
 340

<210> 261
 <211> 330
 <212> PRT
 <213> E. Coli

<400> 261

Met Arg Ile Arg Tyr Gly Trp Glu Leu Ala Leu Ala Ala Leu Leu Val
 1 5 10 15
 Ile Glu Ile Val Ala Phe Gly Ala Ile Asn Pro Arg Met Leu Asp Leu
 20 25 30
 Asn Met Leu Leu Phe Ser Thr Ser Asp Phe Ile Cys Ile Gly Ile Val
 35 40 45
 Ala Leu Pro Leu Thr Met Val Ile Val Ser Gly Gly Ile Asp Ile Ser
 50 55 60
 Phe Gly Ser Thr Ile Gly Leu Cys Ala Ile Ala Leu Gly Val Leu Phe
 65 70 75 80
 Gln Ser Gly Val Pro Met Pro Leu Ala Ile Leu Leu Thr Leu Leu Leu
 85 90 95
 Gly Ala Leu Cys Gly Leu Ile Asn Ala Gly Leu Ile Ile Tyr Thr Lys
 100 105 110
 Val Asn Pro Leu Val Ile Thr Leu Gly Thr Leu Tyr Leu Phe Ala Gly
 115 120 125
 Ser Ala Leu Leu Leu Ser Gly Met Ala Gly Ala Thr Gly Tyr Glu Gly
 130 135 140
 Ile Gly Gly Phe Pro Met Ala Phe Thr Asp Phe Ala Asn Leu Asp Val
 145 150 155 160
 Leu Gly Leu Pro Val Pro Leu Ile Ile Phe Leu Ile Cys Leu Leu Val
 165 170 175
 Phe Trp Leu Trp Leu His Lys Thr His Ala Gly Arg Asn Val Phe Leu
 180 185 190
 Ile Gly Gln Ser Pro Arg Val Ala Leu Tyr Ser Ala Ile Pro Val Asn
 195 200 205
 Arg Thr Leu Cys Ala Leu Tyr Ala Met Thr Gly Leu Ala Ser Ala Val
 210 215 220

Ala Ala Val Leu Leu Val Ser Tyr Phe Gly Ser Ala Arg Ser Asp Leu
 225 230 235 240
 Gly Ala Ser Phe Leu Met Pro Ala Ile Thr Ala Val Val Leu Gly Gly
 245 250 255
 Ala Asn Ile Tyr Gly Gly Ser Gly Ser Ile Ile Gly Thr Ala Ile Ala
 260 265 270
 Val Leu Leu Val Gly Tyr Leu Gln Gln Gly Leu Gln Met Ala Gly Val
 275 280 285
 Pro Asn Gln Val Ser Ser Ala Leu Ser Gly Ala Leu Leu Ile Val Val
 290 295 300
 Val Val Gly Arg Ser Val Ser Leu His Arg Gln Gln Ile Lys Glu Trp
 305 310 315 320
 Leu Ala Arg Arg Ala Asn Asn Pro Leu Pro
 325 330

<210> 262
 <211> 340
 <212> PRT
 <213> E. Coli

<400> 262
 Met Thr Leu His Arg Phe Lys Lys Ile Ala Leu Leu Ser Ala Leu Gly
 1 5 10 15
 Ile Ala Ala Ile Ser Met Asn Val Gln Ala Ala Glu Arg Ile Ala Phe
 20 25 30
 Ile Pro Lys Leu Val Gly Val Gly Phe Phe Thr Ser Gly Gly Asn Gly
 35 40 45
 Ala Gln Gln Ala Gly Lys Glu Leu Gly Val Asp Val Thr Tyr Asp Gly
 50 55 60
 Pro Thr Glu Pro Ser Val Ser Gly Gln Val Gln Leu Ile Asn Asn Phe
 65 70 75 80
 Val Asn Gln Gly Tyr Asn Ala Ile Ile Val Ser Ala Val Ser Pro Asp
 85 90 95
 Gly Leu Cys Pro Ala Leu Lys Arg Ala Met Gln Arg Gly Val Arg Val
 100 105 110
 Leu Thr Trp Asp Ser Asp Thr Lys Pro Glu Cys Arg Ser Tyr Tyr Ile
 115 120 125
 Asn Gln Gly Thr Pro Ala Gln Leu Gly Gly Met Leu Val Asp Met Ala
 130 135 140
 Ala Arg Gln Val Asn Lys Asp Lys Ala Lys Val Ala Phe Phe Tyr Ser
 145 150 155 160
 Ser Pro Thr Val Thr Asp Gln Asn Gln Trp Val Lys Glu Ala Lys Ala
 165 170 175
 Lys Ile Ala Lys Glu His Pro Gly Trp Glu Ile Val Thr Thr Gln Phe
 180 185 190
 Gly Tyr Asn Asp Ala Thr Lys Ser Leu Gln Thr Ala Glu Gly Ile Leu
 195 200 205
 Lys Ala Tyr Ser Asp Leu Asp Ala Ile Ile Ala Pro Asp Ala Asn Ala
 210 215 220
 Leu Pro Ala Ala Ala Gln Ala Ala Glu Asn Leu Lys Asn Asp Lys Val
 225 230 235 240
 Ala Ile Val Gly Phe Ser Thr Pro Asn Val Met Arg Pro Tyr Val Glu
 245 250 255
 Arg Gly Thr Val Lys Glu Phe Gly Leu Trp Asp Val Val Gln Gln Gly
 260 265 270
 Lys Ile Ser Val Tyr Val Ala Asp Ala Leu Leu Lys Lys Gly Ser Met
 275 280 285
 Lys Thr Gly Asp Lys Leu Asp Ile Lys Gly Val Gly Gln Val Glu Val

290 295 300
 Ser Pro Asn Ser Val Gln Gly Tyr Asp Tyr Glu Ala Asp Gly Asn Gly
 305 310 315 320
 Ile Val Leu Leu Pro Glu Arg Val Ile Phe Asn Lys Glu Asn Ile Gly
 325 330 335
 Lys Tyr Asp Phe
 340

<210> 263
 <211> 291
 <212> PRT
 <213> E. Coli

<400> 263
 Met Ala Asp Leu Asp Asp Ile Lys Asp Gly Lys Asp Phe Arg Thr Asp
 1 5 10 15
 Gln Pro Gln Lys Asn Ile Pro Phe Thr Leu Lys Gly Cys Gly Ala Leu
 20 25 30
 Asp Trp Gly Met Gln Ser Arg Leu Ser Arg Ile Phe Asn Pro Lys Thr
 35 40 45
 Gly Lys Thr Val Met Leu Ala Phe Asp His Gly Tyr Phe Gln Gly Pro
 50 55 60
 Thr Thr Gly Leu Glu Arg Ile Asp Ile Asn Ile Ala Pro Leu Phe Glu
 65 70 75 80
 His Ala Asp Val Leu Met Cys Thr Arg Gly Ile Leu Arg Ser Val Val
 85 90 95
 Pro Pro Ala Thr Asn Arg Pro Val Val Leu Arg Ala Ser Gly Ala Asn
 100 105 110
 Ser Ile Leu Ala Glu Leu Ser Asn Glu Ala Val Ala Leu Ser Met Asp
 115 120 125
 Asp Ala Val Arg Leu Asn Ser Cys Ala Val Ala Ala Gln Val Tyr Ile
 130 135 140
 Gly Ser Glu Tyr Glu His Gln Ser Ile Lys Asn Ile Ile Gln Leu Val
 145 150 155 160
 Asp Ala Gly Met Lys Val Gly Met Pro Thr Met Ala Val Thr Gly Val
 165 170 175
 Gly Lys Asp Met Val Arg Asp Gln Arg Tyr Phe Ser Leu Ala Thr Arg
 180 185 190
 Ile Ala Ala Glu Met Gly Ala Gln Ile Ile Lys Thr Tyr Tyr Val Glu
 195 200 205
 Lys Gly Phe Glu Arg Ile Val Ala Gly Cys Pro Val Pro Ile Val Ile
 210 215 220
 Ala Gly Gly Lys Lys Leu Pro Glu Arg Glu Ala Leu Glu Met Cys Trp
 225 230 235 240
 Gln Ala Ile Asp Gln Gly Ala Ser Gly Val Asp Met Gly Arg Asn Ile
 245 250 255
 Phe Gln Ser Asp His Pro Val Ala Met Met Lys Ala Val Gln Ala Val
 260 265 270
 Val His His Asn Glu Thr Ala Asp Arg Ala Tyr Glu Leu Tyr Leu Ser
 275 280 285
 Glu Lys Gln
 290

<210> 264
 <211> 96
 <212> PRT
 <213> E. Coli

<400> 264

Met His Val Thr Leu Val Glu Ile Asn Val His Glu Asp Lys Val Asp
 1 5 10 15
 Glu Phe Ile Glu Val Phe Arg Gln Asn His Leu Gly Ser Val Gln Glu
 20 25 30
 Glu Gly Asn Leu Arg Phe Asp Val Leu Gln Asp Pro Glu Val Asn Ser
 35 40 45
 Arg Phe Tyr Ile Tyr Glu Ala Tyr Lys Asp Glu Asp Ala Val Ala Phe
 50 55 60
 His Lys Thr Thr Pro His Tyr Lys Thr Cys Val Ala Lys Leu Glu Ser
 65 70 75 80
 Leu Met Thr Gly Pro Arg Lys Lys Arg Leu Phe Asn Gly Leu Met Pro
 85 90 95

<210> 265

<211> 383

<212> PRT

<213> E. Coli

<400> 265

Met Phe Glu Pro Met Glu Leu Thr Asn Asp Ala Val Ile Lys Val Ile
 1 5 10 15
 Gly Val Gly Gly Gly Gly Asn Ala Val Glu His Met Val Arg Glu
 20 25 30
 Arg Ile Glu Gly Val Glu Phe Phe Ala Val Asn Thr Asp Ala Gln Ala
 35 40 45
 Leu Arg Lys Thr Ala Val Gly Gln Thr Ile Gln Ile Gly Ser Gly Ile
 50 55 60
 Thr Lys Gly Leu Gly Ala Gly Ala Asn Pro Glu Val Gly Arg Asn Ala
 65 70 75 80
 Ala Asp Glu Asp Arg Asp Ala Leu Arg Ala Ala Leu Glu Gly Ala Asp
 85 90 95
 Met Val Phe Ile Ala Ala Gly Met Gly Gly Thr Gly Thr Gly Ala
 100 105 110
 Ala Pro Val Val Ala Glu Val Ala Lys Asp Leu Gly Ile Leu Thr Val
 115 120 125
 Ala Val Val Thr Lys Pro Phe Asn Phe Glu Gly Lys Lys Arg Met Ala
 130 135 140
 Phe Ala Glu Gln Gly Ile Thr Glu Leu Ser Lys His Val Asp Ser Leu
 145 150 155 160
 Ile Thr Ile Pro Asn Asp Lys Leu Leu Lys Val Leu Gly Arg Gly Ile
 165 170 175
 Ser Leu Leu Asp Ala Phe Gly Ala Ala Asn Asp Val Leu Lys Gly Ala
 180 185 190
 Val Gln Gly Ile Ala Glu Leu Ile Thr Arg Pro Gly Leu Met Asn Val
 195 200 205
 Asp Phe Ala Asp Val Arg Thr Val Met Ser Glu Met Gly Tyr Ala Met
 210 215 220
 Met Gly Ser Gly Val Ala Ser Gly Glu Asp Arg Ala Glu Glu Ala Ala
 225 230 235 240
 Glu Met Ala Ile Ser Ser Pro Leu Leu Glu Asp Ile Asp Leu Ser Gly
 245 250 255
 Ala Arg Gly Val Leu Val Asn Ile Thr Ala Gly Phe Asp Leu Arg Leu
 260 265 270
 Asp Glu Phe Glu Thr Val Gly Asn Thr Ile Arg Ala Phe Ala Ser Asp
 275 280 285
 Asn Ala Thr Val Val Ile Gly Thr Ser Leu Asp Pro Asp Met Asn Asp
 290 295 300
 Glu Leu Arg Val Thr Val Ala Thr Gly Ile Gly Met Asp Lys Arg
 305 310 315 320
 Pro Glu Ile Thr Leu Val Thr Asn Lys Gln Val Gln Gln Pro Val Met

325 330 335
 Asp Arg Tyr Gln Gln His Gly Met Ala Pro Leu Thr Gln Glu Gln Lys
 340 345 350
 Pro Val Ala Lys Val Val Asn Asp Asn Ala Pro Gln Thr Ala Lys Glu
 355 360 365
 Pro Asp Tyr Leu Asp Ile Pro Ala Phe Leu Arg Lys Gln Ala Asp
 370 375 380

<210> 266
 <211> 1014
 <212> PRT
 <213> E. Coli

<400> 266

Met Asp Val Ser Arg Arg Gln Phe Phe Lys Ile Cys Ala Gly Gly Met
 1 5 10 15
 Ala Gly Thr Thr Val Ala Ala Leu Gly Phe Ala Pro Lys Gln Ala Leu
 20 25 30
 Ala Gln Ala Arg Asn Tyr Lys Leu Leu Arg Ala Lys Glu Ile Arg Asn
 35 40 45
 Thr Cys Thr Tyr Cys Ser Val Gly Cys Gly Leu Leu Met Tyr Ser Leu
 50 55 60
 Gly Asp Gly Ala Lys Asn Ala Arg Glu Ala Ile Tyr His Ile Glu Gly
 65 70 75 80
 Asp Pro Asp His Pro Val Ser Arg Gly Ala Leu Cys Pro Lys Gly Ala
 85 90 95
 Gly Leu Leu Asp Tyr Val Asn Ser Glu Asn Arg Leu Arg Tyr Pro Glu
 100 105 110
 Tyr Arg Ala Pro Gly Ser Asp Lys Trp Gln Arg Ile Ser Trp Glu Glu
 115 120 125
 Ala Phe Ser Arg Ile Ala Lys Leu Met Lys Ala Asp Arg Asp Ala Asn
 130 135 140
 Phe Ile Glu Lys Asn Glu Gln Gly Val Thr Val Asn Arg Trp Leu Ser
 145 150 155 160
 Thr Gly Met Leu Cys Ala Ser Gly Ala Ser Asn Glu Thr Gly Met Leu
 165 170 175
 Thr Gln Lys Phe Ala Arg Ser Leu Gly Met Leu Ala Val Asp Asn Gln
 180 185 190
 Ala Arg Val His Gly Pro Thr Val Ala Ser Leu Ala Pro Thr Phe Gly
 195 200 205
 Arg Gly Ala Met Thr Asn His Trp Val Asp Ile Lys Asn Ala Asn Val
 210 215 220
 Val Met Val Met Gly Gly Asn Ala Ala Glu Ala His Pro Val Gly Phe
 225 230 235 240
 Arg Trp Ala Met Glu Ala Lys Asn Asn Asn Asp Ala Thr Leu Ile Val
 245 250 255
 Val Asp Pro Arg Phe Thr Arg Thr Ala Ser Val Ala Asp Ile Tyr Ala
 260 265 270
 Pro Ile Arg Ser Gly Thr Asp Ile Thr Phe Leu Ser Gly Val Leu Arg
 275 280 285
 Tyr Leu Ile Glu Asn Asn Lys Ile Asn Ala Glu Tyr Val Lys His Tyr
 290 295 300
 Thr Asn Ala Ser Leu Leu Val Arg Asp Asp Phe Ala Phe Glu Asp Gly
 305 310 315 320
 Leu Phe Ser Gly Tyr Asp Ala Glu Lys Arg Gln Tyr Asp Lys Ser Ser
 325 330 335
 Trp Asn Tyr Gln Leu Asp Glu Asn Gly Tyr Ala Lys Arg Asp Glu Thr
 340 345 350
 Leu Thr His Pro Arg Cys Val Trp Asn Leu Leu Lys Glu His Val Ser
 355 360 365

Arg Tyr Thr Pro Asp Val Val Glu Asn Ile Cys Gly Thr Pro Lys Ala
 370 375 380
 Asp Phe Leu Lys Val Cys Glu Val Leu Ala Ser Thr Ser Ala Pro Asp
 385 390 395 400
 Arg Thr Thr Thr Phe Leu Tyr Ala Leu Gly Trp Thr Gln His Thr Val
 405 410 415
 Gly Ala Gln Asn Ile Arg Thr Met Ala Met Ile Gln Leu Leu Leu Gly
 420 425 430
 Asn Met Gly Met Ala Gly Gly Gly Val Asn Ala Leu Arg Gly His Ser
 435 440 445
 Asn Ile Gln Gly Leu Thr Asp Leu Gly Leu Leu Ser Thr Ser Leu Pro
 450 455 460
 Gly Tyr Leu Thr Leu Pro Ser Glu Lys Gln Val Asp Leu Gln Ser Tyr
 465 470 475 480
 Leu Glu Ala Asn Thr Pro Lys Ala Thr Leu Ala Asp Gln Val Asn Tyr
 485 490 495
 Trp Ser Asn Tyr Pro Lys Phe Phe Val Ser Leu Met Lys Ser Phe Tyr
 500 505 510
 Gly Asp Ala Ala Gln Lys Glu Asn Asn Trp Gly Tyr Asp Trp Leu Pro
 515 520 525
 Lys Trp Asp Gln Thr Tyr Asp Val Ile Lys Tyr Phe Asn Met Met Asp
 530 535 540
 Glu Gly Lys Val Thr Gly Tyr Phe Cys Gln Gly Phe Asn Pro Val Ala
 545 550 555 560
 Ser Phe Pro Asp Lys Asn Lys Val Val Ser Cys Leu Ser Lys Leu Lys
 565 570 575
 Tyr Met Val Val Ile Asp Pro Leu Val Thr Glu Thr Ser Thr Phe Trp
 580 585 590
 Gln Asn His Gly Glu Ser Asn Asp Val Asp Pro Ala Ser Ile Gln Thr
 595 600 605
 Glu Val Phe Arg Leu Pro Ser Thr Cys Phe Ala Glu Glu Asp Gly Ser
 610 615 620
 Ile Ala Asn Ser Gly Arg Trp Leu Gln Trp His Trp Lys Gly Gln Asp
 625 630 635 640
 Ala Pro Gly Glu Ala Arg Asn Asp Gly Glu Ile Leu Ala Gly Ile Tyr
 645 650 655
 His His Leu Arg Glu Leu Tyr Gln Ser Glu Gly Gly Lys Gly Val Glu
 660 665 670
 Pro Leu Met Lys Met Ser Trp Asn Tyr Lys Gln Pro His Glu Pro Gln
 675 680 685
 Ser Asp Glu Val Ala Lys Glu Asn Asn Gly Tyr Ala Leu Glu Asp Leu
 690 695 700
 Tyr Asp Ala Asn Gly Val Leu Ile Ala Lys Lys Gly Gln Leu Leu Ser
 705 710 715 720
 Ser Phe Ala His Leu Arg Asp Asp Gly Thr Thr Ala Ser Ser Cys Trp
 725 730 735
 Ile Tyr Thr Gly Ser Trp Thr Glu Gln Gly Asn Gln Met Ala Asn Arg
 740 745 750
 Asp Asn Ser Asp Pro Ser Gly Leu Gly Asn Thr Leu Gly Trp Ala Trp
 755 760 765
 Ala Trp Pro Leu Asn Arg Arg Val Leu Tyr Asn Arg Ala Ser Ala Asp
 770 775 780
 Ile Asn Gly Lys Pro Trp Asp Pro Lys Arg Met Leu Ile Gln Trp Asn
 785 790 795 800
 Gly Ser Lys Trp Thr Gly Asn Asp Ile Pro Asp Phe Gly Asn Ala Ala
 805 810 815
 Pro Gly Thr Pro Thr Gly Pro Phe Ile Met Gln Pro Glu Gly Met Gly
 820 825 830
 Arg Leu Phe Ala Ile Asn Lys Met Ala Glu Gly Pro Phe Pro Glu His
 835 840 845
 Tyr Glu Pro Ile Glu Thr Pro Leu Gly Thr Asn Pro Leu His Pro Asn

850	855	860
Val Val Ser Asn Pro	Val Val Arg Leu Tyr	Glu Gln Asp Ala Leu Arg
865	870	875
Met Gly Lys Lys	Glu Gln Phe Pro Tyr	Val Gly Thr Thr Tyr Arg Leu
	885	890
Thr Glu His Phe His Thr Trp Thr	Lys His Ala Leu Leu Asn Ala Ile	895
	900	905
Ala Gln Pro Glu Gln Phe Val Glu Ile Ser Glu Thr	Leu Ala Ala Ala	910
	915	920
Lys Gly Ile Asn Asn Gly Asp Arg Val Thr Val Ser Ser Lys Arg Gly		925
	930	935
Phe Ile Arg Ala Val Ala Val Thr Arg Arg Leu Lys Pro Leu Asn		940
	945	950
Val Asn Gly Gln Gln Val Glu Thr Val Gly Ile Pro Ile His Trp Gly		955
	965	970
Phe Glu Gly Val Ala Arg Lys Gly Tyr Ile Ala Asn Thr Leu Thr Pro		975
	980	985
Asn Val Gly Asp Ala Asn Ser Gln Thr Pro Glu Tyr Lys Ala Phe Leu		990
	995	1000
Val Asn Ile Glu Lys Ala		1005
1010		

<210> 267

<211> 294

<212> PRT

<213> E. Coli

<400> 267

Met Ala Met Glu Thr Gln Asp Ile Ile Lys Arg Ser Ala Thr Asn Ser	
1	5
Ile Thr Pro Pro Ser Gln Val Arg Asp Tyr Lys Ala Glu Val Ala Lys	10
	20
Leu Ile Asp Val Ser Thr Cys Ile Gly Cys Lys Ala Cys Gln Val Ala	25
	35
Cys Ser Glu Trp Asn Asp Ile Arg Asp Glu Val Gly His Cys Val Gly	40
	50
Val Tyr Asp Asn Pro Ala Asp Leu Ser Ala Lys Ser Trp Thr Val Met	55
	65
Arg Phe Ser Glu Thr Glu Gln Asn Gly Lys Leu Glu Trp Leu Ile Arg	70
	85
Lys Asp Gly Cys Met His Cys Glu Asp Pro Gly Cys Leu Lys Ala Cys	90
	100
Pro Ser Ala Gly Ala Ile Ile Gln Tyr Ala Asn Gly Ile Val Asp Phe	105
	115
Gln Ser Glu Asn Cys Ile Gly Cys Gly Tyr Cys Ile Ala Gly Cys Pro	120
	130
Phe Asn Ile Pro Arg Leu Asn Lys Glu Asp Asn Arg Val Tyr Lys Cys	135
	145
Thr Leu Cys Val Asp Arg Val Ser Val Gly Gln Glu Pro Ala Cys Val	150
	165
Lys Thr Cys Pro Thr Gly Ala Ile His Phe Gly Thr Lys Lys Glu Met	170
	180
Leu Glu Leu Ala Glu Gln Arg Val Ala Lys Leu Lys Ala Arg Gly Tyr	185
	195
Glu His Ala Gly Val Tyr Asn Pro Glu Gly Val Gly Gly Thr His Val	200
	210
Met Tyr Val Leu His His Ala Asp Gln Pro Glu Leu Tyr His Gly Leu	215
	225
Pro Lys Asp Pro Lys Ile Asp Thr Ser Val Ser Leu Trp Lys Gly Ala	230
	245
Leu Lys Pro Leu Ala Ala Ala Gly Phe Ile Ala Thr Phe Ala Gly Leu	250
	255

260
 Ile Phe His Tyr Ile Gly Ile Gly 265
 275 280 285
 Glu Glu Asp His His Glu
 290

<210> 268
 <211> 217
 <212> PRT
 <213> E. Coli

<400> 268
 Met Ser Lys Ser Lys Met Ile Val Arg Thr Lys Phe Ile Asp Arg Ala
 1 5 10 15
 Cys His Trp Thr Val Val Ile Cys Phe Phe Leu Val Ala Leu Ser Gly
 20 25 30
 Ile Ser Phe Phe Pro Thr Leu Gln Trp Leu Thr Gln Thr Phe Gly
 35 40 45
 Thr Pro Gln Met Gly Arg Ile Leu His Pro Phe Phe Gly Ile Ala Ile
 50 55 60
 Phe Val Ala Leu Met Phe Met Phe Val Arg Phe Val His His Asn Ile
 65 70 75 80
 Pro Asp Lys Lys Asp Ile Pro Trp Leu Leu Asn Ile Val Glu Val Leu
 85 90 95
 Lys Gly Asn Glu His Lys Val Ala Asp Val Gly Lys Tyr Asn Ala Gly
 100 105 110
 Gln Lys Met Met Phe Trp Ser Ile Met Ser Met Ile Phe Val Leu Leu
 115 120 125
 Val Thr Gly Val Ile Ile Trp Arg Pro Tyr Phe Ala Gln Tyr Phe Pro
 130 135 140
 Met Gln Val Val Arg Tyr Ser Leu Leu Ile His Ala Ala Ala Gly Ile
 145 150 155 160
 Ile Leu Ile His Ala Ile Leu Ile His Met Tyr Met Ala Phe Trp Val
 165 170 175
 Lys Gly Ser Ile Lys Gly Met Ile Glu Gly Lys Val Ser Arg Arg Trp
 180 185 190
 Ala Lys Lys His His Pro Arg Trp Tyr Arg Glu Ile Glu Lys Ala Glu
 195 200 205
 Ala Lys Lys Glu Ser Glu Glu Gly Ile
 210 215

<210> 269
 <211> 86
 <212> PRT
 <213> E. Coli

<400> 269
 Met Ala Leu Leu Ile Thr Lys Lys Cys Ile Asn Cys Asp Met Cys_Glu
 1 5 10 15
 Pro Glu Cys Pro Asn Glu Ala Ile Ser Met Gly Asp His Ile Tyr Glu
 20 25 30
 Ile Asn Ser Asp Lys Cys Thr Glu Cys Val Gly His Tyr Glu Thr Pro
 35 40 45
 Thr Cys Gln Lys Val Cys Pro Ile Pro Asn Thr Ile Val Lys Asp Pro
 50 55 60
 Ala His Val Glu Thr Glu Glu Gln Leu Trp Asp Lys Phe Val Leu Met
 65 70 75 80
 His His Ala Asp Lys Ile
 85

<210> 270
 <211> 400
 <212> PRT
 <213> E. Coli

<400> 270

```

Met Gln Ser Val Asp Val Ala Ile Val Gly Gly Gly Met Val Gly Leu
 1          5          10          15
Ala Val Ala Cys Gly Leu Gln Gly Ser Gly Leu Arg Val Ala Val Leu
 20          25          30
Glu Gln Arg Val Gln Glu Pro Leu Ala Ala Asn Ala Pro Pro Gln Leu
 35          40          45
Arg Val Ser Ala Ile Asn Ala Ala Ser Glu Lys Leu Leu Thr Arg Leu
 50          55          60
Gly Val Trp Gln Asp Ile Leu Ser Arg Arg Ala Ser Cys Tyr His Gly
 65          70          75          80
Met Glu Val Trp Asp Lys Asp Ser Phe Gly His Ile Ser Phe Asp Asp
 85          90          95
Gln Ser Met Gly Tyr Ser His Leu Gly His Ile Val Glu Asn Ser Val
 100         105         110
Ile His Tyr Ala Leu Trp Asn Lys Ala His Gln Ser Ser Asp Ile Thr
 115         120         125
Leu Leu Ala Pro Ala Glu Leu Gln Gln Val Ala Trp Gly Glu Asn Glu
 130         135         140
Thr Phe Leu Thr Leu Lys Asp Gly Ser Met Leu Thr Ala Arg Leu Val
 145         150         155         160
Ile Gly Ala Asp Gly Ala Asn Ser Trp Leu Arg Asn Lys Ala Asp Ile
 165         170         175
Pro Leu Thr Phe Trp Asp Tyr Gln His His Ala Leu Val Ala Thr Ile
 180         185         190
Arg Thr Glu Glu Pro His Asp Ala Val Ala Arg Gln Val Phe His Gly
 195         200         205
Glu Gly Ile Leu Ala Phe Leu Pro Leu Ser Asp Pro His Leu Cys Ser
 210         215         220
Ile Val Trp Ser Leu Ser Pro Glu Glu Ala Gln Arg Met Gln Gln Ala
 225         230         235         240
Ser Glu Asp Glu Phe Asn Arg Ala Leu Asn Ile Ala Phe Asp Asn Arg
 245         250         255
Leu Gly Leu Cys Lys Val Glu Ser Ala Arg Gln Val Phe Pro Leu Thr
 260         265         270
Gly Arg Tyr Ala Arg Gln Phe Ala Ser His Arg Leu Ala Leu Val Gly
 275         280         285
Asp Ala Ala His Thr Ile His Pro Leu Ala Gly Gln Gly Val Asn Leu
 290         295         300
Gly Phe Met Asp Ala Ala Glu Leu Ile Ala Glu Leu Lys Arg Leu His
 305         310         315         320
Arg Gln Gly Lys Asp Ile Gly Gln Tyr Ile Tyr Leu Arg Arg Tyr Glu
 325         330         335
Arg Ser Arg Lys His Ser Ala Ala Leu Met Leu Ala Gly Met Gln Gly
 340         345         350
Phe Arg Asp Leu Phe Ser Gly Thr Asn Pro Ala Lys Lys Leu Leu Arg
 355         360         365
Asp Ile Gly Leu Lys Leu Ala Asp Thr Leu Pro Gly Val Lys Pro Gln
 370         375         380
Leu Ile Arg Gln Ala Met Gly Leu Asn Asp Leu Pro Glu Trp Leu Arg
 385         390         395         400

```

<210> 271

<211> 392
 <212> PRT
 <213> E. Coli

<400> 271

```

Met Ser Val Ile Ile Val Gly Gly Gly Met Ala Gly Ala Thr Leu Ala
 1          5          10          15
Leu Ala Ile Ser Arg Leu Ser His Gly Ala Leu Pro Val His Leu Ile
 20          25          30
Glu Ala Thr Ala Pro Glu Ser His Ala His Pro Gly Phe Asp Gly Arg
 35          40          45
Ala Ile Ala Leu Ala Ala Gly Thr Cys Gln Gln Leu Ala Arg Ile Gly
 50          55          60
Val Trp Gln Ser Leu Ala Asp Cys Ala Thr Ala Ile Thr Thr Val His
 65          70          75          80
Val Ser Asp Arg Gly His Ala Gly Phe Val Thr Leu Ala Ala Glu Asp
 85          90          95
Tyr Gln Leu Ala Ala Leu Gly Gln Val Val Glu Leu His Asn Val Gly
100          105          110
Gln Arg Leu Phe Ala Leu Leu Arg Lys Ala Pro Gly Val Thr Leu His
115          120          125
Cys Pro Asp Arg Val Ala Asn Val Ala Arg Thr Gln Ser His Val Glu
130          135          140
Val Thr Leu Glu Ser Gly Glu Thr Leu Thr Gly Arg Val Leu Val Ala
145          150          155          160
Ala Asp Gly Thr His Ser Ala Leu Ala Thr Ala Cys Gly Val Asp Trp
165          170          175
Gln Gln Glu Pro Tyr Glu Gln Leu Ala Val Ile Ala Asn Val Ala Thr
180          185          190
Ser Val Ala His Glu Gly Arg Ala Phe Glu Arg Phe Thr Gln His Gly
195          200          205
Pro Leu Ala Met Leu Pro Met Ser Asp Gly Arg Cys Ser Leu Val Trp
210          215          220
Cys His Pro Leu Glu Arg Arg Glu Glu Val Leu Ser Trp Ser Asp Glu
225          230          235          240
Lys Phe Cys Arg Glu Leu Gln Ser Ala Phe Gly Trp Arg Leu Gly Lys
245          250          255
Ile Thr His Ala Gly Lys Arg Ser Ala Tyr Pro Leu Ala Leu Thr His
260          265          270
Ala Ala Arg Ser Ile Thr His Arg Thr Val Leu Val Gly Asn Ala Ala
275          280          285
Gln Thr Leu His Pro Ile Ala Gly Gln Gly Phe Asn Leu Gly Met Arg
290          295          300
Asp Val Met Ser Leu Ala Glu Thr Leu Thr Gln Ala Gln Glu Arg Gly
305          310          315          320
Glu Asp Met Gly Asp Tyr Gly Val Leu Cys Arg Tyr Gln Gln Arg Arg
325          330          335
Gln Ser Asp Arg Glu Ala Thr Ile Gly Val Thr Asp Ser Leu Val His
340          345          350
Leu Phe Ala Asn Arg Trp Ala Pro Leu Val Val Gly Arg Asn Ile Gly
355          360          365
Leu Met Thr Met Glu Leu Phe Thr Pro Ala Arg Asp Val Leu Ala Gln
370          375          380
Arg Thr Leu Gly Trp Val Ala Arg
385          390

```

<210> 272
 <211> 441
 <212> PRT
 <213> E. Coli

<400> 272
Met Ser Glu Ile Ser Arg Gln Glu Phe Gln Arg Arg Arg Gln Ala Leu
1 5 10 15
Val Glu Gln Met Gln Pro Gly Ser Ala Ala Leu Ile Phe Ala Ala Pro
20 25 30
Glu Val Thr Arg Ser Ala Asp Ser Glu Tyr Pro Tyr Arg Gln Asn Ser
35 40 45
Asp Phe Trp Tyr Phe Thr Gly Phe Asn Glu Pro Glu Ala Val Leu Val
50 55 60
Leu Ile Lys Ser Asp Asp Thr His Asn His Ser Val Leu Phe Asn Arg
65 70 75 80
Val Arg Asp Leu Thr Ala Glu Ile Trp Phe Gly Arg Arg Leu Gly Gln
85 90 95
Asp Ala Ala Pro Glu Lys Leu Gly Val Asp Arg Ala Leu Ala Phe Ser
100 105 110
Glu Ile Asn Gln Gln Leu Tyr Gln Leu Leu Asn Gly Leu Asp Val Val
115 120 125
Tyr His Ala Gln Gly Glu Tyr Ala Tyr Ala Asp Val Ile Val Asn Ser
130 135 140
Ala Leu Glu Lys Leu Arg Lys Gly Ser Arg Gln Asn Leu Thr Ala Pro
145 150 155 160
Ala Thr Met Ile Asp Trp Arg Pro Val Val His Glu Met Arg Leu Phe
165 170 175
Lys Ser Pro Glu Glu Ile Ala Val Leu Arg Arg Ala Gly Glu Ile Thr
180 185 190
Ala Met Ala His Thr Arg Ala Met Glu Lys Cys Arg Pro Gly Met Phe
195 200 205
Glu Tyr His Leu Glu Gly Glu Ile His His Glu Phe Asn Arg His Gly
210 215 220
Ala Arg Tyr Pro Ser Tyr Asn Thr Ile Val Gly Ser Gly Glu Asn Gly
225 230 235 240
Cys Ile Leu His Tyr Thr Glu Asn Glu Cys Glu Met Arg Asp Gly Asp
245 250 255
Leu Val Leu Ile Asp Ala Gly Cys Glu Tyr Lys Gly Tyr Ala Gly Asp
260 265 270
Ile Thr Arg Thr Phe Pro Val Asn Gly Lys Phe Thr Gln Ala Gln Arg
275 280 285
Glu Ile Tyr Asp Ile Val Leu Glu Ser Leu Glu Thr Ser Leu Arg Leu
290 295 300
Tyr Arg Pro Gly Thr Ser Ile Leu Glu Val Thr Gly Glu Val Val Arg
305 310 315 320
Ile Met Val Ser Gly Leu Val Lys Leu Gly Ile Leu Lys Gly Asp Val
325 330 335
Asp Glu Leu Ile Ala Gln Asn Ala His Arg Pro Phe Phe Met His Gly
340 345 350
Leu Ser His Trp Leu Gly Leu Asp Val His Asp Val Gly Val Tyr Gly
355 360 365
Gln Asp Arg Ser Arg Ile Leu Glu Pro Gly Met Val Leu Thr Val Glu
370 375 380
Pro Gly Leu Tyr Ile Ala Pro Asp Ala Glu Val Pro Glu Gln Tyr Arg
385 390 395 400
Gly Ile Gly Ile Arg Ile Glu Asp Asp Ile Val Ile Thr Glu Thr Gly
405 410 415
Asn Glu Asn Leu Thr Ala Ser Val Val Lys Lys Pro Glu Glu Ile Glu
420 425 430
Ala Leu Met Val Ala Ala Arg Lys Gln
435 440

<210> 273

<211> 194
 <212> PRT
 <213> E. Coli

<400> 273
 Met Leu Met Ser Ile Gln Asn Glu Met Pro Gly Tyr Asn Glu Met Asn
 1 5 10 15
 Gln Tyr Leu Asn Gln Gln Gly Thr Gly Leu Thr Pro Ala Glu Met His
 20 25 30
 Gly Leu Ile Ser Gly Met Ile Cys Gly Gly Asn Asp Asp Ser Ser Trp
 35 40 45
 Leu Pro Leu Leu His Asp Leu Thr Asn Glu Gly Met Ala Phe Gly His
 50 55 60
 Glu Leu Ala Gln Ala Leu Arg Lys Met His Ser Ala Thr Ser Asp Ala
 65 70 75 80
 Leu Gln Asp Asp Gly Phe Leu Phe Gln Leu Tyr Leu Pro Asp Gly Asp
 85 90 95
 Asp Val Ser Val Phe Asp Arg Ala Asp Ala Leu Ala Gly Trp Val Asn
 100 105 110
 His Phe Leu Leu Gly Leu Gly Val Thr Gln Pro Lys Leu Asp Lys Val
 115 120 125
 Thr Gly Glu Thr Gly Glu Ala Ile Asp Asp Leu Arg Asn Ile Ala Gln
 130 135 140
 Leu Gly Tyr Asp Glu Asp Glu Asp Gln Glu Glu Met Ser Leu
 145 150 155 160
 Glu Glu Ile Ile Glu Tyr Val Arg Val Ala Ala Leu Leu Cys His Asp
 165 170 175
 Thr Phe Thr His Pro Gln Pro Thr Ala Pro Glu Val Gln Lys Pro Thr
 180 185 190
 Leu His

<210> 274
 <211> 120
 <212> PRT
 <213> E. Coli

<400> 274
 Met Leu Lys Leu Phe Ala Lys Tyr Thr Ser Ile Gly Val Leu Asn Thr
 1 5 10 15
 Leu Ile His Trp Val Val Phe Gly Val Cys Ile Tyr Val Ala His Thr
 20 25 30
 Asn Gln Ala Leu Ala Asn Phe Ala Gly Phe Val Val Ala Val Ser Phe
 35 40 45
 Ser Phe Phe Ala Asn Ala Lys Phe Thr Phe Lys Ala Ser Thr Thr Thr
 50 55 60
 Met Arg Tyr Met Leu Tyr Val Gly Phe Met Gly Thr Leu Ser Ala Thr
 65 70 75 80
 Val Gly Trp Ala Ala Asp Arg Cys Ala Leu Pro Pro Met Ile Thr Leu
 85 90 95
 Val Thr Phe Ser Ala Ile Ser Leu Val Cys Gly Phe Val Tyr Ser Lys
 100 105 110
 Phe Ile Val Phe Arg Asp Ala Lys
 115 120

<210> 275
 <211> 306
 <212> PRT
 <213> E. Coli

<400> 275

```

Met Lys Ile Ser Leu Val Val Pro Val Phe Asn Glu Glu Glu Ala Ile
 1           5           10           15
Pro Ile Phe Tyr Lys Thr Val Arg Glu Phe Glu Glu Leu Lys Ser Tyr
      20           25           30
Glu Val Glu Ile Val Phe Ile Asn Asp Gly Ser Lys Asp Ala Thr Glu
      35           40           45
Ser Ile Ile Asn Ala Leu Ala Val Ser Asp Pro Leu Val Val Pro Leu
 50           55           60
Ser Phe Thr Arg Asn Phe Gly Lys Glu Pro Ala Leu Phe Ala Gly Leu
65           70           75           80
Asp His Ala Thr Gly Asp Ala Ile Ile Pro Ile Asp Val Asp Leu Gln
      85           90           95
Asp Pro Ile Glu Val Ile Pro His Leu Ile Glu Lys Trp Gln Ala Gly
      100          105          110
Ala Asp Met Val Leu Ala Lys Arg Ser Asp Arg Ser Thr Asp Gly Arg
      115          120          125
Leu Lys Arg Lys Thr Ala Glu Trp Phe Tyr Lys Leu His Asn Lys Ile
      130          135          140
Ser Asn Pro Lys Ile Glu Asn Val Gly Asp Phe Arg Leu Met Ser
145          150          155          160
Arg Asp Val Val Glu Asn Ile Lys Leu Met Pro Glu Arg Asn Leu Phe
      165          170          175
Met Lys Gly Ile Leu Ser Trp Val Gly Gly Lys Thr Asp Ile Val Glu
      180          185          190
Tyr Val Arg Ala Glu Arg Ile Ala Gly Asp Thr Lys Phe Asn Gly Trp
      195          200          205
Lys Leu Trp Asn Leu Ala Leu Glu Gly Ile Thr Ser Phe Ser Thr Phe
      210          215          220
Pro Leu Arg Ile Trp Thr Tyr Ile Gly Leu Val Ala Ser Val Ala
225          230          235          240
Phe Ile Tyr Gly Ala Trp Met Ile Leu Asp Thr Ile Ile Phe Gly Asn
      245          250          255
Ala Val Arg Gly Tyr Pro Ser Leu Leu Val Ser Ile Leu Phe Leu Gly
      260          265          270
Gly Ile Gln Met Ile Gly Ile Gly Val Leu Gly Glu Tyr Ile Gly Arg
      275          280          285
Thr Tyr Ile Glu Thr Lys Lys Arg Pro Lys Tyr Ile Ile Lys Arg Val
      290          295          300
Lys Lys
305

```

<210> 276

<211> 443

<212> PRT

<213> E. Coli

<400> 276

```

Met Asn Lys Ala Ile Lys Val Ser Leu Tyr Ile Ser Phe Val Leu Ile
 1           5           10           15
Ile Cys Ala Leu Ser Lys Asn Ile Met Met Leu Asn Thr Ser Asp Phe
      20           25           30
Gly Arg Ala Ile Lys Pro Leu Ile Glu Asp Ile Pro Ala Phe Thr Tyr
      35           40           45
Asp Leu Pro Leu Leu Tyr Lys Leu Lys Gly His Ile Asp Ser Ile Asp
 50           55           60
Ser Tyr Glu Tyr Ile Ser Ser Tyr Ser Tyr Ile Leu Tyr Thr Tyr Val
65           70           75           80
Leu Phe Ile Ser Ile Phe Thr Glu Tyr Leu Asp Ala Arg Val Leu Ser
      85           90           95

```

```

Leu Phe Leu Lys Val Ile Tyr Ile Tyr Ser Leu Tyr Ala Ile Phe Thr
    100                      105                      110
Ser Tyr Ile Lys Thr Glu Arg Tyr Val Thr Leu Phe Thr Phe Phe Ile
    115                      120                      125
Leu Ala Phe Leu Met Cys Ser Ser Ser Thr Leu Ser Met Phe Ala Ser
    130                      135                      140
Phe Tyr Gln Glu Gln Ile Val Ile Ile Phe Leu Pro Phe Leu Val Tyr
    145                      150                      155                      160
Ser Leu Thr Cys Lys Asn Asn Lys Ser Met Leu Leu Leu Phe Phe Ser
    165                      170                      175
Leu Leu Ile Ile Ser Thr Ala Lys Asn Gln Phe Ile Leu Thr Pro Leu
    180                      185                      190
Ile Val Tyr Ser Tyr Tyr Ile Phe Phe Asp Arg His Lys Leu Ile Ile
    195                      200                      205
Lys Ser Val Ile Cys Val Val Cys Leu Leu Ala Ser Ile Phe Ala Ile
    210                      215                      220
Ser Tyr Ser Lys Gly Val Val Glu Leu Asn Lys Tyr His Ala Thr Tyr
    225                      230                      235                      240
Phe Gly Ser Tyr Leu Tyr Met Lys Asn Asn Gly Tyr Lys Met Pro Ser
    245                      250                      255
Tyr Val Asp Asp Lys Cys Val Gly Leu Asp Ala Trp Gly Asn Lys Phe
    260                      265                      270
Asp Ile Ser Phe Gly Ala Thr Pro Thr Glu Val Gly Thr Glu Cys Phe
    275                      280                      285
Glu Ser His Lys Asp Glu Thr Phe Ser Asn Ala Leu Phe Leu Leu Val
    290                      295                      300
Ser Lys Pro Ser Thr Ile Phe Lys Leu Pro Phe Asp Asp Gly Val Met
    305                      310                      315                      320
Ser Gln Tyr Lys Glu Asn Tyr Phe His Val Tyr Lys Lys Leu His Val
    325                      330                      335
Ile Tyr Gly Glu Ser Asn Ile Leu Thr Thr Ile Thr Asn Ile Lys Asp
    340                      345                      350
Asn Ile Phe Lys Asn Ile Arg Phe Ile Ser Leu Leu Leu Phe Phe Ile
    355                      360                      365
Ala Ser Ile Phe Ile Arg Asn Asn Lys Ile Lys Ala Ser Leu Phe Val
    370                      375                      380
Val Ser Leu Phe Gly Ile Ser Gln Phe Tyr Val Ser Phe Phe Gly Glu
    385                      390                      395                      400
Gly Tyr Arg Asp Leu Ser Lys His Leu Phe Gly Met Tyr Phe Ser Phe
    405                      410                      415
Asp Leu Cys Leu Tyr Ile Thr Val Val Phe Leu Ile Tyr Lys Ile Ile
    420                      425                      430
Gln Arg Asn Gln Asp Asn Ser Asp Val Lys His
    435                      440

```

<210> 277
 <211> 82
 <212> PRT
 <213> E. Coli

<400> 277

```

Met Gly Ile Leu Ser Trp Ile Ile Phe Gly Leu Ile Ala Gly Ile Leu
  1                      5                      10                      15
Ala Lys Trp Ile Met Pro Gly Lys Asp Gly Gly Gly Phe Phe Met Thr
    20                      25                      30
Ile Leu Leu Gly Ile Val Gly Ala Val Val Gly Gly Trp Ile Ser Thr
    35                      40                      45
Leu Phe Gly Phe Gly Lys Val Asp Gly Phe Asn Phe Gly Ser Phe Val
    50                      55                      60

```


Val Ala Val Ile Gly Ala Ile Val Val Leu Phe Ile Tyr Arg Lys Ile
 65 70 75 80
 Lys Ser

<210> 278
 <211> 60
 <212> PRT
 <213> E. Coli

<400> 278
 Met Gly Lys Ala Thr Tyr Thr Val Thr Val Thr Asn Asn Ser Asn Gly
 1 5 10 15
 Val Ser Val Asp Tyr Glu Thr Glu Thr Pro Met Thr Leu Leu Val Pro
 20 25 30
 Glu Val Ala Ala Glu Val Ile Lys Asp Leu Val Asn Thr Val Arg Ser
 35 40 45
 Tyr Asp Thr Glu Asn Glu His Asp Val Cys Gly Trp
 50 55 60

<210> 279
 <211> 119
 <212> PRT
 <213> E. Coli

<400> 279
 Met Leu Gln Ile Pro Gln Asn Tyr Ile His Thr Arg Ser Thr Pro Phe
 1 5 10 15
 Trp Asn Lys Gln Thr Ala Pro Ala Gly Ile Phe Glu Arg His Leu Asp
 20 25 30
 Lys Gly Thr Arg Pro Gly Val Tyr Pro Arg Leu Ser Val Met His Gly
 35 40 45
 Ala Val Lys Tyr Leu Gly Tyr Ala Asp Glu His Ser Ala Glu Pro Asp
 50 55 60
 Gln Val Ile Leu Ile Glu Ala Gly Gln Phe Ala Val Phe Pro Pro Glu
 65 70 75 80
 Lys Trp His Asn Ile Glu Ala Met Thr Asp Asp Thr Tyr Phe Asn Ile
 85 90 95
 Asp Phe Phe Val Ala Pro Glu Val Leu Met Glu Gly Ala Gln Gln Arg
 100 105 110
 Lys Val Ile His Asn Gly Lys
 115

<210> 280
 <211> 246
 <212> PRT
 <213> E. Coli

<400> 280
 Met Lys Phe Lys Val Ile Ala Leu Ala Ala Leu Met Gly Ile Ser Gly
 1 5 10 15
 Met Ala Ala Gln Ala Asn Glu Leu Pro Asp Gly Pro His Ile Val Thr
 20 25 30
 Ser Gly Thr Ala Ser Val Asp Ala Val Pro Asp Ile Ala Thr Leu Ala
 35 40 45
 Ile Glu Val Asn Val Ala Lys Asp Ala Ala Thr Ala Lys Lys Gln
 50 55 60
 Ala Asp Glu Arg Val Ala Gln Tyr Ile Ser Phe Leu Glu Leu Asn Gln

```

65          70          75          80
Ile Ala Lys Lys Asp Ile Ser Ser Ala Asn Leu Arg Thr Gln Pro Asp
      85          90          95
Tyr Asp Tyr Gln Asp Gly Lys Ser Ile Leu Lys Gly Tyr Arg Ala Val
      100          105          110
Arg Thr Val Glu Val Thr Leu Arg Gln Leu Asp Lys Leu Asn Ser Leu
      115          120          125
Leu Asp Gly Ala Leu Lys Ala Gly Leu Asn Glu Ile Arg Ser Val Ser
      130          135          140
Leu Gly Val Ala Gln Pro Asp Ala Tyr Lys Asp Lys Ala Arg Lys Ala
      145          150          155          160
Ala Ile Asp Asn Ala Ile His Gln Ala Gln Glu Leu Ala Asn Gly Phe
      165          170          175
His Arg Lys Leu Gly Pro Val Tyr Ser Val Arg Tyr His Val Ser Asn
      180          185          190
Tyr Gln Pro Ser Pro Met Val Arg Met Met Lys Ala Asp Ala Ala Pro
      195          200          205
Val Ser Ala Gln Glu Thr Tyr Glu Gln Ala Ala Ile Gln Phe Asp Asp
      210          215          220
Gln Val Asp Val Val Phe Gln Leu Glu Pro Val Asp Gln Gln Pro Ala
      225          230          235          240
Lys Thr Pro Ala Ala Gln
      245

```

<210> 281
 <211> 464
 <212> PRT
 <213> E. Coli

```

<400> 281
Met Leu Leu Leu Asp Ala Cys Ser Gln Met Cys Pro Ser Phe Arg Arg
  1          5          10          15
Phe Gln Thr Val Phe His Asn Ser Ser Ile Phe Leu Pro Tyr Trp Leu
      20          25          30
Ala Thr Leu Val Ser Phe Arg Glu Thr Phe Gln Glu Glu Lys Leu Leu
      35          40          45
Thr Met Lys Gly Ser Tyr Lys Ser Arg Trp Val Ile Val Ile Val Val
      50          55          60
Val Ile Ala Ala Ile Ala Ala Phe Trp Phe Trp Gln Gly Arg Asn Asp
      65          70          75          80
Ser Arg Ser Ala Ala Pro Gly Ala Thr Lys Gln Ala Gln Gln Ser Pro
      85          90          95
Ala Gly Gly Arg Arg Gly Met Arg Ser Gly Pro Leu Ala Pro Val Gln
      100          105          110
Ala Ala Thr Ala Val Glu Gln Ala Val Pro Arg Tyr Leu Thr Gly Leu
      115          120          125
Gly Thr Ile Thr Ala Ala Asn Thr Val Thr Val Arg Ser Arg Val Asp
      130          135          140
Gly Gln Leu Ile Ala Leu His Phe Gln Glu Gly Gln Gln Val Lys Ala
      145          150          155          160
Gly Asp Leu Leu Ala Glu Ile Asp Pro Ser Gln Phe Lys Val Ala Leu
      165          170          175
Ala Gln Ala Gln Gly Gln Leu Ala Lys Asp Lys Ala Thr Leu Ala Asn
      180          185          190
Ala Arg Arg Asp Leu Ala Arg Tyr Gln Gln Leu Ala Lys Thr Asn Leu
      195          200          205
Val Ser Arg Gln Glu Leu Asp Ala Gln Gln Ala Leu Val Ser Glu Thr
      210          215          220
Glu Gly Thr Ile Lys Ala Asp Glu Ala Ser Val Ala Ser Ala Gln Leu
      225          230          235          240

```

Gln Leu Asp Trp Ser Arg Ile Thr Ala Pro Val Asp Gly Arg Val Gly
 245 250 255
 Leu Lys Gln Val Asp Val Gly Asn Gln Ile Ser Ser Gly Asp Thr Thr
 260 265 270
 Gly Ile Val Val Ile Thr Gln Thr His Pro Ile Asp Leu Val Phe Thr
 275 280 285
 Leu Pro Glu Ser Asp Ile Ala Thr Val Val Gln Ala Gln Lys Ala Gly
 290 295 300
 Lys Pro Leu Val Val Glu Ala Trp Asp Arg Thr Asn Ser Lys Lys Leu
 305 310 315 320
 Ser Glu Gly Thr Leu Leu Ser Leu Asp Asn Gln Ile Asp Ala Thr Thr
 325 330 335
 Gly Thr Ile Lys Val Lys Ala Arg Phe Asn Asn Gln Asp Asp Ala Leu
 340 345 350
 Phe Pro Asn Gln Phe Val Asn Ala Arg Met Leu Val Asp Thr Glu Gln
 355 360 365
 Asn Ala Val Val Ile Pro Thr Ala Ala Leu Gln Met Gly Asn Glu Gly
 370 375 380
 His Phe Val Trp Val Leu Asn Ser Glu Asn Lys Val Ser Lys His Leu
 385 390 395 400
 Val Thr Pro Gly Ile Gln Asp Ser Gln Lys Val Val Ile Arg Ala Gly
 405 410 415
 Ile Ser Ala Gly Asp Arg Val Val Thr Asp Gly Ile Asp Arg Leu Thr
 420 425 430
 Glu Gly Ala Lys Val Glu Val Val Glu Ala Gln Ser Ala Thr Thr Pro
 435 440 445
 Glu Glu Lys Ala Thr Ser Arg Glu Tyr Ala Lys Lys Gly Ala Arg Ser
 450 455 460

<210> 282

<211> 1040

<212> PRT

<213> E. Coli

<400> 282

Met Gln Val Leu Pro Ser Ser Thr Gly Gly Pro Ser Arg Leu Phe
 1 5 10 15
 Ile Met Arg Pro Val Ala Thr Thr Leu Leu Met Val Ala Ile Leu Leu
 20 25 30
 Ala Gly Ile Ile Gly Tyr Arg Ala Leu Pro Val Ser Ala Leu Pro Glu
 35 40 45
 Val Asp Tyr Pro Thr Ile Gln Val Val Thr Leu Tyr Pro Gly Ala Ser
 50 55 60
 Pro Asp Val Met Thr Ser Ala Val Thr Ala Pro Leu Glu Arg Gln Phe
 65 70 75 80
 Gly Gln Met Ser Gly Leu Lys Gln Met Ser Ser Gln Ser Ser Gly Gly
 85 90 95
 Ala Ser Val Ile Thr Leu Gln Phe Gln Leu Thr Leu Pro Leu Asp Val
 100 105 110
 Ala Glu Gln Glu Val Gln Ala Ala Ile Asn Ala Ala Thr Asn Leu Leu
 115 120 125
 Pro Ser Asp Leu Pro Asn Pro Pro Val Tyr Ser Lys Val Asn Pro Ala
 130 135 140
 Asp Pro Pro Ile Met Thr Leu Ala Val Thr Ser Thr Ala Met Pro Met
 145 150 155 160
 Thr Gln Val Glu Asp Met Val Glu Thr Arg Val Ala Gln Lys Ile Ser
 165 170 175
 Gln Ile Ser Gly Val Gly Leu Val Thr Leu Ser Gly Gly Gln Arg Pro
 180 185 190
 Ala Val Arg Val Lys Leu Asn Ala Gln Ala Ile Ala Ala Leu Gly Leu

195	200	205
Thr Ser Glu Thr Val Arg Thr Ala Ile Thr Gly Ala Asn Val Asn Ser		
210	215	220
Ala Lys Gly Ser Leu Asp Gly Pro Ser Arg Ala Val Thr Leu Ser Ala		
225	230	235
Asn Asp Gln Met Gln Ser Ala Glu Glu Tyr Arg Gln Leu Ile Ile Ala		
245	250	255
Tyr Gln Asn Gly Ala Pro Ile Arg Leu Gly Asp Val Ala Thr Val Glu		
260	265	270
Gln Gly Ala Glu Asn Ser Trp Leu Gly Ala Trp Ala Asn Lys Glu Gln		
275	280	285
Ala Ile Val Met Asn Val Gln Arg Gln Pro Gly Ala Asn Ile Ile Ser		
290	295	300
Thr Ala Asp Ser Ile Arg Gln Met Leu Pro Gln Leu Thr Glu Ser Leu		
305	310	315
Pro Lys Ser Val Lys Val Thr Val Leu Ser Asp Arg Thr Thr Asn Ile		
325	330	335
Arg Ala Ser Val Asp Asp Thr Gln Phe Glu Leu Met Met Ala Ile Ala		
340	345	350
Leu Val Val Met Ile Ile Tyr Leu Phe Leu Arg Asn Ile Pro Ala Thr		
355	360	365
Ile Ile Pro Gly Val Ala Val Pro Leu Ser Leu Ile Gly Thr Phe Ala		
370	375	380
Val Met Val Phe Leu Asp Phe Ser Ile Asn Asn Leu Thr Leu Met Ala		
385	390	395
Leu Thr Ile Ala Thr Gly Phe Val Val Asp Asp Ala Ile Val Val Ile		
405	410	415
Glu Asn Ile Ser Arg Tyr Ile Glu Lys Gly Glu Lys Pro Leu Ala Ala		
420	425	430
Ala Leu Lys Gly Ala Gly Glu Ile Gly Phe Thr Ile Ile Ser Leu Thr		
435	440	445
Phe Ser Leu Ile Ala Val Leu Ile Pro Leu Leu Phe Met Gly Asp Ile		
450	455	460
Val Gly Arg Leu Phe Arg Glu Phe Ala Ile Thr Leu Ala Val Ala Ile		
465	470	475
Leu Ile Ser Ala Val Val Ser Leu Thr Leu Thr Pro Met Met Cys Ala		
485	490	495
Arg Met Leu Ser Gln Glu Ser Leu Arg Lys Gln Asn Arg Phe Ser Arg		
500	505	510
Ala Ser Glu Lys Met Phe Asp Arg Ile Ile Ala Ala Tyr Gly Arg Gly		
515	520	525
Leu Ala Lys Val Leu Asn His Pro Trp Leu Thr Leu Ser Val Ala Leu		
530	535	540
Ser Thr Leu Leu Leu Ser Val Leu Leu Trp Val Phe Ile Pro Lys Gly		
545	550	555
Phe Phe Pro Val Gln Asp Asn Gly Ile Ile Gln Gly Thr Leu Gln Ala		
565	570	575
Pro Gln Ser Ser Ser Phe Ala Asn Met Ala Gln Arg Gln Arg Gln Val		
580	585	590
Ala Asp Val Ile Leu Gln Asp Pro Ala Val Gln Ser Leu Thr Ser Phe		
595	600	605
Val Gly Val Asp Gly Thr Asn Pro Ser Leu Asn Ser Ala Arg Leu Gln		
610	615	620
Ile Asn Leu Lys Pro Leu Asp Glu Arg Asp Asp Arg Val Gln Lys Val		
625	630	635
Ile Ala Arg Leu Gln Thr Ala Val Asp Lys Val Pro Gly Val Asp Leu		
645	650	655
Phe Leu Gln Pro Thr Gln Asp Leu Thr Ile Asp Thr Gln Val Ser Arg		
660	665	670
Thr Gln Tyr Gln Phe Thr Leu Gln Ala Thr Ser Leu Asp Ala Leu Ser		
675	680	685

Thr Trp Val Pro Gln Leu Met Glu Lys Leu Gln Gln Leu Pro Gln Leu
 690 695 700
 Ser Asp Val Ser Ser Asp Trp Gln Asp Lys Gly Leu Val Ala Tyr Val
 705 710 715 720
 Asn Val Asp Arg Asp Ser Ala Ser Arg Leu Gly Ile Ser Met Ala Asp
 725 730 735
 Val Asp Asn Ala Leu Tyr Asn Ala Phe Gly Gln Arg Leu Ile Ser Thr
 740 745 750
 Ile Tyr Thr Gln Ala Asn Gln Tyr Arg Val Val Leu Glu His Asn Thr
 755 760 765
 Glu Asn Thr Pro Gly Leu Ala Ala Leu Asp Thr Ile Arg Leu Thr Ser
 770 775 780
 Ser Asp Gly Gly Val Val Pro Leu Ser Ser Ile Ala Lys Ile Glu Gln
 785 790 795 800
 Arg Phe Ala Pro Leu Ser Ile Asn His Leu Asp Gln Phe Pro Val Thr
 805 810 815
 Thr Ile Ser Phe Asn Val Pro Asp Asn Tyr Ser Leu Gly Asp Ala Val
 820 825 830
 Gln Ala Ile Met Asp Thr Glu Lys Thr Leu Asn Leu Pro Val Asp Ile
 835 840 845
 Thr Thr Gln Phe Gln Gly Ser Thr Leu Ala Phe Gln Ser Ala Leu Gly
 850 855 860
 Ser Thr Val Trp Leu Ile Val Ala Ala Val Val Ala Met Tyr Ile Val
 865 870 875 880
 Leu Gly Ile Leu Tyr Glu Ser Phe Ile His Pro Ile Thr Ile Leu Ser
 885 890 895
 Thr Leu Pro Thr Ala Gly Val Gly Ala Leu Leu Ala Leu Ile Ala
 900 905 910
 Gly Ser Glu Leu Asp Val Ile Ala Ile Ile Gly Ile Ile Leu Leu Ile
 915 920 925
 Gly Ile Val Lys Lys Asn Ala Ile Met Met Ile Asp Phe Ala Leu Ala
 930 935 940
 Ala Glu Arg Glu Gln Gly Met Ser Pro Arg Glu Ala Ile Tyr Gln Ala
 945 950 955 960
 Cys Leu Leu Arg Phe Arg Pro Ile Leu Met Thr Thr Leu Ala Ala Leu
 965 970 975
 Leu Gly Ala Leu Pro Leu Met Leu Ser Thr Gly Val Gly Ala Glu Leu
 980 985 990
 Arg Arg Pro Leu Gly Ile Gly Met Val Gly Gly Leu Ile Val Ser Gln
 995 1000 1005
 Val Leu Thr Leu Phe Thr Thr Pro Val Ile Tyr Leu Leu Phe Asp Arg
 1010 1015 1020
 Leu Ala Leu Trp Thr Lys Ser Arg Phe Ala Arg His Glu Glu Glu Ala
 1025 1030 1035 1040

<210> 283

<211> 1025

<212> PRT

<213> E. Coli

<400> 283

Met Lys Phe Phe Ala Leu Phe Ile Tyr Arg Pro Val Ala Thr Ile Leu
 1 5 10 15
 Leu Ser Val Ala Ile Thr Leu Cys Gly Ile Leu Gly Phe Arg Met Leu
 20 25 30
 Pro Val Ala Pro Leu Pro Gln Val Asp Phe Pro Val Ile Ile Val Ser
 35 40 45
 Ala Ser Leu Pro Gly Ala Ser Pro Glu Thr Met Ala Ser Ser Val Ala
 50 55 60
 Thr Pro Leu Glu Arg Ser Leu Gly Arg Ile Ala Gly Val Ser Glu Met

65					70					75				80	
Thr	Ser	Ser	Ser	Ser	Leu	Gly	Ser	Thr	Arg	Ile	Ile	Leu	Gln	Phe	Asp
				85					90					95	
Phe	Asp	Arg	Asp	Ile	Asn	Gly	Ala	Ala	Arg	Asp	Val	Gln	Ala	Ala	Ile
			100						105				110		
Asn	Ala	Ala	Gln	Ser	Leu	Leu	Pro	Ser	Gly	Met	Pro	Ser	Arg	Pro	Thr
			115				120					125			
Tyr	Arg	Lys	Ala	Asn	Pro	Ser	Asp	Ala	Pro	Ile	Met	Ile	Leu	Thr	Leu
	130					135					140				
Thr	Ser	Asp	Thr	Tyr	Ser	Gln	Gly	Glu	Leu	Tyr	Asp	Phe	Ala	Ser	Thr
	145				150					155				160	
Gln	Leu	Ala	Pro	Thr	Ile	Ser	Gln	Ile	Asp	Gly	Val	Gly	Asp	Val	Asp
				165					170					175	
Val	Gly	Gly	Ser	Ser	Leu	Pro	Ala	Val	Arg	Val	Gly	Leu	Asn	Pro	Gln
			180					185					190		
Ala	Leu	Phe	Asn	Gln	Gly	Val	Ser	Leu	Asp	Asp	Val	Arg	Thr	Ala	Val
			195				200					205			
Ser	Asn	Ala	Asn	Val	Arg	Lys	Pro	Gln	Gly	Ala	Leu	Glu	Asp	Gly	Thr
	210					215					220				
His	Arg	Trp	Gln	Ile	Gln	Thr	Asn	Asp	Glu	Leu	Lys	Thr	Ala	Ala	Glu
	225				230					235				240	
Tyr	Gln	Pro	Leu	Ile	Ile	His	Tyr	Asn	Asn	Gly	Gly	Ala	Val	Arg	Leu
			245					250						255	
Gly	Asp	Val	Ala	Thr	Val	Thr	Asp	Ser	Val	Gln	Asp	Val	Arg	Asn	Ala
			260				265					270			
Gly	Met	Thr	Asn	Ala	Lys	Pro	Ala	Ile	Leu	Leu	Met	Ile	Arg	Lys	Leu
	275					280						285			
Pro	Glu	Ala	Asn	Ile	Ile	Gln	Thr	Val	Asp	Ser	Ile	Arg	Ala	Lys	Leu
	290					295					300				
Pro	Glu	Leu	Gln	Glu	Thr	Ile	Pro	Ala	Ala	Ile	Asp	Leu	Gln	Ile	Ala
	305				310					315				320	
Gln	Asp	Arg	Ser	Pro	Thr	Ile	Arg	Ala	Ser	Leu	Glu	Glu	Val	Glu	Gln
			325				330							335	
Thr	Leu	Ile	Ile	Ser	Val	Ala	Leu	Val	Ile	Leu	Val	Val	Phe	Leu	Phe
			340				345						350		
Leu	Arg	Ser	Gly	Arg	Ala	Thr	Ile	Ile	Pro	Ala	Val	Ser	Val	Pro	Val
	355					360						365			
Ser	Leu	Ile	Gly	Thr	Phe	Ala	Ala	Met	Tyr	Leu	Cys	Gly	Phe	Ser	Leu
	370				375					380					
Asn	Asn	Leu	Ser	Leu	Met	Ala	Leu	Thr	Ile	Ala	Thr	Gly	Phe	Val	Val
	385				390					395				400	
Asp	Asp	Ala	Ile	Val	Val	Leu	Glu	Asn	Ile	Ala	Arg	His	Leu	Glu	Ala
			405					410					415		
Gly	Met	Lys	Pro	Leu	Gln	Ala	Ala	Leu	Gln	Gly	Thr	Arg	Glu	Val	Gly
		420					425						430		
Phe	Thr	Val	Leu	Ser	Met	Ser	Leu	Ser	Leu	Val	Ala	Val	Phe	Leu	Pro
		435				440						445			
Leu	Leu	Leu	Met	Gly	Gly	Leu	Pro	Gly	Arg	Leu	Leu	Arg	Glu	Phe	Ala
	450				455					460					
Val	Thr	Leu	Ser	Val	Ala	Ile	Gly	Ile	Ser	Leu	Leu	Val	Ser	Leu	Thr
	465				470					475				480	
Leu	Thr	Pro	Met	Met	Cys	Gly	Trp	Met	Leu	Lys	Ala	Ser	Lys	Pro	Arg
			485					490					495		
Glu	Gln	Lys	Arg	Leu	Arg	Gly	Phe	Gly	Arg	Met	Leu	Val	Ala	Leu	Gln
		500					505						510		
Gln	Gly	Tyr	Gly	Lys	Ser	Leu	Lys	Trp	Val	Leu	Asn	His	Thr	Arg	Leu
	515					520						525			
Val	Gly	Val	Val	Leu	Leu	Gly	Thr	Ile	Ala	Leu	Asn	Ile	Trp	Leu	Tyr
	530				535					540					
Ile	Ser	Ile	Pro	Lys	Thr	Phe	Phe	Pro	Glu	Gln	Asp	Thr	Gly	Val	Leu
	545				550					555				560	

Met Gly Gly Ile Gln Ala Asp Gln Ser Ile Ser Phe Gln Ala Met Arg
 565 570 575
 Gly Lys Leu Gln Asp Phe Met Lys Ile Ile Arg Asp Asp Pro Ala Val
 580 585 590
 Asp Asn Val Thr Gly Phe Thr Gly Gly Ser Arg Val Asn Ser Gly Met
 595 600 605
 Met Phe Ile Thr Leu Lys Pro Arg Asp Glu Arg Ser Glu Thr Ala Gln
 610 615 620
 Gln Ile Ile Asp Arg Leu Arg Val Lys Leu Ala Lys Glu Pro Gly Ala
 625 630 635 640
 Asn Leu Phe Leu Met Ala Val Gln Asp Ile Arg Val Gly Gly Arg Gln
 645 650 655
 Ser Asn Ala Ser Tyr Gln Tyr Thr Leu Leu Ser Asp Asp Leu Ala Ala
 660 665 670
 Leu Arg Glu Trp Glu Pro Lys Ile Arg Lys Lys Leu Ala Thr Leu Pro
 675 680 685
 Glu Leu Ala Asp Val Asn Ser Asp Gln Gln Asp Asn Gly Ala Glu Met
 690 695 700
 Asn Leu Val Tyr Asp Arg Asp Thr Met Ala Arg Leu Gly Ile Asp Val
 705 710 715 720
 Gln Ala Ala Asn Ser Leu Leu Asn Asn Ala Phe Gly Gln Arg Gln Ile
 725 730 735
 Ser Thr Ile Tyr Gln Pro Met Asn Gln Tyr Lys Val Val Met Glu Val
 740 745 750
 Asp Pro Arg Tyr Thr Gln Asp Ile Ser Ala Leu Glu Lys Met Phe Val
 755 760 765
 Ile Asn Asn Glu Gly Lys Ala Ile Pro Leu Ser Tyr Phe Ala Lys Trp
 770 775 780
 Gln Pro Ala Asn Ala Pro Leu Ser Val Asn His Gln Gly Leu Ser Ala
 785 790 795 800
 Ala Ser Thr Ile Ser Phe Asn Leu Pro Thr Gly Lys Ser Leu Ser Asp
 805 810 815
 Ala Ser Ala Ala Ile Asp Arg Ala Met Thr Gln Leu Gly Val Pro Ser
 820 825 830
 Thr Val Arg Gly Ser Phe Ala Gly Thr Ala Gln Val Phe Gln Glu Thr
 835 840 845
 Met Asn Ser Gln Val Ile Leu Ile Ile Ala Ala Ile Ala Thr Val Tyr
 850 855 860
 Ile Val Leu Gly Ile Leu Tyr Glu Ser Tyr Val His Pro Leu Thr Ile
 865 870 875 880
 Leu Ser Thr Leu Pro Ser Ala Gly Val Gly Ala Leu Leu Ala Leu Glu
 885 890 895
 Leu Phe Asn Ala Pro Phe Ser Leu Ile Ala Leu Ile Gly Ile Met Leu
 900 905 910
 Leu Ile Gly Ile Val Lys Lys Asn Ala Ile Met Met Val Asp Phe Ala
 915 920 925
 Leu Glu Ala Gln Arg His Gly Asn Leu Thr Pro Gln Glu Ala Ile Phe
 930 935 940
 Gln Ala Cys Leu Leu Arg Phe Arg Pro Ile Met Met Thr Thr Leu Ala
 945 950 955 960
 Ala Leu Phe Gly Ala Leu Pro Leu Val Leu Ser Gly Gly Asp Gly Ser
 965 970 975
 Glu Leu Arg Gln Pro Leu Gly Ile Thr Ile Val Gly Gly Leu Val Met
 980 985 990
 Ser Gln Leu Leu Thr Leu Tyr Thr Thr Pro Val Val Tyr Leu Phe Phe
 995 1000 1005
 Asp Arg Leu Arg Leu Arg Phe Ser Arg Lys Pro Lys Gln Thr Val Thr
 1010 1015 1020
 Glu
 1025

<210> 284
 <211> 471
 <212> PRT
 <213> E. Coli

<400> 284

```

Met Thr Asp Leu Pro Asp Ser Thr Arg Trp Gln Leu Trp Ile Val Ala
1      5      10      15
Phe Gly Phe Phe Met Gln Ser Leu Asp Thr Thr Ile Val Asn Thr Ala
20     25     30
Leu Pro Ser Met Ala Gln Ser Leu Gly Glu Ser Pro Leu His Met His
35     40     45
Met Val Ile Val Ser Tyr Val Leu Thr Val Ala Val Met Leu Pro Ala
50     55     60
Ser Gly Trp Leu Ala Asp Lys Val Gly Val Arg Asn Ile Phe Phe Thr
65     70     75     80
Ala Ile Val Leu Phe Thr Leu Gly Ser Leu Phe Cys Ala Leu Ser Gly
85     90     95
Thr Leu Asn Glu Leu Leu Leu Ala Arg Ala Leu Gln Gly Val Gly Gly
100    105    110
Ala Met Met Val Pro Val Gly Arg Leu Thr Val Met Lys Ile Val Pro
115    120    125
Arg Glu Gln Tyr Met Ala Ala Met Thr Phe Val Thr Leu Pro Gly Gln
130    135    140
Val Gly Pro Leu Leu Gly Pro Ala Leu Gly Gly Leu Leu Val Glu Tyr
145    150    155    160
Ala Ser Trp His Trp Ile Phe Leu Ile Asn Ile Pro Val Gly Ile Ile
165    170    175
Gly Ala Ile Ala Thr Leu Leu Leu Met Pro Asn Tyr Thr Met Gln Thr
180    185    190
Arg Arg Phe Asp Leu Ser Gly Phe Leu Leu Leu Ala Val Gly Met Ala
195    200    205
Val Leu Thr Leu Ala Leu Asp Gly Ser Lys Gly Thr Gly Leu Ser Pro
210    215    220
Leu Thr Ile Ala Gly Leu Val Ala Val Gly Val Val Ala Leu Val Leu
225    230    235    240
Tyr Leu Leu His Ala Arg Asn Asn Asn Arg Ala Leu Phe Ser Leu Lys
245    250    255
Leu Phe Arg Thr Arg Thr Phe Ser Leu Gly Leu Ala Gly Ser Phe Ala
260    265    270
Gly Arg Ile Gly Ser Gly Met Leu Pro Phe Met Thr Pro Val Phe Leu
275    280    285
Gln Ile Gly Leu Gly Phe Ser Pro Phe His Ala Gly Leu Met Met Ile
290    295    300
Pro Met Val Leu Gly Ser Met Gly Met Lys Arg Ile Val Val Gln Val
305    310    315    320
Val Asn Arg Phe Gly Tyr Arg Arg Val Leu Val Ala Thr Thr Leu Gly
325    330    335
Leu Ser Leu Val Thr Leu Leu Phe Met Thr Thr Ala Leu Leu Gly Trp
340    345    350
Tyr Tyr Val Leu Pro Phe Val Leu Phe Leu Gln Gly Met Val Asn Ser
355    360    365
Thr Arg Phe Ser Ser Met Asn Thr Leu Thr Leu Lys Asp Leu Pro Asp
370    375    380
Asn Leu Ala Ser Ser Gly Asn Ser Leu Leu Ser Met Ile Met Gln Leu
385    390    395    400
Ser Met Ser Ile Gly Val Thr Ile Ala Gly Leu Leu Leu Gly Leu Phe
405    410    415
Gly Ser Gln His Val Ser Val Asp Ser Gly Thr Thr Gln Thr Val Phe
420    425    430

```


Met Tyr Thr Trp Leu Ser Met Ala Leu Ile Ile Ala Leu Pro Ala Phe
 435 440 445
 Ile Phe Ala Arg Val Pro Asn Asp Thr His Gln Asn Val Ala Ile Ser
 450 455 460
 Arg Arg Lys Arg Ser Ala Gln
 465 470

<210> 285
 <211> 344
 <212> PRT
 <213> E. Coli

<400> 285

Met Glu Ile Arg Ile Met Leu Phe Ile Leu Met Met Met Val Met Pro
 1 5 10 15
 Val Ser Tyr Ala Ala Cys Tyr Ser Glu Leu Ser Val Gln His Asn Leu
 20 25 30
 Val Val Gln Gly Asp Phe Ala Leu Thr Gln Thr Gln Met Ala Thr Tyr
 35 40 45
 Glu His Asn Phe Asn Asp Ser Ser Cys Val Ser Thr Asn Thr Ile Thr
 50 55 60
 Pro Met Ser Pro Ser Asp Ile Ile Val Gly Leu Tyr Asn Asp Thr Ile
 65 70 75 80
 Lys Leu Asn Leu His Phe Glu Trp Thr Asn Lys Asn Asn Ile Thr Leu
 85 90 95
 Ser Asn Asn Gln Thr Ser Phe Thr Ser Gly Tyr Ser Val Thr Val Thr
 100 105 110
 Pro Ala Ala Ser Asn Ala Lys Val Asn Val Ser Ala Gly Gly Gly Gly
 115 120 125
 Ser Val Met Ile Asn Gly Val Ala Thr Leu Ser Ser Ala Ser Ser Ser
 130 135 140
 Thr Arg Gly Ser Ala Ala Val Gln Phe Leu Leu Cys Leu Leu Gly Gly
 145 150 155 160
 Lys Ser Trp Asp Ala Cys Val Asn Ser Tyr Arg Asn Ala Leu Ala Gln
 165 170 175
 Asn Ala Gly Val Tyr Ser Phe Asn Leu Thr Leu Ser Tyr Asn Pro Ile
 180 185 190
 Thr Thr Thr Cys Lys Pro Asp Asp Leu Leu Ile Thr Leu Asp Ser Ile
 195 200 205
 Pro Val Ser Gln Leu Pro Ala Thr Gly Asn Lys Ala Thr Ile Asn Ser
 210 215 220
 Lys Gln Gly Asp Ile Ile Leu Arg Cys Lys Asn Leu Leu Gly Gln Gln
 225 230 235 240
 Asn Gln Thr Ser Arg Lys Met Gln Val Tyr Leu Ser Ser Ser Asp Leu
 245 250 255
 Leu Thr Asn Ser Asn Thr Ile Leu Lys Gly Ala Glu Asp Asn Gly Val
 260 265 270
 Gly Phe Ile Leu Glu Ser Asn Gly Ser Pro Val Thr Leu Leu Asn Ile
 275 280 285
 Thr Asn Ser Ser Lys Gly Tyr Thr Asn Leu Lys Glu Val Ala Ala Lys
 290 295 300
 Ser Lys Leu Thr Asp Thr Val Ser Ile Pro Ile Thr Ala Ser Tyr
 305 310 315 320
 Tyr Val Tyr Asp Thr Asn Lys Val Lys Ser Gly Ala Leu Glu Ala Thr
 325 330 335
 Ala Leu Ile Asn Val Lys Tyr Asp
 340

<210> 286

<211> 826
 <212> PRT
 <213> E. Coli

<400> 286

```

Met Leu Arg Met Thr Pro Leu Ala Ser Ala Ile Val Ala Leu Leu Leu
1      5      10      15
Gly Ile Glu Ala Tyr Ala Ala Glu Glu Thr Phe Asp Thr His Phe Met
20      25      30
Ile Gly Gly Met Lys Asp Gln Gln Val Ala Asn Ile Arg Leu Asp Asp
35      40      45
Asn Gln Pro Leu Pro Gly Gln Tyr Asp Ile Asp Ile Tyr Val Asn Lys
50      55      60
Gln Trp Arg Gly Lys Tyr Glu Ile Ile Val Lys Asp Asn Pro Gln Glu
65      70      75      80
Thr Cys Leu Ser Arg Glu Val Ile Lys Arg Leu Gly Ile Asn Ser Asp
85      90      95
Asn Phe Ala Ser Gly Lys Gln Cys Leu Thr Phe Glu Gln Leu Val Gln
100     105     110
Gly Gly Ser Tyr Thr Trp Asp Ile Gly Val Phe Arg Leu Asp Phe Ser
115     120     125
Val Pro Gln Ala Trp Val Glu Glu Leu Glu Ser Gly Tyr Val Pro Pro
130     135     140
Glu Asn Trp Glu Arg Gly Ile Asn Ala Phe Tyr Thr Ser Tyr Tyr Leu
145     150     155     160
Ser Gln Tyr Tyr Ser Asp Tyr Lys Ala Ser Gly Asn Asn Lys Ser Thr
165     170     175
Tyr Val Arg Phe Asn Ser Gly Leu Asn Leu Leu Gly Trp Gln Leu His
180     185     190
Ser Asp Ala Ser Phe Ser Lys Thr Asn Asn Asn Pro Gly Val Trp Lys
195     200     205
Ser Asn Thr Leu Tyr Leu Glu Arg Gly Phe Ala Gln Leu Leu Gly Thr
210     215     220
Leu Arg Val Gly Asp Met Tyr Thr Ser Ser Asp Ile Phe Asp Ser Val
225     230     235     240
Arg Phe Arg Gly Val Arg Leu Phe Arg Asp Met Gln Met Leu Pro Asn
245     250     255
Ser Lys Gln Asn Phe Thr Pro Arg Val Gln Gly Ile Ala Gln Ser Asn
260     265     270
Ala Leu Val Thr Ile Glu Gln Asn Gly Phe Val Val Tyr Gln Lys Glu
275     280     285
Val Pro Pro Gly Pro Phe Ala Ile Thr Asp Leu Gln Leu Ala Gly Gly
290     295     300
Gly Ala Asp Leu Asp Val Ser Val Lys Glu Ala Asp Gly Ser Val Thr
305     310     315     320
Thr Tyr Leu Val Pro Tyr Ala Ala Val Pro Asn Met Leu Gln Pro Gly
325     330     335
Val Ser Lys Tyr Asp Leu Ala Ala Gly Arg Ser His Ile Glu Gly Ala
340     345     350
Ser Lys Gln Ser Asp Phe Val Gln Ala Gly Tyr Gln Tyr Gly Phe Asn
355     360     365
Asn Leu Leu Thr Leu Tyr Gly Gly Ser Met Val Ala Asn Asn Tyr Tyr
370     375     380
Ala Phe Thr Leu Gly Ala Gly Trp Asn Thr Arg Ile Gly Ala Ile Ser
385     390     395     400
Val Asp Ala Thr Lys Ser His Ser Lys Gln Asp Asn Gly Asp Val Phe
405     410     415
Asp Gly Gln Ser Tyr Gln Ile Ala Tyr Asn Lys Phe Val Ser Gln Thr
420     425     430
Ser Thr Arg Phe Gly Leu Ala Ala Trp Arg Tyr Ser Ser Arg Asp Tyr
435     440     445

```

```

Arg Thr Phe Asn Asp His Val Trp Ala Asn Asn Lys Asp Asn Tyr Arg
450                               455                               460
Arg Asp Glu Asn Asp Val Tyr Asp Ile Ala Asp Tyr Tyr Gln Asn Asp
465                               470                               475                               480
Phe Gly Arg Lys Asn Ser Phe Ser Ala Asn Met Ser Gln Ser Leu Pro
485                               490                               495
Glu Gly Trp Gly Ser Val Ser Leu Ser Thr Leu Trp Arg Asp Tyr Trp
500                               505                               510
Gly Arg Ser Gly Ser Ser Lys Asp Tyr Gln Leu Ser Tyr Ser Asn Asn
515                               520                               525
Leu Arg Arg Ile Ser Tyr Thr Leu Ala Ala Ser Gln Ala Tyr Asp Glu
530                               535                               540
Asn His His Glu Glu Lys Arg Phe Asn Ile Phe Ile Ser Ile Pro Phe
545                               550                               555                               560
Asp Trp Gly Asp Asp Val Ser Thr Pro Arg Arg Gln Ile Tyr Met Ser
565                               570                               575
Asn Ser Thr Thr Phe Asp Asp Gln Gly Phe Ala Ser Asn Asn Thr Gly
580                               585                               590
Leu Ser Gly Thr Val Gly Ser Arg Asp Gln Phe Asn Tyr Gly Val Asn
595                               600                               605
Leu Ser His Gln His Gln Gly Asn Glu Thr Thr Ala Gly Ala Asn Leu
610                               615                               620
Thr Trp Asn Ala Pro Val Ala Thr Val Asn Gly Ser Tyr Ser Gln Ser
625                               630                               635                               640
Ser Thr Tyr Arg Gln Ala Gly Ala Ser Val Ser Gly Gly Ile Val Ala
645                               650                               655
Trp Ser Gly Gly Val Asn Leu Ala Asn Arg Leu Ser Glu Thr Phe Ala
660                               665                               670
Val Met Asn Ala Pro Gly Ile Lys Asp Ala Tyr Val Asn Gly Gln Lys
675                               680                               685
Tyr Arg Thr Thr Asn Arg Asn Gly Val Val Ile Tyr Asp Gly Met Thr
690                               695                               700
Pro Tyr Arg Glu Asn His Leu Met Leu Asp Val Ser Gln Ser Asp Ser
705                               710                               715                               720
Glu Ala Glu Leu Arg Gly Asn Arg Lys Ile Ala Ala Pro Tyr Arg Gly
725                               730                               735
Ala Val Val Leu Val Asn Phe Asp Thr Asp Gln Arg Lys Pro Trp Phe
740                               745                               750
Ile Lys Ala Leu Arg Ala Asp Gly Gln Ser Leu Thr Phe Gly Tyr Glu
755                               760                               765
Val Asn Asp Ile His Gly His Asn Ile Gly Val Val Gly Gln Gly Ser
770                               775                               780
Gln Leu Phe Ile Arg Thr Asn Glu Val Pro Pro Ser Val Asn Val Ala
785                               790                               795                               800
Ile Asp Lys Gln Gln Gly Leu Ser Cys Thr Ile Thr Phe Gly Lys Glu
805                               810                               815
Ile Asp Glu Ser Arg Asn Tyr Ile Cys Gln
820                               825

```

<210> 287

<211> 239

<212> PRT

<213> E. Coli

<400> 287

```

Met Ala Ala Ile Pro Trp Arg Pro Phe Asn Leu Arg Gly Ile Lys Met
1                               5                               10                               15
Lys Gly Leu Leu Ser Leu Leu Ile Phe Ser Met Val Leu Pro Ala His
20                               25                               30
Ala Gly Ile Val Ile Tyr Gly Thr Arg Ile Ile Tyr Pro Ala Glu Asn

```

```

      35      40      45
Lys Glu Val Met Val Gln Leu Met Asn Gln Gly Asn Arg Ser Ser Leu
  50      55      60
Leu Gln Ala Trp Ile Asp Asp Gly Asp Thr Ser Leu Pro Pro Glu Lys
  65      70      75      80
Ile Gln Val Pro Phe Met Leu Thr Pro Pro Val Ala Lys Ile Gly Ala
      85      90      95
Asn Ser Gly Gln Gln Val Lys Ile Lys Ile Met Pro Asn Lys Leu Pro
      100      105      110
Thr Asn Lys Glu Ser Ile Phe Tyr Leu Asn Val Leu Asp Ile Pro Pro
      115      120      125
Asn Ser Pro Glu Gln Glu Gly Lys Asn Ala Leu Lys Phe Ala Met Gln
      130      135      140
Asn Arg Ile Lys Leu Phe Tyr Arg Pro Ala Gly Ile Ala Pro Val Asn
      145      150      155      160
Lys Ala Thr Phe Lys Lys Leu Leu Val Asn Arg Ser Gly Asn Gly Leu
      165      170      175
Val Ile Lys Asn Asp Ser Ala Asn Trp Val Thr Ile Ser Asp Val Lys
      180      185      190
Ala Asn Asn Val Lys Val Asn Tyr Glu Thr Ile Met Ile Ala Pro Leu
      195      200      205
Glu Ser Gln Ser Val Asn Val Lys Ser Asn Asn Ala Asn Asn Trp His
      210      215      220
Leu Thr Ile Ile Asp Asp His Gly Asn Tyr Ile Ser Asp Lys Ile
      225      230      235

```

<210> 288
 <211> 180
 <212> PRT
 <213> E. Coli

```

      <400> 288
Met Lys Arg Ser Ile Ile Ala Ala Ala Val Phe Ser Ser Phe Phe Met
  1      5      10      15
Ser Ala Gly Val Phe Ala Ala Asp Val Asp Thr Gly Thr Leu Thr Ile
      20      25      30      35
Lys Gly Asn Ile Ala Glu Ser Pro Cys Lys Phe Glu Ala Gly Gly Asp
      40      45
Ser Val Ser Ile Asn Met Pro Thr Val Pro Thr Ser Val Phe Glu Gly
      50      55      60
Lys Ala Lys Tyr Ser Thr Tyr Asp Asp Ala Val Gly Val Thr Ser Ser
      65      70      75      80
Met Leu Lys Ile Ser Cys Pro Lys Glu Val Ala Gly Val Lys Leu Ser
      85      90      95
Leu Ile Thr Asn Asp Lys Ile Thr Gly Asn Asp Lys Ala Ile Ala Ser
      100      105      110
Ser Asn Asp Thr Val Gly Tyr Tyr Leu Tyr Leu Gly Asp Asn Ser Asp
      115      120      125
Val Leu Asp Val Ser Ala Pro Phe Asn Ile Glu Ser Tyr Lys Thr Ala
      130      135      140
Glu Gly Gln Tyr Ala Ile Pro Phe Lys Ala Lys Tyr Leu Lys Leu Thr
      145      150      155      160
Asp Asn Ser Val Gln Ser Gly Asp Val Leu Ser Ser Leu Val Met Arg
      165      170      175
Val Ala Gln Asp
      180

```

<210> 289

<211> 112
 <212> PRT
 <213> E. Coli

<400> 289
 Met Ser Ser Glu Arg Asp Leu Val Asn Phe Leu Gly Asp Phe Ser Met
 1 5 10 15
 Asp Val Ala Lys Ala Val Ile Ala Gly Gly Val Ala Thr Ala Ile Gly
 20 25 30
 Ser Leu Ala Ser Phe Ala Cys Val Ser Phe Gly Phe Pro Val Ile Leu
 35 40 45
 Val Gly Gly Ala Ile Leu Leu Thr Gly Ile Val Cys Thr Val Val Leu
 50 55 60
 Asn Glu Ile Asp Ala Gln Cys His Leu Ser Glu Lys Leu Lys Tyr Ala
 65 70 75 80
 Ile Arg Asp Gly Leu Lys Arg Gln Gln Glu Leu Asp Lys Trp Lys Arg
 85 90 95
 Glu Asn Met Thr Pro Phe Met Tyr Val Leu Asn Thr Pro Pro Val Ile
 100 105 110

<210> 290
 <211> 193
 <212> PRT
 <213> E. Coli

<400> 290
 Met Thr Asp Tyr Leu Leu Leu Phe Val Gly Thr Val Leu Val Asn Asn
 1 5 10 15
 Phe Val Leu Val Lys Phe Leu Gly Leu Cys Pro Phe Met Gly Val Ser
 20 25 30
 Lys Lys Leu Glu Thr Ala Met Gly Met Gly Leu Ala Thr Thr Phe Val
 35 40 45
 Met Thr Leu Ala Ser Ile Cys Ala Trp Leu Ile Asp Thr Trp Ile Leu
 50 55 60
 Ile Pro Leu Asn Leu Ile Tyr Leu Arg Thr Leu Ala Phe Ile Leu Val
 65 70 75 80
 Ile Ala Val Val Val Gln Phe Thr Glu Met Val Val Arg Lys Thr Ser
 85 90 95
 Pro Val Leu Tyr Arg Leu Leu Gly Ile Phe Leu Pro Leu Ile Thr Thr
 100 105 110
 Asn Cys Ala Val Leu Gly Val Ala Leu Leu Asn Ile Asn Leu Gly His
 115 120 125
 Asn Phe Leu Gln Ser Ala Leu Tyr Gly Phe Ser Ala Ala Val Gly Phe
 130 135 140
 Ser Leu Val Met Val Leu Phe Ala Ala Ile Arg Glu Arg Leu Ala Val
 145 150 155 160
 Ala Asp Val Pro Ala Pro Phe Arg Gly Asn Ala Ile Ala Leu Ile Thr
 165 170 175
 Ala Gly Leu Met Ser Leu Ala Phe Met Gly Phe Ser Gly Leu Val Lys
 180 185 190
 Leu

<210> 291
 <211> 192
 <212> PRT
 <213> E. Coli

<400> 291

```

Met Asn Ala Ile Trp Ile Ala Val Ala Ala Val Ser Leu Leu Gly Leu
 1           5           10           15
Ala Phe Gly Ala Ile Leu Gly Tyr Ala Ser Arg Arg Phe Ala Val Glu
          20           25           30
Asp Asp Pro Val Val Glu Lys Ile Asp Glu Ile Leu Pro Gln Ser Gln
          35           40           45
Cys Gly Gln Cys Gly Tyr Pro Gly Cys Arg Pro Tyr Ala Glu Ala Ile
 50           55           60
Ser Cys Asn Gly Glu Lys Ile Asn Arg Cys Ala Pro Gly Gly Glu Ala
 65           70           75           80
Val Met Leu Lys Ile Ala Glu Leu Leu Asn Val Glu Pro Gln Pro Leu
          85           90           95
Asp Gly Glu Ala Gln Glu Ile Thr Pro Ala Arg Met Val Ala Val Ile
          100          105          110
Asp Glu Asn Asn Cys Ile Gly Cys Thr Lys Cys Ile Gln Ala Cys Pro
          115          120          125
Val Asp Ala Ile Val Gly Ala Thr Arg Ala Met His Thr Val Met Ser
          130          135          140
Asp Leu Cys Thr Gly Cys Asn Leu Cys Val Asp Pro Cys Pro Thr His
 145          150          155          160
Cys Ile Ser Leu Gln Pro Val Ala Glu Thr Pro Asp Ser Trp Lys Trp
          165          170          175
Asp Leu Asn Thr Ile Pro Val Arg Ile Ile Pro Val Glu His His Ala
          180          185          190

```

<210> 292

<211> 740

<212> PRT

<213> E. Coli

<400> 292

```

Met Leu Lys Leu Phe Ser Ala Phe Arg Lys Asn Lys Ile Trp Asp Phe
 1           5           10           15
Asn Gly Gly Ile His Pro Pro Glu Met Lys Thr Gln Ser Asn Gly Thr
          20           25           30
Pro Leu Arg Gln Val Pro Leu Ala Gln Arg Phe Val Ile Pro Leu Lys
          35           40           45
Gln His Ile Gly Ala Glu Gly Glu Leu Cys Val Ser Val Gly Asp Lys
 50           55           60
Val Leu Arg Gly Gln Pro Leu Thr Arg Gly Arg Gly Lys Met Leu Pro
 65           70           75           80
Val His Ala Pro Thr Ser Gly Thr Val Thr Ala Ile Ala Pro His Ser
          85           90           95
Thr Ala His Pro Ser Ala Leu Ala Glu Leu Ser Val Ile Ile Asp Ala
          100          105          110
Asp Gly Glu Asp Cys Trp Ile Pro Arg Asp Gly Trp Ala Asp Tyr Arg
          115          120          125
Thr Arg Ser Arg Glu Glu Leu Ile Glu Arg Ile His Gln Phe Gly Val
          130          135          140
Ala Gly Leu Gly Gly Ala Gly Phe Pro Thr Gly Val Lys Leu Gln Gly
 145          150          155          160
Gly Gly Asp Lys Ile Glu Thr Leu Ile Ile Asn Ala Ala Glu Cys Glu
          165          170          175
Pro Tyr Ile Thr Ala Asp Asp Arg Leu Met Gln Asp Cys Ala Ala Gln
          180          185          190
Val Val Glu Gly Ile Arg Ile Leu Ala His Ile Leu Gln Pro Arg Glu
          195          200          205
Ile Leu Ile Gly Ile Glu Asp Asn Lys Pro Gln Ala Ile Ser Met Leu
          210          215          220

```

```

Arg Ala Val Leu Ala Asp Ser Asn Asp Ile Ser Leu Arg Val Ile Pro
225                230                235                240
Thr Lys Tyr Pro Ser Gly Gly Ala Lys Gln Leu Thr Tyr Ile Leu Thr
                245                250                255
Gly Lys Gln Val Pro His Gly Gly Arg Ser Ser Asp Ile Gly Val Leu
                260                265                270
Met Gln Asn Val Gly Thr Ala Tyr Ala Val Lys Arg Ala Val Ile Asp
275                280                285
Gly Glu Pro Ile Thr Glu Arg Val Val Thr Leu Thr Gly Glu Ala Ile
290                295                300
Ala Arg Pro Gly Asn Val Trp Ala Arg Leu Gly Thr Pro Val Arg His
305                310                315                320
Leu Leu Asn Asp Ala Gly Phe Cys Pro Ser Ala Asp Gln Met Val Ile
                325                330                335
Met Gly Gly Pro Leu Met Gly Phe Thr Leu Pro Trp Leu Asp Val Pro
                340                345                350
Val Val Lys Ile Thr Asn Cys Leu Leu Ala Pro Ser Ala Asn Glu Leu
                355                360                365
Gly Glu Pro Gln Glu Glu Gln Ser Cys Ile Arg Cys Ser Ala Cys Ala
                370                375                380
Asp Ala Cys Pro Ala Asp Leu Leu Pro Gln Gln Leu Tyr Trp Phe Ser
385                390                395                400
Lys Gly Gln Gln His Asp Lys Ala Thr Thr His Asn Ile Ala Asp Cys
                405                410                415
Ile Glu Cys Gly Ala Cys Ala Trp Val Cys Pro Ser Asn Ile Pro Leu
                420                425                430
Val Gln Tyr Phe Arg Gln Glu Lys Ala Glu Ile Ala Ala Ile Arg Gln
                435                440                445
Glu Glu Lys Arg Ala Ala Glu Ala Lys Ala Arg Phe Glu Ala Arg Gln
                450                455                460
Ala Arg Leu Glu Arg Glu Lys Ala Ala Arg Leu Glu Arg His Lys Ser
465                470                475                480
Ala Ala Val Gln Pro Ala Ala Lys Asp Lys Asp Ala Ile Ala Ala Ala
                485                490                495
Leu Ala Arg Val Lys Glu Lys Gln Ala Gln Ala Thr Gln Pro Ile Val
                500                505                510
Ile Lys Ala Gly Glu Arg Pro Asp Asn Ser Ala Ile Ile Ala Ala Arg
                515                520                525
Glu Ala Arg Lys Ala Gln Ala Arg Ala Lys Gln Ala Glu Leu Gln Gln
                530                535                540
Thr Asn Asp Ala Ala Thr Val Ala Asp Pro Arg Lys Thr Ala Val Glu
545                550                555                560
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
                565                570                575
Asn Ala Glu Pro Glu Gln Gln Val Asp Pro Arg Lys Ala Ala Val Glu
                580                585                590
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
                595                600                605
Asn Ala Glu Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Glu
                610                615                620
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
                625                630                635                640
Asn Ala Glu Pro Glu Gln Gln Val Asp Pro Arg Lys Ala Ala Val Glu
                645                650                655
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Arg Glu Gln Gln Pro Ala
                660                665                670
Asn Ala Glu Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Glu
                675                680                685
Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Gln Ala
                690                695                700
Asn Ala Val Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Ala

```

```
<210> 293
<211> 352
<212> PRT
<213> E. Coli
```

Met	Val	Phe	Arg	Ile	Ala	Ser	Ser	Pro	Tyr	Thr	His	Asn	Gln	Arg	Gln
1				5				10						15	
Thr	Ser	Arg	Ile	Met	Leu	Leu	Val	Leu	Leu	Ala	Ala	Val	Pro	Gly	Ile
			20					25					30		
Ala	Ala	Gln	Leu	Trp	Phe	Phe	Gly	Trp	Gly	Thr	Leu	Val	Gln	Ile	Leu
		35					40					45			
Leu	Ala	Ser	Val	Ser	Ala	Leu	Leu	Ala	Glu	Ala	Leu	Val	Leu	Lys	Leu
		50				55					60				
Arg	Lys	Gln	Ser	Val	Ala	Ala	Thr	Leu	Lys	Asp	Asn	Ser	Ala	Leu	Leu
65				70						75				80	
Thr	Gly	Leu	Leu	Leu	Ala	Val	Ser	Ile	Pro	Pro	Leu	Ala	Pro	Trp	Trp
			85						90				95		
Met	Val	Val	Leu	Gly	Thr	Val	Phe	Ala	Val	Ile	Ile	Ala	Lys	Gln	Leu
			100					105					110		
Tyr	Gly	Gly	Leu	Gly	Gln	Asn	Pro	Phe	Asn	Pro	Ala	Met	Ile	Gly	Tyr
		115					120					125			
Val	Val	Leu	Leu	Ile	Ser	Phe	Pro	Val	Gln	Met	Thr	Ser	Trp	Leu	Pro
		130				135					140				
Pro	His	Glu	Ile	Ala	Val	Asn	Ile	Pro	Gly	Phe	Ile	Asp	Ala	Ile	Gln
145				150						155				160	
Val	Ile	Phe	Ser	Gly	His	Thr	Ala	Ser	Gly	Gly	Asp	Met	Asn	Thr	Leu
			165					170					175		
Arg	Leu	Gly	Ile	Asp	Gly	Ile	Ser	Gln	Ala	Thr	Pro	Leu	Asp	Thr	Phe
		180					185					190			
Lys	Thr	Ser	Val	Arg	Ala	Gly	His	Ser	Val	Glu	Gln	Ile	Met	Gln	Tyr
		195					200					205			
Pro	Ile	Tyr	Ser	Gly	Ile	Leu	Ala	Gly	Ala	Gly	Trp	Gln	Trp	Val	Asn
		210				215					220				
Leu	Ala	Trp	Leu	Ala	Gly	Gly	Val	Trp	Leu	Leu	Trp	Gln	Lys	Ala	Ile
225				230						235				240	
Arg	Trp	His	Ile	Pro	Leu	Ser	Phe	Leu	Val	Thr	Leu	Ala	Leu	Cys	Ala
			245					250					255		
Met	Leu	Gly	Trp	Leu	Phe	Ser	Pro	Glu	Thr	Leu	Ala	Ala	Pro	Gln	Ile
		260						265					270		
His	Leu	Leu	Ser	Gly	Ala	Thr	Met	Leu	Gly	Ala	Phe	Phe	Ile	Leu	Thr
		275					280					285			
Asp	Pro	Val	Thr	Ala	Ser	Thr	Thr	Asn	Arg	Gly	Arg	Leu	Ile	Phe	Gly
		290				295					300				
Ala	Leu	Ala	Gly	Leu	Leu	Val	Trp	Leu	Ile	Arg	Ser	Phe	Gly	Gly	Tyr
305				310						315				320	
Pro	Asp	Gly	Val	Ala	Phe	Ala	Val	Leu	Leu	Ala	Asn	Ile	Thr	Val	Pro
			325					330					335		
Leu	Ile	Asp	Tyr	Tyr	Thr	Arg	Pro	Arg	Val	Tyr	Gly	His	Arg	Lys	Gly
		340						345					350		

<210> 294

<211> 206
 <212> PRT
 <213> E. Coli

<400> 294

```

Met Leu Lys Thr Ile Arg Lys His Gly Ile Thr Leu Ala Leu Phe Ala
 1          5          10          15
Ala Gly Ser Thr Gly Leu Thr Ala Ala Ile Asn Gln Met Thr Lys Thr
 20          25          30
Thr Ile Ala Glu Gln Ala Ser Leu Gln Gln Lys Ala Leu Phe Asp Gln
 35          40          45
Val Leu Pro Ala Glu Arg Tyr Asn Asn Ala Leu Ala Gln Ser Cys Tyr
 50          55          60
Leu Val Thr Ala Pro Glu Leu Gly Lys Gly Glu His Arg Val Tyr Ile
 65          70          75
Ala Lys Gln Asp Asp Lys Pro Val Ala Ala Val Leu Glu Ala Thr Ala
 85          90          95
Pro Asp Gly Tyr Ser Gly Ala Ile Gln Leu Leu Val Gly Ala Asp Phe
100          105          110
Asn Gly Thr Val Leu Gly Thr Arg Val Thr Glu His His Glu Thr Pro
115          120          125
Gly Leu Gly Asp Lys Ile Glu Leu Arg Leu Ser Asp Trp Ile Thr His
130          135          140
Phe Ala Gly Lys Lys Ile Ser Gly Ala Asp Asp Ala His Trp Ala Val
145          150          155
Lys Lys Asp Gly Gly Asp Phe Asp Gln Phe Thr Gly Ala Thr Ile Thr
165          170          175
Pro Arg Ala Val Val Asn Ala Val Lys Arg Ala Gly Leu Tyr Ala Gln
180          185          190
Thr Leu Pro Ala Gln Leu Ser Gln Leu Pro Ala Cys Gly Glu
195          200          205

```

<210> 295
 <211> 231
 <212> PRT
 <213> E. Coli

<400> 295

```

Met Ser Glu Ile Lys Asp Val Ile Val Gln Gly Leu Trp Lys Asn Asn
 1          5          10          15
Ser Ala Leu Val Gln Leu Leu Gly Leu Cys Pro Leu Leu Ala Val Thr
 20          25          30
Ser Thr Ala Thr Asn Ala Leu Gly Leu Gly Leu Ala Thr Thr Leu Val
 35          40          45
Leu Thr Leu Thr Asn Leu Thr Ile Ser Thr Leu Arg His Trp Thr Pro
 50          55          60
Ala Glu Ile Arg Ile Pro Ile Tyr Val Met Ile Ile Ala Ser Val Val
 65          70          75
Ser Ala Val Gln Met Leu Ile Asn Ala Tyr Ala Phe Gly Leu Tyr Gln
 85          90          95
Ser Leu Gly Ile Phe Ile Pro Leu Ile Val Thr Asn Cys Ile Val Val
100          105          110
Gly Arg Ala Glu Ala Phe Ala Ala Lys Lys Gly Pro Ala Leu Ser Ala
115          120          125
Leu Asp Gly Phe Ser Ile Gly Met Gly Ala Thr Cys Ala Met Phe Val
130          135          140
Leu Gly Ser Leu Arg Glu Ile Ile Gly Asn Gly Thr Leu Phe Asp Gly
145          150          155
Ala Asp Ala Leu Leu Gly Ser Trp Ala Lys Val Leu Arg Val Glu Ile
165          170          175

```

Phe His Thr Asp Ser Pro Phe Leu Leu Ala Met Leu Pro Pro Gly Ala
 180 185 190
 Phe Ile Gly Leu Gly Leu Met Leu Ala Gly Lys Tyr Leu Ile Asp Glu
 195 200 205
 Arg Met Lys Lys Arg Arg Ala Glu Ala Ala Ala Glu Arg Ala Leu Pro
 210 215 220
 Asn Gly Glu Thr Gly Asn Val
 225 230

<210> 296
 <211> 211
 <212> PRT
 <213> E. Coli

<400> 296
 Met Asn Lys Ala Lys Arg Leu Glu Ile Leu Thr Arg Leu Arg Glu Asn
 1 5 10 15
 Asn Pro His Pro Thr Thr Glu Leu Asn Phe Ser Ser Pro Phe Glu Leu
 20 25 30
 Leu Ile Ala Val Leu Leu Ser Ala Gln Ala Thr Asp Val Ser Val Asn
 35 40 45
 Lys Ala Thr Ala Lys Leu Tyr Pro Val Ala Asn Thr Pro Ala Ala Met
 50 55 60
 Leu Glu Leu Gly Val Glu Gly Val Lys Thr Tyr Ile Lys Thr Ile Gly
 65 70 75 80
 Leu Tyr Asn Ser Lys Ala Glu Asn Ile Ile Lys Thr Cys Arg Ile Leu
 85 90 95
 Leu Glu Gln His Asn Gly Glu Val Pro Glu Asp Arg Ala Ala Leu Glu
 100 105 110
 Ala Leu Pro Gly Val Gly Arg Lys Thr Ala Asn Val Val Leu Asn Thr
 115 120 125
 Ala Phe Gly Trp Pro Thr Ile Ala Val Asp Thr His Ile Phe Arg Val
 130 135 140
 Cys Asn Arg Thr Gln Phe Ala Pro Gly Lys Asn Val Glu Gln Val Glu
 145 150 155 160
 Glu Lys Leu Leu Lys Val Val Pro Ala Glu Phe Lys Val Asp Cys His
 165 170 175
 His Trp Leu Ile Leu His Gly Arg Tyr Thr Cys Ile Ala Arg Lys Pro
 180 185 190
 Arg Cys Gly Ser Cys Ile Ile Glu Asp Leu Cys Glu Tyr Lys Glu Lys
 195 200 205
 Val Asp Ile
 210

<210> 297
 <211> 167
 <212> PRT
 <213> E. Coli

<400> 297
 Met Lys Arg Leu His Lys Arg Phe Leu Leu Ala Thr Phe Cys Ala Leu
 1 5 10 15
 Phe Thr Ala Thr Leu Gln Ala Ala Asp Val Thr Ile Thr Val Asn Gly
 20 25 30
 Arg Val Val Ala Lys Pro Cys Thr Ile Gln Thr Lys Glu Ala Asn Val
 35 40 45
 Asn Leu Gly Asp Leu Tyr Thr Arg Asn Leu Gln Gln Pro Gly Ser Ala
 50 55 60
 Ser Gly Trp His Asn Ile Thr Leu Ser Leu Thr Asp Cys Pro Val Glu

```

65              70              75              80
Thr Ser Ala Val Thr Ala Ile Val Thr Gly Ser Thr Asp Asn Thr Gly
      85              90              95
Tyr Tyr Lys Asn Glu Gly Thr Ala Glu Asn Ile Gln Ile Glu Leu Arg
      100             105             110
Asp Asp Gln Asp Ala Ala Leu Lys Asn Gly Asp Ser Lys Thr Val Ile
      115             120             125
Val Asp Glu Ile Thr Arg Asn Ala Gln Phe Pro Leu Lys Ala Arg Ala
      130             135             140
Ile Thr Val Asn Gly Asn Ala Ser Gln Gly Thr Ile Glu Ala Leu Ile
145             150             155             160
Asn Val Ile Tyr Thr Trp Gln
      165

```

<210> 298
 <211> 176
 <212> PRT
 <213> E. Coli

```

<400> 298
Met Lys Tyr Asn Asn Ile Ile Phe Leu Gly Leu Cys Leu Gly Leu Thr
1      5      10      15
Thr Tyr Ser Ala Leu Ser Ala Asp Ser Val Ile Lys Ile Ser Gly Arg
      20      25      30
Val Leu Asp Tyr Gly Cys Thr Val Ser Ser Asp Ser Leu Asn Phe Thr
      35      40      45
Val Asp Leu Gln Lys Asn Ser Ala Arg Gln Phe Pro Thr Thr Gly Ser
      50      55      60
Thr Ser Pro Ala Val Pro Phe Gln Ile Thr Leu Ser Glu Cys Ser Lys
65      70      75      80
Gly Thr Thr Gly Val Arg Val Ala Phe Asn Gly Ile Glu Asp Ala Glu
      85      90      95
Asn Asn Thr Leu Leu Lys Leu Asp Glu Gly Ser Asn Thr Ala Ser Gly
      100     105     110
Leu Gly Ile Glu Ile Leu Asp Ala Asn Met Arg Pro Val Lys Leu Asn
      115     120     125
Asp Leu His Ala Gly Met Gln Trp Ile Pro Leu Val Pro Glu Gln Asn
      130     135     140
Asn Ile Leu Pro Tyr Ser Ala Arg Leu Lys Ser Thr Gln Lys Ser Val
145     150     155     160
Asn Pro Gly Leu Val Arg Ala Ser Ala Thr Phe Thr Leu Glu Phe Gln
      165     170     175

```

<210> 299
 <211> 382
 <212> PRT
 <213> E. Coli

```

<400> 299
Met Ser Gly Tyr Thr Val Lys Pro Pro Thr Gly Asp Thr Asn Glu Gln
1      5      10      15
Thr Gln Phe Ile Asp Tyr Phe Asn Leu Phe Tyr Ser Lys Arg Gly Gln
      20      25      30
Glu Gln Ile Ser Ile Ser Gln Gln Leu Gly Asn Tyr Gly Thr Thr Phe
      35      40      45
Phe Ser Ala Ser Arg Gln Ser Tyr Trp Asn Thr Ser Arg Ser Asp Gln
50      55      60

```

Gln Ile Ser Phe Gly Leu Asn Val Pro Phe Gly Asp Ile Thr Thr Ser
 65 70 75 80
 Leu Asn Tyr Ser Tyr Ser Asn Asn Ile Trp Gln Asn Asp Arg Asp His
 85 90 95
 Leu Leu Ala Phe Thr Leu Asn Val Pro Phe Ser His Trp Met Arg Thr
 100 105 110
 Asp Ser Gln Ser Ala Phe Arg Asn Ser Asn Ala Ser Tyr Ser Met Ser
 115 120 125
 Asn Asp Leu Lys Gly Gly Met Thr Asn Leu Ser Gly Val Tyr Gly Thr
 130 135 140
 Leu Leu Pro Asp Asn Asn Leu Asn Tyr Ser Val Gln Val Gly Asn Thr
 145 150 155 160
 His Gly Gly Asn Thr Ser Ser Gly Thr Ser Gly Tyr Ser Ser Leu Asn
 165 170 175
 Tyr Arg Gly Ala Tyr Gly Asn Thr Asn Val Gly Tyr Ser Arg Ser Gly
 180 185 190
 Asp Ser Ser Gln Ile Tyr Tyr Gly Met Ser Gly Gly Ile Ile Ala His
 195 200 205
 Ala Asp Gly Ile Thr Phe Gly Gln Pro Leu Gly Asp Thr Met Val Leu
 210 215 220
 Val Lys Ala Pro Gly Ala Asp Asn Val Lys Ile Glu Asn Gln Thr Gly
 225 230 235 240
 Ile His Thr Asp Trp Arg Gly Tyr Ala Ile Leu Pro Phe Ala Thr Glu
 245 250 255
 Tyr Arg Glu Asn Arg Val Ala Leu Asn Ala Asn Ser Leu Ala Asp Asn
 260 265 270
 Val Glu Leu Asp Glu Thr Val Val Thr Val Ile Pro Thr His Gly Ala
 275 280 285
 Ile Ala Arg Ala Thr Phe Asn Ala Gln Ile Gly Gly Lys Val Leu Met
 290 295 300
 Thr Leu Lys Tyr Gly Asn Lys Ser Val Pro Phe Gly Ala Ile Val Thr
 305 310 315 320
 His Gly Glu Asn Lys Asn Gly Ser Ile Val Ala Glu Asn Gly Gln Val
 325 330 335
 Tyr Leu Thr Gly Leu Pro Gln Ser Gly Gln Leu Gln Val Ser Trp Gly
 340 345 350
 Lys Asp Lys Asn Ser Asn Cys Ile Val Glu Tyr Lys Leu Pro Glu Val
 355 360 365
 Ser Pro Gly Thr Leu Leu Asn Gln Gln Thr Ala Ile Cys Arg
 370 375 380

<210> 300

<211> 138

<212> PRT

<213> E. Coli

<400> 300

Met Ile Ala Ile Ala Asp Ile Leu Gln Ala Gly Glu Lys Leu Thr Ala
 1 5 10 15
 Val Ala Pro Phe Leu Ala Gly Ile Gln Asn Glu Glu Gln Tyr Thr Gln
 20 25 30
 Ala Leu Glu Leu Val Asp His Leu Leu Asn Asp Pro Glu Asn Pro
 35 40 45
 Leu Leu Asp Leu Val Cys Ala Lys Ile Thr Ala Trp Glu Glu Ser Ala
 50 55 60
 Pro Glu Phe Ala Glu Phe Asn Ala Met Ala Gln Ala Met Pro Gly Gly
 65 70 75 80
 Ile Ala Val Ile Arg Thr Leu Met Asp Gln Tyr Gly Leu Thr Leu Ser
 85 90 95
 Asp Leu Pro Glu Ile Gly Ser Lys Ser Met Val Ser Arg Val Leu Ser

100 105 110
 Gly Lys Arg Lys Leu Thr Leu Glu His Ala Lys Lys Leu Ala Thr Arg
 115 120 125
 Phe Gly Ile Ser Pro Ala Leu Phe Ile Asp
 130 135

<210> 301
 <211> 104
 <212> PRT
 <213> E. Coli

<400> 301
 Met His Leu Ile Thr Gln Lys Ala Leu Lys Asp Ala Ala Glu Lys Tyr
 1 5 10 15
 Pro Gln His Lys Thr Glu Leu Val Ala Leu Gly Asn Thr Ile Ala Lys
 20 25 30
 Gly Tyr Phe Lys Lys Pro Glu Ser Leu Lys Ala Val Phe Pro Ser Leu
 35 40 45
 Asp Asn Phe Lys Tyr Leu Asp Lys His Tyr Val Phe Asn Val Gly Gly
 50 55 60
 Asn Glu Leu Arg Val Val Ala Met Val Phe Phe Glu Ser Gln Lys Cys
 65 70 75 80
 Tyr Ile Arg Glu Val Met Thr His Lys Glu Tyr Asp Phe Phe Thr Ala
 85 90 95
 Val His Arg Thr Lys Gly Lys Lys
 100

<210> 302
 <211> 2383
 <212> PRT
 <213> E. Coli

<400> 302
 Met Leu Ser Val Phe Thr Phe Phe Arg Cys Ala Arg Lys Gly Ala Phe
 1 5 10 15
 Met Leu Ala Arg Ser Gly Lys Val Ser Met Ala Thr Lys Lys Arg Ser
 20 25 30
 Gly Glu Glu Ile Asn Asp Arg Gln Ile Leu Cys Gly Met Gly Ile Lys
 35 40 45
 Leu Arg Arg Leu Thr Ala Gly Ile Cys Leu Ile Thr Gln Leu Ala Phe
 50 55 60
 Pro Met Ala Ala Ala Ala Gln Gly Val Val Asn Ala Ala Thr Gln Gln
 65 70 75 80
 Pro Val Pro Ala Gln Ile Ala Ile Ala Asn Ala Asn Thr Val Pro Tyr
 85 90 95
 Thr Leu Gly Ala Leu Glu Ser Ala Gln Ser Val Ala Glu Arg Phe Gly
 100 105 110
 Ile Ser Val Ala Glu Leu Arg Lys Leu Asn Gln Phe Arg Thr Phe Ala
 115 120 125
 Arg Ser Phe Asp Asn Val Arg Gln Gly Asp Glu Leu Asp Val Pro Ala
 130 135 140
 Gln Val Ser Glu Lys Lys Leu Thr Pro Pro Pro Gly Asn Ser Ser Asp
 145 150 155 160
 Asn Leu Glu Gln Gln Ile Ala Ser Thr Ser Gln Gln Ile Gly Ser Leu
 165 170 175
 Leu Ala Glu Asp Met Asn Ser Glu Gln Ala Ala Asn Met Ala Arg Gly
 180 185 190
 Trp Ala Ser Ser Gln Ala Ser Gly Ala Met Thr Asp Trp Leu Ser Arg

195	200	205
Phe Gly Thr Ala Arg Ile Thr	Leu Gly Val Asp Glu Asp Phe Ser Leu	
210	215	220
Lys Asn Ser Gln Phe Asp Phe	Leu His Pro Trp Tyr Glu Thr Pro Asp	
225	230	235
Asn Leu Phe Phe Ser Gln His Thr	Leu His Arg Thr Asp Glu Arg Thr	
245	250	255
Gln Ile Asn Asn Gly Leu Gly Trp	Arg His Phe Thr Pro Thr Trp Met	
260	265	270
Ser Gly Ile Asn Phe Phe Phe	Asp His Asp Leu Ser Arg Tyr His Ser	
275	280	285
Arg Ala Gly Ile Gly Ala Glu	Tyr Trp Arg Asp Tyr Leu Lys Leu Ser	
290	295	300
Ser Asn Gly Tyr Leu Arg Leu Thr	Asn Trp Arg Ser Ala Pro Glu Leu	
305	310	315
Asp Asn Asp Tyr Glu Ala Arg Pro	Ala Asn Gly Trp Asp Val Arg Ala	
325	330	335
Glu Ser Trp Leu Pro Ala Trp Pro	His Leu Gly Gly Lys Leu Val Tyr	
340	345	350
Glu Gln Tyr Tyr Gly Asp Glu Val	Ala Leu Phe Asp Lys Asp Asp Arg	
355	360	365
Gln Ser Asn Pro His Ala Ile Thr	Ala Gly Leu Asn Tyr Thr Pro Phe	
370	375	380
Pro Leu Met Thr Phe Ser Ala Glu	Gln Arg Gln Gly Lys Gln Gly Glu	
385	390	395
Asn Asp Thr Arg Phe Ala Val Asp	Phe Thr Trp Gln Pro Gly Ser Ala	
405	410	415
Met Gln Lys Gln Leu Asp Pro Asn	Glu Val Ala Ala Arg Arg Ser Leu	
420	425	430
Ala Gly Ser Arg Tyr Asp Leu Val	Asp Arg Asn Asn Asn Ile Val Leu	
435	440	445
Glu Tyr Arg Lys Lys Glu Leu Val	Arg Leu Thr Leu Thr Asp Pro Val	
450	455	460
Thr Gly Lys Ser Gly Glu Val Lys	Ser Leu Val Ser Ser Leu Gln Thr	
465	470	475
Lys Tyr Ala Leu Lys Gly Tyr Asn	Val Glu Ala Thr Ala Leu Glu Ala	
485	490	495
Ala Gly Gly Lys Val Val Thr Thr	Gly Lys Asp Ile Leu Val Thr Leu	
500	505	510
Pro Ala Tyr Arg Phe Thr Ser Thr	Pro Glu Thr Asp Asn Thr Trp Pro	
515	520	525
Ile Glu Val Thr Ala Glu Asp Val	Lys Gly Asn Leu Ser Asn Arg Glu	
530	535	540
Gln Ser Met Val Val Val Gln Ala	Pro Thr Leu Ser Gln Lys Asp Ser	
545	550	555
Ser Val Ser Leu Ser Thr Gln Thr	Leu Asn Ala Asp Ser His Ser Thr	
565	570	575
Ala Thr Leu Thr Phe Ile Ala His	Asp Ala Ala Gly Asn Pro Val Val	
580	585	590
Gly Leu Val Leu Ser Thr Arg His	Glu Gly Val Gln Asp Ile Thr Leu	
595	600	605
Ser Asp Trp Lys Asp Asn Gly Asp	Gly Ser Tyr Thr Gln Ile Leu Thr	
610	615	620
Thr Gly Ala Met Ser Gly Thr Leu	Thr Leu Met Pro Gln Leu Asn Gly	
625	630	635
Val Asp Ala Ala Lys Ala Pro Ala	Val Val Asn Ile Ile Ser Val Ser	
645	650	655
Ser Ser Arg Thr His Ser Ser Ile	Lys Ile Asp Lys Asp Arg Tyr Leu	
660	665	670
Ser Gly Asn Pro Ile Glu Val Thr	Val Glu Leu Arg Asp Glu Asn Asp	
675	680	685

Lys Pro Val Lys Glu Gln Lys Gln Gln Leu Asn Asn Ala Val Ser Ile
 690 695 700
 Asp Asn Val Lys Pro Gly Val Thr Thr Asp Trp Lys Glu Thr Ala Asp
 705 710 715 720
 Gly Val Tyr Lys Ala Thr Tyr Thr Ala Tyr Thr Lys Gly Ser Gly Leu
 725 730 735
 Thr Ala Lys Leu Leu Met Gln Asn Trp Asn Glu Asp Leu His Thr Ala
 740 745 750
 Gly Phe Ile Ile Asp Ala Asn Pro Gln Ser Ala Lys Ile Ala Thr Leu
 755 760 765
 Ser Ala Ser Asn Asn Gly Val Leu Ala Asn Glu Asn Ala Ala Asn Thr
 770 775 780
 Val Ser Val Asn Val Ala Asp Glu Gly Ser Asn Pro Ile Asn Asp His
 785 790 795 800
 Thr Val Thr Phe Ala Val Leu Ser Gly Ser Ala Thr Ser Phe Asn Asn
 805 810 815
 Gln Asn Thr Ala Lys Thr Asp Val Asn Gly Leu Ala Thr Phe Asp Leu
 820 825 830
 Lys Ser Ser Lys Gln Glu Asp Asn Thr Val Glu Val Thr Leu Glu Asn
 835 840 845
 Gly Val Lys Gln Thr Leu Ile Val Ser Phe Val Gly Asp Ser Ser Thr
 850 855 860
 Ala Gln Val Asp Leu Gln Lys Ser Lys Asn Glu Val Val Ala Asp Gly
 865 870 875 880
 Asn Asp Ser Val Thr Met Thr Ala Thr Val Arg Asp Ala Lys Gly Asn
 885 890 895
 Leu Leu Asn Asp Val Met Val Thr Phe Asn Val Asn Ser Ala Glu Ala
 900 905 910
 Lys Leu Ser Gln Thr Glu Val Asn Ser His Asp Gly Ile Ala Thr Ala
 915 920 925
 Thr Leu Thr Ser Leu Lys Asn Gly Asp Tyr Arg Val Thr Ala Ser Val
 930 935 940
 Ser Ser Gly Ser Gln Ala Asn Gln Gln Val Asn Phe Ile Gly Asp Gln
 945 950 955 960
 Ser Thr Ala Ala Leu Thr Leu Ser Val Pro Ser Gly Asp Ile Thr Val
 965 970 975
 Thr Asn Thr Ala Pro Gln Tyr Met Thr Ala Thr Leu Gln Asp Lys Asn
 980 985 990
 Gly Asn Pro Leu Lys Asp Lys Glu Ile Thr Phe Ser Val Pro Asn Asp
 995 1000 1005
 Val Ala Ser Lys Phe Ser Ile Ser Asn Gly Gly Lys Gly Met Thr Asp
 1010 1015 1020
 Ser Asn Gly Val Ala Ile Ala Ser Leu Thr Gly Thr Leu Ala Gly Thr
 1025 1030 1035 1040
 His Met Ile Met Ala Arg Leu Ala Asn Ser Asn Val Ser Asp Ala Gln
 1045 1050 1055
 Pro Met Thr Phe Val Ala Asp Lys Asp Arg Ala Val Val Val Leu Gln
 1060 1065 1070
 Thr Ser Lys Ala Glu Ile Ile Gly Asn Gly Val Asp Glu Thr Thr Leu
 1075 1080 1085
 Thr Ala Thr Val Lys Asp Pro Ser Asn His Pro Val Ala Gly Ile Thr
 1090 1095 1100
 Val Asn Phe Thr Met Pro Gln Asp Val Ala Ala Asn Phe Thr Leu Glu
 1105 1110 1115 1120
 Asn Asn Gly Ile Ala Ile Thr Gln Ala Asn Gly Glu Ala His Val Thr
 1125 1130 1135
 Leu Lys Gly Lys Lys Ala Gly Thr His Thr Val Thr Ala Thr Leu Gly
 1140 1145 1150
 Asn Asn Asn Thr Ser Asp Ser Gln Pro Val Thr Phe Val Ala Asp Lys
 1155 1160 1165
 Ala Ser Ala Gln Val Val Leu Gln Ile Ser Lys Asp Glu Ile Thr Gly

1170	1175	1180
Asn Gly Val Asp Ser Ala Thr Leu Thr Ala Thr Val Lys Asp Gln Phe		
1185	1190	1195
Asp Asn Glu Val Asn Asn Leu Pro Val Thr Phe Ser Ser Ala Ser Ser		1200
	1205	1210
Gly Leu Thr Leu Thr Pro Gly Val Ser Asn Thr Asn Glu Ser Gly Ile		1215
	1220	1225
Ala Gln Ala Thr Leu Ala Gly Val Ala Phe Gly Glu Lys Thr Val Thr		1230
	1235	1240
Ala Ser Leu Ala Asn Asn Gly Ala Ser Asp Asn Lys Thr Val His Phe		1245
	1250	1255
Ile Gly Asp Thr Ala Ala Lys Ile Ile Glu Leu Ala Pro Val Pro		1260
	1265	1270
Asp Ser Ile Ile Ala Gly Thr Pro Gln Asn Ser Ser Gly Ser Val Ile		1275
	1285	1290
Thr Ala Thr Val Val Asp Asn Asn Gly Phe Pro Val Lys Gly Val Thr		1295
	1300	1305
Val Asn Phe Thr Ser Asn Ala Ala Thr Ala Glu Met Thr Asn Gly Gly		1310
	1315	1320
Gln Ala Val Thr Asn Glu Gln Gly Lys Ala Thr Val Thr Tyr Thr Asn		1325
	1330	1335
Thr Arg Ser Ser Ile Glu Ser Gly Ala Arg Pro Asp Thr Val Glu Ala		1340
	1345	1350
Ser Leu Glu Asn Gly Ser Ser Thr Leu Ser Thr Ser Ile Asn Val Asn		1355
	1365	1370
Ala Asp Ala Ser Thr Ala His Leu Thr Leu Leu Gln Ala Leu Phe Asp		1375
	1380	1385
Thr Val Ser Ala Gly Glu Thr Thr Ser Leu Tyr Ile Glu Val Lys Asp		1390
	1395	1400
Asn Tyr Gly Asn Gly Val Pro Gln Gln Glu Val Thr Leu Ser Val Ser		1405
	1410	1415
Pro Ser Glu Gly Val Thr Pro Ser Asn Asn Ala Ile Tyr Thr Thr Asn		1420
	1425	1430
His Asp Gly Asn Phe Tyr Ala Ser Phe Thr Ala Thr Lys Ala Gly Val		1435
	1445	1450
Tyr Gln Leu Thr Ala Thr Leu Glu Asn Gly Asp Ser Met Gln Gln Thr		1455
	1460	1465
Val Thr Tyr Val Pro Asn Val Ala Asn Ala Glu Ile Thr Leu Ala Ala		1470
	1475	1480
Ser Lys Asp Pro Val Ile Ala Asp Asn Asn Asp Leu Thr Thr Leu Thr		1485
	1490	1495
Ala Thr Val Ala Asp Thr Glu Gly Asn Ala Ile Ala Asn Thr Glu Val		1500
	1505	1510
Thr Phe Thr Leu Pro Glu Asp Val Lys Ala Asn Phe Thr Leu Ser Asp		1515
	1525	1530
Gly Gly Lys Val Ile Thr Asp Ala Glu Gly Lys Ala Lys Val Thr Leu		1535
	1540	1545
Lys Gly Thr Lys Ala Gly Ala His Thr Val Thr Ala Ser Met Thr Gly		1550
	1555	1560
Gly Lys Ser Glu Gln Leu Val Val Asn Phe Ile Ala Asp Thr Leu Thr		1565
	1570	1575
Ala Gln Val Asn Leu Asn Val Thr Glu Asp Asn Phe Ile Ala Asn Asn		1580
	1585	1590
Val Gly Met Thr Arg Leu Gln Ala Thr Val Thr Asp Gly Asn Gly Asn		1595
	1605	1610
Pro Leu Ala Asn Glu Ala Val Thr Phe Thr Leu Pro Ala Asp Val Ser		1615
	1620	1625
Ala Ser Phe Thr Leu Gly Gln Gly Gly Ser Ala Ile Thr Asp Ile Asn		1630
	1635	1640
Gly Lys Ala Glu Val Thr Leu Ser Gly Thr Lys Ser Gly Thr Tyr Pro		1645
	1650	1655
		1660

Val Thr Val Ser Val Asn Asn Tyr Gly Val Ser Asp Thr Lys Gln Val
 1665 1670 1675 1680
 Thr Leu Ile Ala Asp Ala Gly Thr Ala Lys Leu Ala Ser Leu Thr Ser
 1685 1690 1695
 Val Tyr Ser Phe Val Val Ser Thr Thr Glu Gly Ala Thr Met Thr Ala
 1700 1705 1710
 Ser Val Thr Asp Ala Asn Gly Asn Pro Val Glu Gly Ile Lys Val Asn
 1715 1720 1725
 Phe Arg Gly Thr Ser Val Thr Leu Ser Ser Thr Ser Val Glu Thr Asp
 1730 1735 1740
 Asp Arg Gly Phe Ala Glu Ile Leu Val Thr Ser Thr Glu Val Gly Leu
 1745 1750 1755 1760
 Lys Thr Val Ser Ala Ser Leu Ala Asp Lys Pro Thr Glu Val Ile Ser
 1765 1770 1775
 Arg Leu Leu Asn Ala Ser Ala Asp Val Asn Ser Ala Thr Ile Thr Ser
 1780 1785 1790
 Leu Glu Ile Pro Glu Gly Gln Val Met Val Ala Gln Asp Val Ala Val
 1795 1800 1805
 Lys Ala His Val Asn Asp Gln Phe Gly Asn Pro Val Ala His Gln Pro
 1810 1815 1820
 Val Thr Phe Ser Ala Glu Pro Ser Ser Gln Met Ile Ile Ser Gln Asn
 1825 1830 1835 1840
 Thr Val Ser Thr Asn Thr Gln Gly Val Ala Glu Val Thr Met Thr Pro
 1845 1850 1855
 Glu Arg Asn Gly Ser Tyr Met Val Lys Ala Ser Leu Pro Asn Gly Ala
 1860 1865 1870
 Ser Leu Glu Lys Gln Leu Glu Ala Ile Asp Glu Lys Leu Thr Leu Thr
 1875 1880 1885
 Ala Ser Ser Pro Leu Ile Gly Val Tyr Ala Pro Thr Gly Ala Thr Leu
 1890 1895 1900
 Thr Ala Thr Leu Thr Ser Ala Asn Gly Thr Pro Val Glu Gly Gln Val
 1905 1910 1915 1920
 Ile Asn Phe Ser Val Thr Pro Glu Gly Ala Thr Leu Ser Gly Gly Lys
 1925 1930 1935
 Val Arg Thr Asn Ser Ser Gly Gln Ala Pro Val Val Leu Thr Ser Asn
 1940 1945 1950
 Lys Val Gly Thr Tyr Thr Val Thr Ala Ser Phe His Asn Gly Val Thr
 1955 1960 1965
 Ile Gln Thr Gln Thr Thr Val Lys Val Thr Gly Asn Ser Ser Thr Ala
 1970 1975 1980
 His Val Ala Ser Phe Ile Ala Asp Pro Ser Thr Ile Ala Ala Thr Asn
 1985 1990 1995 2000
 Thr Asp Leu Ser Thr Leu Lys Ala Thr Val Glu Asp Gly Ser Gly Asn
 2005 2010 2015
 Leu Ile Glu Gly Leu Thr Val Tyr Phe Ala Leu Lys Ser Gly Ser Ala
 2020 2025 2030
 Thr Leu Thr Ser Leu Thr Ala Val Thr Asp Gln Asn Gly Ile Ala Thr
 2035 2040 2045
 Thr Ser Val Lys Gly Ala Met Thr Gly Ser Val Thr Val Ser Ala Val
 2050 2055 2060
 Thr Thr Ala Gly Gly Met Gln Thr Val Asp Ile Thr Leu Val Ala Gly
 2065 2070 2075 2080
 Pro Ala Asp Thr Ser Gln Ser Val Leu Lys Ser Asn Arg Ser Ser Leu
 2085 2090 2095
 Lys Gly Asp Tyr Thr Asp Ser Ala Glu Leu Arg Leu Val Leu His Asp
 2100 2105 2110
 Ile Ser Gly Asn Pro Ile Lys Val Ser Glu Gly Met Glu Phe Val Gln
 2115 2120 2125
 Ser Gly Thr Asn Val Pro Tyr Ile Lys Ile Ser Ala Ile Asp Tyr Ser
 2130 2135 2140
 Leu Asn Ile Asn Gly Asp Tyr Lys Ala Thr Val Thr Gly Gly Gly Glu

2145 2150 2155 2160
 Gly Ile Ala Thr Leu Ile Pro Val Leu Asn Gly Val His Gln Ala Gly
 2165 2170 2175
 Leu Ser Thr Thr Ile Gln Phe Thr Arg Ala Glu Asp Lys Ile Met Ser
 2180 2185 2190
 Gly Thr Val Ser Val Asn Gly Thr Asp Leu Pro Thr Thr Thr Phe Pro
 2195 2200 2205
 Ser Gln Gly Phe Thr Gly Ala Tyr Tyr Gln Leu Asn Asn Asp Asn Phe
 2210 2215 2220
 Ala Pro Gly Lys Thr Ala Ala Asp Tyr Glu Phe Ser Ser Ser Ala Ser
 2225 2230 2235 2240
 Trp Val Asp Val Asp Ala Thr Gly Lys Val Thr Phe Lys Asn Val Gly
 2245 2250 2255
 Ser Asn Ser Glu Arg Ile Thr Ala Thr Pro Lys Ser Gly Gly Pro Ser
 2260 2265 2270
 Tyr Val Tyr Glu Ile Arg Val Lys Ser Trp Trp Val Asn Ala Gly Glu
 2275 2280 2285
 Ala Phe Met Ile Tyr Ser Leu Ala Glu Asn Phe Cys Ser Ser Asn Gly
 2290 2295 2300
 Tyr Thr Leu Pro Arg Ala Asn Tyr Leu Asn His Cys Ser Ser Arg Gly
 2305 2310 2315 2320
 Ile Gly Ser Leu Tyr Ser Glu Trp Gly Asp Met Gly His Tyr Thr Thr
 2325 2330 2335
 Asp Ala Gly Phe Gln Ser Asn Met Tyr Trp Ser Ser Ser Pro Ala Asn
 2340 2345 2350
 Ser Ser Glu Gln Tyr Val Val Ser Leu Ala Thr Gly Asp Gln Ser Val
 2355 2360 2365
 Phe Glu Lys Leu Gly Phe Ala Tyr Ala Thr Cys Tyr Lys Asn Leu
 2370 2375 2380

<210> 303
 <211> 61
 <212> PRT
 <213> E. Coli

<400> 303
 Met Ser Lys Gly Ala Leu Tyr Glu Phe Asn Asn Pro Asp Gln Leu Lys
 1 5 10 15
 Ile Pro Leu Pro His Lys His Ile Ala Ser Thr Phe Asn Asp Ile Met
 20 25 30
 Ser Lys Asp Val Gly Tyr Ala Tyr Val Ser Leu Leu Tyr Ala Cys Pro
 35 40 45
 Leu Lys Thr His Ser Leu Arg Leu Asn Pro Phe Ser Lys
 50 55 60

<210> 304
 <211> 398
 <212> PRT
 <213> E. Coli

<400> 304
 Met Gln Val Ala Glu Gln Arg Ile Gln Leu Ala Glu Ala Gln Ala Lys
 1 5 10 15
 Ala Val Ala Thr Gln Asp Gly Pro Gln Ile Asp Phe Ser Ala Asp Met
 20 25 30
 Glu Arg Gln Lys Met Ser Ala Glu Gly Leu Met Gly Pro Phe Ala Leu
 35 40 45
 Asn Asp Pro Ala Ala Gly Thr Thr Gly Pro Trp Tyr Thr Asn Gly Thr
 50 55 60

Phe Gly Leu Thr Ala Gly Trp His Leu Asp Ile Trp Gly Lys Asn Arg
 65 70 75 80
 Ala Glu Val Thr Ala Arg Leu Gly Thr Val Lys Ala Arg Ala Ala Glu
 85 90 95
 Arg Glu Gln Thr Arg Gln Leu Leu Ala Gly Ser Val Ala Arg Leu Tyr
 100 105 110
 Trp Glu Trp Gln Thr Gln Ala Ala Leu Asn Thr Val Leu Gln Gln Ile
 115 120 125
 Glu Lys Glu Gln Asn Thr Ile Ile Ala Thr Asp Arg Gln Leu Tyr Gln
 130 135 140
 Asn Gly Ile Thr Ser Ser Val Glu Gly Val Glu Thr Asp Ile Asn Ala
 145 150 155 160
 Ser Lys Thr Arg Gln Gln Leu Asn Asp Val Ala Gly Lys Met Lys Ile
 165 170 175
 Ile Glu Ala Arg Leu Ser Ala Leu Thr Asn Asn Gln Thr Lys Ser Leu
 180 185 190
 Lys Leu Lys Pro Val Ala Leu Pro Lys Val Ala Ser Gln Leu Pro Asp
 195 200 205
 Glu Leu Gly Tyr Ser Leu Leu Ala Arg Arg Ala Asp Leu Gln Ala Ala
 210 215 220
 His Trp Tyr Val Glu Ser Ser Leu Ser Thr Ile Asp Ala Ala Lys Ala
 225 230 235 240
 Ala Phe Tyr Pro Asp Ile Asn Leu Met Ala Phe Leu Gln Gln Asp Ala
 245 250 255
 Leu His Leu Ser Asp Leu Phe Arg His Ser Ala Gln Gln Met Gly Val
 260 265 270
 Thr Ala Gly Leu Thr Leu Pro Ile Phe Asp Ser Gly Arg Leu Asn Ala
 275 280 285
 Asn Leu Asp Ile Ala Lys Ala Glu Ser Asn Leu Ser Ile Ala Ser Tyr
 290 295 300
 Asn Lys Ala Val Val Glu Ala Val Asn Asp Val Ala Arg Ala Ala Ser
 305 310 315 320
 Gln Val Gln Thr Leu Ala Glu Lys Asn Gln His Gln Ala Gln Ile Glu
 325 330 335
 Arg Asp Ala Leu Arg Val Val Gly Leu Ala Gln Ala Arg Phe Asn Ala
 340 345 350
 Gly Ile Ile Ala Gly Ser Arg Val Ser Glu Ala Arg Ile Pro Ala Leu
 355 360 365
 Arg Glu Arg Ala Asn Gly Leu Leu Leu Gln Gly Gln Trp Leu Asp Ala
 370 375 380
 Ser Ile Gln Leu Thr Gly Ala Leu Gly Gly Gly Tyr Lys Arg
 385 390 395

<210> 305
 <211> 96
 <212> PRT
 <213> E. Coli

<400> 305
 Met Tyr Cys His Ala Lys Leu Lys Asn Ile Ser Gln His Thr Val Ile
 1 5 10 15
 Ser Ala His Leu Phe Leu Pro Asp Tyr Ser Pro Met Asn Arg Asp Ser
 20 25 30
 Phe Tyr Pro Ala Ile Ala Cys Phe Pro Leu Leu Leu Met Leu Ala Gly
 35 40 45
 Cys Ala Pro Met His Glu Thr Arg Gln Ala Leu Ser Gln Gln Thr Pro
 50 55 60
 Ala Ala Gln Val Asp Thr Ala Leu Pro Thr Ala Leu Lys Met Val Gly
 65 70 75 80
 Gln Thr Ala Asn Gly Gly Trp Ser Ile Thr Ile Ile Asn Ser Leu Pro

85

90

95

<210> 306
 <211> 315
 <212> PRT
 <213> E. Coli

<400> 306

```

Met Arg Val Leu Leu Ala Pro Met Glu Gly Val Leu Asp Ser Leu Val
 1      5      10      15
Arg Glu Leu Leu Thr Glu Val Asn Asp Tyr Asp Leu Cys Ile Thr Glu
 20      25      30
Phe Val Arg Val Val Asp Gln Leu Pro Val Lys Val Phe His Arg
 35      40      45
Ile Cys Pro Glu Leu Gln Asn Ala Ser Arg Thr Pro Ser Gly Thr Leu
 50      55      60
Val Arg Val Gln Leu Leu Gly Gln Phe Pro Gln Trp Leu Ala Glu Asn
 65      70      75      80
Ala Ala Arg Ala Val Glu Leu Gly Ser Trp Gly Val Asp Leu Asn Cys
 85      90      95
Gly Cys Pro Ser Lys Thr Val Asn Gly Ser Gly Gly Gly Ala Thr Leu
100      105      110
Leu Lys Asp Pro Glu Leu Ile Tyr Gln Gly Ala Lys Ala Met Arg Glu
115      120      125
Ala Val Pro Ala His Leu Pro Val Ser Val Lys Val Arg Leu Gly Trp
130      135      140
Asp Ser Gly Glu Lys Lys Phe Glu Ile Ala Asp Ala Val Gln Gln Ala
145      150      155      160
Gly Ala Thr Glu Leu Val Val His Gly Arg Thr Lys Glu Gln Gly Tyr
165      170      175
Arg Ala Glu His Ile Asp Trp Gln Ala Ile Gly Asp Ile Arg Gln Arg
180      185      190
Leu Asn Ile Pro Val Ile Ala Asn Gly Glu Ile Trp Asp Trp Gln Ser
195      200      205
Ala Gln Gln Cys Met Ala Ile Ser Gly Cys Asp Ala Val Met Ile Gly
210      215      220
Arg Gly Ala Leu Asn Ile Pro Asn Leu Ser Arg Val Val Lys Tyr Asn
225      230      235      240
Glu Pro Arg Met Pro Trp Pro Glu Val Val Ala Leu Leu Gln Lys Tyr
245      250      255
Thr Arg Leu Glu Lys Gln Gly Asp Thr Gly Leu Tyr His Val Ala Arg
260      265      270
Ile Lys Gln Trp Leu Ser Tyr Leu Arg Lys Glu Tyr Asp Glu Ala Thr
275      280      285
Glu Leu Phe Gln His Val Arg Val Leu Asn Asn Ser Pro Asp Ile Ala
290      295      300
Arg Ala Ile Gln Ala Ile Asp Ile Glu Lys Leu
305      310      315

```

<210> 307
 <211> 296
 <212> PRT
 <213> E. Coli

<400> 307

```

Met Thr Ile Ser Thr Thr Ser Thr Pro His Asp Ala Val Phe Lys Ser
 1      5      10      15
Phe Leu Arg His Pro Asp Thr Ala Arg Asp Phe Ile Asp Ile His Leu
 20      25      30

```

Pro Ala Pro Leu Arg Lys Leu Cys Asp Leu Thr Thr Leu Lys Leu Glu
 35 40 45
 Pro Asn Ser Phe Ile Asp Glu Asp Leu Arg Gln Tyr Tyr Ser Asp Leu
 50 55 60
 Leu Trp Ser Val Lys Thr Gln Glu Gly Val Gly Tyr Ile Tyr Val Val
 65 70 75 80
 Ile Glu His Gln Ser Lys Pro Glu Glu Leu Met Ala Phe Arg Met Met
 85 90 95
 Arg Tyr Ser Ile Ala Ala Met Gln Asn His Leu Asp Ala Gly Tyr Lys
 100 105 110
 Glu Leu Pro Leu Val Leu Pro Met Leu Phe Tyr His Gly Cys Arg Ser
 115 120 125
 Pro Tyr Pro Tyr Ser Leu Cys Trp Leu Asp Glu Phe Ala Glu Pro Ala
 130 135 140
 Ile Ala Arg Lys Ile Tyr Ser Ser Ala Phe Pro Leu Val Asp Ile Thr
 145 150 155 160
 Val Val Pro Asp Asp Glu Ile Met Gln His Arg Lys Met Ala Leu Leu
 165 170 175
 Glu Leu Ile Gln Lys His Ile Arg Gln Arg Asp Leu Leu Gly Leu Val
 180 185 190
 Asp Gln Ile Val Ser Leu Leu Val Thr Gly Asn Thr Asn Asp Arg Gln
 195 200 205
 Leu Lys Ala Leu Phe Asn Tyr Val Leu Gln Thr Gly Asp Ala Gln Arg
 210 215 220
 Phe Arg Ala Phe Ile Gly Glu Ile Ala Glu Arg Ala Pro Gln Glu Lys
 225 230 235 240
 Glu Lys Leu Met Thr Ile Ala Asp Arg Leu Arg Glu Glu Gly Ala Met
 245 250 255
 Gln Gly Lys His Glu Glu Ala Leu Arg Ile Ala Gln Glu Met Leu Asp
 260 265 270
 Arg Gly Leu Asp Arg Glu Leu Val Met Met Val Thr Arg Leu Ser Pro
 275 280 285
 Asp Asp Leu Ile Ala Gln Ser His
 290 295

<210> 308
 <211> 555
 <212> PRT
 <213> E. Coli

<400> 308

<400> 3
 Met Ala Gln Phe Val Tyr Thr Met His Arg Val Gly Lys Val Val Pro
 1 5 10 15
 Pro Lys Arg His Ile Leu Lys Asn Ile Ser Leu Ser Phe Phe Pro Gly
 20 25 30
 Ala Lys Ile Gly Val Leu Gly Leu Asn Gly Ala Gly Lys Ser Thr Leu
 35 40 45
 Leu Arg Ile Met Ala Gly Ile Asp Lys Asp Ile Glu Gly Glu Ala Arg
 50 55 60
 Pro Gln Pro Asp Ile Lys Ile Gly Tyr Leu Pro Gln Glu Pro Gln Leu
 65 70 75 80
 Asn Pro Glu His Thr Val Arg Glu Ser Ile Glu Glu Ala Val Ser Glu
 85 90 95
 Val Val Asn Ala Leu Lys Arg Leu Asp Glu Val Tyr Ala Leu Tyr Ala
 100 105 110
 Asp Pro Asp Ala Asp Phe Asp Lys Leu Ala Ala Glu Gln Gly Arg Leu
 115 120 125
 Glu Glu Ile Ile Gln Ala His Asp Gly His Asn Leu Asn Val Gln Leu
 130 135 140

Glu Arg Ala Ala Asp Ala Leu Arg Leu Pro Asp Trp Asp Ala Lys Ile
 145 150 155 160
 Ala Asn Leu Ser Gly Gly Glu Arg Arg Arg Val Ala Leu Cys Arg Leu
 165 170 175
 Leu Leu Glu Lys Pro Asp Met Leu Leu Leu Asp Glu Pro Thr Asn His
 180 185 190
 Leu Asp Ala Glu Ser Val Ala Trp Leu Glu Arg Phe Leu His Asp Phe
 195 200 205
 Glu Gly Thr Val Val Ala Ile Thr His Asp Arg Tyr Phe Leu Asp Asn
 210 215 220
 Val Ala Gly Trp Ile Leu Glu Leu Asp Arg Gly Glu Gly Ile Pro Trp
 225 230 235 240
 Glu Gly Asn Tyr Ser Ser Trp Leu Glu Gln Lys Asp Gln Arg Leu Ala
 245 250 255
 Gln Glu Ala Ser Gln Glu Ala Ala Arg Arg Lys Ser Ile Glu Lys Glu
 260 265 270
 Leu Glu Trp Val Arg Gln Gly Thr Lys Gly Arg Gln Ser Lys Gly Lys
 275 280 285
 Ala Arg Leu Ala Arg Phe Glu Glu Leu Asn Ser Thr Glu Tyr Gln Lys
 290 295 300
 Arg Asn Glu Thr Asn Glu Leu Phe Ile Pro Pro Gly Pro Arg Leu Gly
 305 310 315 320
 Asp Lys Val Leu Glu Val Ser Asn Leu Arg Lys Ser Tyr Gly Asp Arg
 325 330 335
 Leu Leu Ile Asp Asp Leu Ser Phe Ser Ile Pro Lys Gly Ala Ile Val
 340 345 350
 Gly Ile Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Phe Arg Met
 355 360 365
 Ile Ser Gly Gln Glu Gln Pro Asp Ser Gly Thr Ile Thr Leu Gly Glu
 370 375 380
 Thr Val Lys Leu Ala Ser Val Asp Gln Phe Arg Asp Ser Met Asp Asn
 385 390 395 400
 Ser Lys Thr Val Trp Glu Glu Val Ser Gly Gly Leu Asp Ile Met Lys
 405 410 415
 Ile Gly Asn Thr Glu Met Pro Ser Arg Ala Tyr Val Gly Arg Phe Asn
 420 425 430
 Phe Lys Gly Val Asp Gln Gly Lys Arg Val Gly Glu Leu Ser Gly Gly
 435 440 445
 Glu Arg Gly Arg Leu His Leu Ala Lys Leu Leu Gln Val Gly Gly Asn
 450 455 460
 Met Leu Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Glu Thr Leu
 465 470 475 480
 Arg Ala Leu Glu Asn Ala Leu Leu Glu Phe Pro Gly Cys Ala Met Val
 485 490 495
 Ile Ser His Asp Arg Trp Phe Leu Asp Arg Ile Ala Thr His Ile Leu
 500 505 510
 Asp Tyr Gln Asp Glu Gly Lys Val Glu Phe Phe Glu Gly Asn Phe Thr
 515 520 525
 Glu Tyr Glu Glu Tyr Lys Lys Arg Thr Leu Gly Ala Asp Ala Leu Glu
 530 535 540
 Pro Lys Arg Ile Lys Tyr Lys Arg Ile Ala Lys
 545 550

<210> 309
 <211> 173
 <212> PRT
 <213> E. Coli

<400> 309

```

Met Ser Lys Pro Lys Tyr Pro Phe Glu Lys Arg Leu Glu Val Val Asn
 1          5          10          15
His Tyr Phe Thr Thr Asp Asp Gly Tyr Arg Ile Ile Ser Ala Arg Phe
          20          25          30
Gly Val Pro Arg Thr Gln Val Arg Thr Trp Val Ala Leu Tyr Glu Lys
          35          40          45
His Gly Glu Lys Gly Leu Ile Pro Lys Pro Lys Gly Val Ser Ala Asp
          50          55          60
Pro Glu Leu Arg Ile Lys Val Val Lys Ala Val Ile Glu Gln His Met
          65          70          75          80
Ser Leu Asn Gln Ala Ala Ala His Phe Met Leu Ala Gly Ser Gly Ser
          85          90          95
Val Ala Arg Trp Leu Lys Val Tyr Glu Glu Arg Gly Glu Ala Gly Leu
          100          105          110
Arg Ala Leu Lys Ile Gly Thr Lys Arg Asn Ile Ala Ile Ser Val Asp
          115          120          125
Pro Glu Lys Ala Ala Ser Ala Leu Glu Leu Ser Lys Asp Arg Arg Ile
          130          135          140
Glu Asp Leu Glu Arg Gln Val Arg Phe Leu Glu Thr Arg Leu Met Tyr
          145          150          155          160
Leu Lys Lys Leu Lys Ala Leu Ala His Pro Thr Lys Lys
          165          170

```

<210> 310
 <211> 283
 <212> PRT
 <213> E. Coli

```

<400> 310
Met Lys Val Leu Asn Glu Leu Arg Gln Phe Tyr Pro Leu Asp Glu Leu
 1          5          10          15
Leu Arg Ala Ala Glu Ile Pro Arg Ser Thr Phe Tyr Tyr His Leu Lys
          20          25          30
Ala Leu Ser Lys Pro Asp Lys Tyr Ala Asp Val Lys Lys Arg Ile Ser
          35          40          45
Glu Ile Tyr His Glu Asn Arg Gly Arg Tyr Gly Tyr Arg Arg Val Thr
          50          55          60
Leu Ser Leu His Arg Glu Gly Lys Gln Ile Asn His Lys Ala Val Gln
          65          70          75          80
Arg Leu Met Gly Thr Leu Ser Leu Lys Ala Ala Ile Lys Val Lys Arg
          85          90          95
Tyr Arg Ser Tyr Arg Gly Glu Val Gly Gln Thr Ala Pro Asn Val Leu
          100          105          110
Gln Arg Asp Phe Lys Ala Thr Arg Pro Asn Glu Lys Trp Val Thr Asp
          115          120          125
Val Thr Glu Phe Ala Val Asn Gly Arg Lys Leu Tyr Leu Ser Pro Val
          130          135          140
Ile Asp Leu Phe Asn Asn Glu Val Ile Ser Tyr Ser Leu Ser Glu Arg
          145          150          155          160
Pro Val Met Asn Met Val Glu Asn Met Leu Asp Gln Ala Phe Lys Lys
          165          170          175
Leu Asn Pro His Glu His Pro Val Leu His Ser Asp Gln Gly Trp Gln
          180          185          190
Tyr Arg Met Arg Arg Tyr Gln Asn Ile Leu Lys Glu His Gly Ile Lys
          195          200          205
Gln Ser Met Ser Arg Lys Gly Asn Cys Leu Asp Asn Ala Val Val Glu
          210          215          220
Cys Phe Phe Gly Thr Lys Ser Glu Cys Phe Tyr Leu Asp Glu Phe
          225          230          235          240
Ser Asn Ile Ser Glu Leu Lys Asp Ala Val Thr Glu Tyr Ile Glu Tyr

```

Tyr Asn Ser Arg 245 Arg Ile Ser Leu Lys 250 Leu Lys Gly Leu Thr 255 Pro Ile
 260 265 270
 Glu Tyr Arg Asn Gln Thr Tyr Met Pro Arg Val
 275 280

<210> 311
 <211> 38
 <212> PRT
 <213> E. Coli

<400> 311
 Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile
 1 5 10 15
 Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys
 20 25 30
 His Lys Gln Arg Gln Gly
 35

<210> 312
 <211> 443
 <212> PRT
 <213> E. Coli

<400> 312
 Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu
 1 5 10 15
 Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val
 20 25 30
 Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val
 35 40 45
 Leu Ala Lys Leu Leu Glu Gln Gln Arg Gly Thr Ile Ile Glu Met Phe
 50 55 60
 Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu
 65 70 75 80
 Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Gln Leu Leu Thr
 85 90 95
 Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly
 100 105 110
 Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala
 115 120 125
 Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly
 130 135 140
 Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala
 145 150 155 160
 Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu
 165 170 175
 Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Phe
 180 185 190
 Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu
 195 200 205
 Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Val Ala
 210 215 220
 Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly
 225 230 235 240
 Gln Arg Arg Ile Val Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg
 245 250 255
 Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala
 260 265 270
 Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala


```

      275      280      285
Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr
290      295      300
Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu
305      310      315
Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val
325      330      335
Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe
340      345      350
Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys
355      360      365
Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile
370      375      380
Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr
385      390      395
Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe
405      410      415
Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala
420      425      430
Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg
435      440

```

<210> 313
 <211> 144
 <212> PRT
 <213> E. Coli

```

      <400> 313
Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly
1      5      10
Lys Arg Leu Gly Arg Gly Ile Gly Ser Gly Leu Gly Lys Thr Gly Gly
20      25      30
Arg Gly His Lys Gly Gln Lys Ser Arg Ser Gly Gly Gly Val Arg Arg
35      40      45
Gly Phe Glu Gly Gly Gln Met Pro Leu Tyr Arg Arg Leu Pro Lys Phe
50      55      60
Gly Phe Thr Ser Arg Lys Ala Ala Ile Thr Ala Glu Ile Arg Leu Ser
65      70      75      80
Asp Leu Ala Lys Val Glu Gly Gly Val Val Asp Leu Asn Thr Leu Lys
85      90      95
Ala Ala Asn Ile Ile Gly Ile Gln Ile Glu Phe Ala Lys Val Ile Leu
100      105      110
Ala Gly Glu Val Thr Thr Pro Val Thr Val Arg Gly Leu Arg Val Thr
115      120      125
Lys Gly Ala Arg Ala Ala Ile Glu Ala Ala Gly Gly Lys Ile Glu Glu
130      135      140

```

<210> 314
 <211> 59
 <212> PRT
 <213> E. Coli

```

      <400> 314
Met Ala Lys Thr Ile Lys Ile Thr Gln Thr Arg Ser Ala Ile Gly Arg
1      5      10
Leu Pro Lys His Lys Ala Thr Leu Leu Gly Leu Gly Leu Arg Arg Ile
20      25      30
Gly His Thr Val Glu Arg Glu Asp Thr Pro Ala Ile Arg Gly Met Ile

```

35 40 45
 Asn Ala Val Ser Phe Met Val Lys Val Glu Glu
 50 55

<210> 315
 <211> 167
 <212> PRT
 <213> E. Coli

<400> 315
 Met Ala His Ile Glu Lys Gln Ala Gly Glu Leu Gln Glu Lys Leu Ile
 1 5 10 15
 Ala Val Asn Arg Val Ser Lys Thr Val Lys Gly Gly Arg Ile Phe Ser
 20 25 30
 Phe Thr Ala Leu Thr Val Val Gly Asp Gly Asn Gly Arg Val Gly Phe
 35 40 45
 Gly Tyr Gly Lys Ala Arg Glu Val Pro Ala Ala Ile Gln Lys Ala Met
 50 55 60
 Glu Lys Ala Arg Arg Asn Met Ile Asn Val Ala Leu Asn Asn Gly Thr
 65 70 75 80
 Leu Gln His Pro Val Lys Gly Val His Thr Gly Ser Arg Val Phe Met
 85 90 95
 Gln Pro Ala Ser Glu Gly Thr Gly Ile Ile Ala Gly Gly Ala Met Arg
 100 105 110
 Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr
 115 120 125
 Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu
 130 135 140
 Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser
 145 150 155 160
 Val Glu Glu Ile Leu Gly Lys
 165

<210> 316
 <211> 117
 <212> PRT
 <213> E. Coli

<400> 316
 Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg
 1 5 10 15
 Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro
 20 25 30
 Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu
 35 40 45
 Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr
 50 55 60
 Thr Gly Asn Lys Asp Ala Ala Ala Val Gly Lys Ala Val Ala Glu
 65 70 75 80
 Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly
 85 90 95
 Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu
 100 105 110
 Ala Gly Leu Gln Phe
 115

<210> 317
 <211> 177

<212> PRT

<213> E. Coli

<400> 317

```

Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp
1      5      10      15
Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu
20      25      30
Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn
35      40      45
Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln
50      55      60
Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr
65      70      75      80
Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala
85      90      95
Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro
100     105     110
Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln
115     120     125
Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val
130     135     140
Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys
145     150     155     160
Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys
165     170     175
Lys

```

<210> 318

<211> 130

<212> PRT

<213> E. Coli

<400> 318

```

Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn
1      5      10      15
Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu
20      25      30
Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp
35      40      45
Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys
50      55      60
Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg
65      70      75      80
Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met
85      90      95
Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr
100     105     110
Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr
115     120     125
Val Ala
130

```

<210> 319

<211> 101

<212> PRT

<213> E. Coli

<400> 319

```

Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu
1      5      10      15
Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser
20      25      30
Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu
35      40      45
Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys
50      55      60
Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser
65      70      75      80
Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu
85      90      95
Lys Lys Ala Ser Trp
100

```

<210> 320

<211> 179

<212> PRT

<213> E. Coli

<400> 320

```

Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu
1      5      10      15
Met Thr Glu Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu
20      25      30
Lys Ile Thr Leu Asn Met Gly Val Gly Glu Ala Ile Ala Asp Lys Lys
35      40      45
Leu Leu Asp Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys
50      55      60
Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg
65      70      75      80
Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met
85      90      95
Trp Glu Phe Phe Glu Arg Leu Ile Thr Ile Ala Val Pro Arg Ile Arg
100      105      110
Asp Phe Arg Gly Leu Ser Ala Lys Ser Phe Asp Gly Arg Gly Asn Tyr
115      120      125
Ser Met Gly Val Arg Glu Gln Ile Ile Phe Pro Glu Ile Asp Tyr Asp
130      135      140
Lys Val Asp Arg Val Arg Gly Leu Asp Ile Thr Ile Thr Thr Thr Ala
145      150      155      160
Lys Ser Asp Glu Glu Gly Arg Ala Leu Leu Ala Ala Phe Asp Phe Pro
165      170      175
Phe Arg Lys

```

<210> 321Z

<211> 104

<212> PRT

<213> E. Coli

<400> 321

```

Met Ala Ala Lys Ile Arg Arg Asp Asp Glu Val Ile Val Leu Thr Gly
1      5      10      15
Lys Asp Lys Gly Lys Arg Gly Lys Val Lys Asn Val Leu Ser Ser Gly
20      25      30

```

Lys Val Ile Val Glu Gly Ile Asn Leu Val Lys Lys His Gln Lys Pro
 35 40 45
 Val Pro Ala Leu Asn Gln Pro Gly Gly Ile Val Glu Lys Glu Ala Ala
 50 55 60
 Ile Gln Val Ser Asn Val Ala Ile Phe Asn Ala Ala Thr Gly Lys Ala
 65 70 75 80
 Asp Arg Val Gly Phe Arg Phe Glu Asp Gly Lys Lys Val Arg Phe Phe
 85 90 95
 Lys Ser Asn Ser Glu Thr Ile Lys
 100

<210> 322
 <211> 123
 <212> PRT
 <213> E. Coli

<400> 322
 Met Ile Gln Glu Gln Thr Met Leu Asn Val Ala Asp Asn Ser Gly Ala
 1 5 10 15
 Arg Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr
 20 25 30
 Ala Gly Val Gly Asp Ile Ile Lys Ile Thr Ile Lys Glu Ala Ile Pro
 35 40 45
 Arg Gly Lys Val Lys Lys Gly Asp Val Leu Lys Ala Val Val Val Arg
 50 55 60
 Thr Lys Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp
 65 70 75 80
 Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly
 85 90 95
 Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe
 100 105 110
 Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu
 115 120

<210> 323
 <211> 188
 <212> PRT
 <213> E. Coli

<400> 323
 Met Phe Lys Gly Gln Lys Thr Leu Ala Ala Leu Ala Val Ser Leu Leu
 1 5 10 15
 Phe Thr Ala Pro Val Tyr Ala Ala Asp Glu Gly Ser Gly Glu Ile His
 20 25 30
 Phe Lys Gly Glu Val Ile Glu Ala Pro Cys Glu Ile His Pro Glu Asp
 35 40 45
 Ile Asp Lys Asn Ile Asp Leu Gly Gln Val Thr Thr Thr His Ile Asn
 50 55 60
 Arg Glu His His Ser Asn Lys Val Ala Val Asp Ile Arg Leu Ile Asn
 65 70 75 80
 Cys Asp Leu Pro Ala Ser Asp Asn Gly Ser Gly Met Pro Val Ser Lys
 85 90 95
 Val Gly Val Thr Phe Asp Ser Thr Ala Lys Thr Thr Gly Ala Thr Pro
 100 105 110
 Leu Leu Ser Asn Thr Ser Ala Gly Glu Ala Thr Gly Val Gly Val Arg
 115 120 125
 Leu Met Asp Lys Asn Asp Gly Asn Ile Val Leu Gly Ser Ala Ala Pro
 130 135 140
 Asp Leu Asp Leu Asp Ala Ser Ser Ser Glu Gln Thr Leu Asn Phe Phe

145 150 155 160
 Ala Trp Met Glu Gln Ile Asp Asn Ala Val Asp Val Thr Ala Gly Glu
 165 170 175
 Val Thr Ala Asn Ala Thr Tyr Val Leu Asp Tyr Lys
 180 185

<210> 324
 <211> 427
 <212> PRT
 <213> E. Coli

<400> 324
 Met Ala Asp Thr Lys Ala Lys Leu Thr Leu Asn Gly Asp Thr Ala Val
 1 5 10 15
 Glu Leu Asp Val Leu Lys Gly Thr Leu Gly Gln Asp Val Ile Asp Ile
 20 25 30
 Arg Thr Leu Gly Ser Lys Gly Val Phe Thr Phe Asp Pro Gly Phe Thr
 35 40 45
 Ser Thr Ala Ser Cys Glu Ser Lys Ile Thr Phe Ile Asp Gly Asp Glu
 50 55 60
 Gly Ile Leu Leu His Arg Gly Phe Pro Ile Asp Gln Leu Ala Thr Asp
 65 70 75 80
 Ser Asn Tyr Leu Glu Val Cys Tyr Ile Leu Leu Asn Gly Glu Lys Pro
 85 90 95
 Thr Gln Glu Gln Tyr Asp Glu Phe Lys Thr Thr Val Thr Arg His Thr
 100 105 110
 Met Ile His Glu Gln Ile Thr Arg Leu Phe His Ala Phe Arg Arg Asp
 115 120 125
 Ser His Pro Met Ala Val Met Cys Gly Ile Thr Gly Ala Leu Ala Ala
 130 135 140
 Phe Tyr His Asp Ser Leu Asp Val Asn Asn Pro Arg His Arg Glu Ile
 145 150 155 160
 Ala Ala Phe Arg Leu Ser Lys Met Pro Thr Met Ala Ala Met Cys
 165 170 175
 Tyr Lys Tyr Ser Ile Gly Gln Pro Phe Val Tyr Pro Arg Asn Asp Leu
 180 185 190
 Ser Tyr Ala Gly Asn Phe Leu Asn Met Met Phe Ser Thr Pro Cys Glu
 195 200 205
 Pro Tyr Glu Val Asn Pro Ile Leu Glu Arg Ala Met Asp Arg Ile Leu
 210 215 220
 Ile Leu His Ala Asp His Glu Gln Asn Ala Ser Thr Ser Thr Val Arg
 225 230 235 240
 Thr Ala Gly Ser Ser Gly Ala Asn Pro Phe Ala Cys Ile Ala Ala Gly
 245 250 255
 Ile Ala Ser Leu Trp Gly Pro Ala His Gly Gly Ala Asn Glu Ala Ala
 260 265 270
 Leu Lys Met Leu Glu Glu Ile Ser Ser Val Lys His Ile Pro Glu Phe
 275 280 285
 Val Arg Arg Ala Lys Asp Lys Asn Asp Ser Phe Arg Leu Met Gly Phe
 290 295 300
 Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Thr Val Met Arg
 305 310 315 320
 Glu Thr Cys His Glu Val Leu Lys Glu Leu Gly Thr Lys Asp Asp Leu
 325 330 335
 Leu Glu Val Ala Met Glu Leu Glu Asn Ile Ala Leu Asn Asp Pro Tyr
 340 345 350
 Phe Ile Glu Lys Lys Leu Tyr Pro Asn Val Asp Phe Tyr Ser Gly Ile
 355 360 365
 Ile Leu Lys Ala Met Gly Ile Pro Ser Ser Met Phe Thr Val Ile Phe
 370 375 380

Ala Met Ala Arg Thr Val Gly Trp Ile Ala His Trp Ser Glu Met His
 385 390 395 400
 Ser Asp Gly Met Lys Ile Ala Arg Pro Arg Gln Leu Tyr Thr Gly Tyr
 405 410 415
 Glu Lys Arg Asp Phe Lys Ser Asp Ile Lys Arg
 420 425

<210> 325
 <211> 477
 <212> PRT
 <213> E. Coli

<400> 325
 Met Lys Val Thr Leu Pro Glu Phe Glu Arg Ala Gly Val Met Val Val
 1 5 10 15
 Gly Asp Val Met Leu Asp Arg Tyr Trp Tyr Gly Pro Thr Ser Arg Ile
 20 25 30
 Ser Pro Glu Ala Pro Val Pro Val Val Lys Val Asn Thr Ile Glu Glu
 35 40 45
 Arg Pro Gly Gly Ala Ala Asn Val Ala Met Asn Ile Ala Ser Leu Gly
 50 55 60
 Ala Asn Ala Arg Leu Val Gly Leu Thr Gly Ile Asp Asp Ala Ala Arg
 65 70 75 80
 Ala Leu Ser Lys Ser Leu Ala Asp Val Asn Val Lys Cys Asp Phe Val
 85 90 95
 Ser Val Pro Thr His Pro Thr Ile Thr Lys Leu Arg Val Leu Ser Arg
 100 105 110
 Asn Gln Gln Leu Ile Arg Leu Asp Phe Glu Glu Gly Phe Glu Gly Val
 115 120 125
 Asp Pro Gln Pro Leu His Glu Arg Ile Asn Gln Ala Leu Ser Ser Ile
 130 135 140
 Gly Ala Leu Val Leu Ser Asp Tyr Ala Lys Gly Ala Leu Ala Ser Val
 145 150 155 160
 Gln Gln Met Ile Gln Leu Ala Arg Lys Ala Gly Val Pro Val Leu Ile
 165 170 175
 Asp Pro Lys Gly Thr Asp Phe Glu Arg Tyr Arg Gly Ala Thr Leu Leu
 180 185 190
 Thr Pro Asn Leu Ser Glu Phe Glu Ala Val Val Gly Lys Cys Lys Thr
 195 200 205
 Glu Glu Glu Ile Val Glu Arg Gly Met Lys Leu Ile Ala Asp Tyr Glu
 210 215 220
 Leu Ser Ala Leu Leu Val Thr Arg Ser Glu Gln Gly Met Ser Leu Leu
 225 230 235 240
 Gln Pro Gly Lys Ala Pro Leu His Met Pro Thr Gln Ala Gln Glu Val
 245 250 255
 Tyr Asp Val Thr Gly Ala Gly Asp Thr Val Ile Gly Val Leu Ala Ala
 260 265 270
 Thr Leu Ala Ala Gly Asn Ser Leu Glu Glu Ala Cys Phe Phe Ala Asn
 275 280 285
 Ala Ala Ala Gly Val Val Val Gly Lys Leu Gly Thr Ser Thr Val Ser
 290 295 300
 Pro Ile Glu Leu Glu Asn Ala Val Arg Gly Arg Ala Asp Thr Gly Phe
 305 310 315 320
 Gly Val Met Thr Glu Glu Glu Leu Lys Leu Ala Val Ala Ala Arg
 325 330 335
 Lys Arg Gly Glu Lys Val Val Met Thr Asn Gly Val Phe Asp Ile Leu
 340 345 350
 His Ala Gly His Val Ser Tyr Leu Ala Asn Ala Arg Lys Leu Gly Asp
 355 360 365
 Arg Leu Ile Val Ala Val Asn Ser Asp Ala Ser Thr Lys Arg Leu Lys

```

      370              375              380
Gly Asp Ser Arg Pro Val Asn Pro Leu Glu Gln Arg Met Ile Val Leu
385              390              395              400
Gly Ala Leu Glu Ala Val Asp Trp Val Val Ser Phe Glu Glu Asp Thr
      405              410              415
Pro Gln Arg Leu Ile Ala Gly Ile Leu Pro Asp Leu Leu Val Lys Gly
      420              425              430
Gly Asp Tyr Lys Pro Glu Glu Ile Ala Gly Ser Lys Glu Val Trp Ala
      435              440              445
Asn Gly Gly Glu Val Leu Val Leu Asn Phe Glu Asp Gly Cys Ser Thr
      450              455              460
Thr Asn Ile Ile Lys Lys Ile Gln Gln Asp Lys Lys Gly
465              470              475

```

```

<210> 326
<211> 946
<212> PRT
<213> E. Coli

```

```

<400> 326
Met Lys Pro Leu Ser Ser Pro Leu Gln Gln Tyr Trp Gln Thr Val Val
1              5              10              15
Glu Arg Leu Pro Glu Pro Leu Ala Glu Glu Ser Leu Ser Ala Gln Ala
      20              25              30
Lys Ser Val Leu Thr Phe Ser Asp Phe Val Gln Asp Ser Val Ile Ala
      35              40              45
His Pro Glu Trp Leu Thr Glu Leu Glu Ser Gln Pro Pro Gln Ala Asp
      50              55              60
Glu Trp Gln His Tyr Ala Ala Trp Leu Gln Glu Ala Leu Cys Asn Val
65              70              75              80
Ser Asp Glu Ala Gly Leu Met Arg Glu Leu Arg Leu Phe Arg Arg Arg
      85              90              95
Ile Met Val Arg Ile Ala Trp Ala Gln Thr Leu Ala Leu Val Thr Glu
      100              105              110
Glu Ser Ile Leu Gln Gln Leu Ser Tyr Leu Ala Glu Thr Leu Ile Val
      115              120              125
Ala Ala Arg Asp Trp Leu Tyr Asp Ala Cys Cys Arg Glu Trp Gly Thr
      130              135              140
Pro Cys Asn Ala Gln Gly Glu Ala Gln Pro Leu Leu Ile Leu Gly Met
145              150              155              160
Gly Lys Leu Gly Gly Gly Glu Leu Asn Phe Ser Ser Asp Ile Asp Leu
      165              170              175
Ile Phe Ala Trp Pro Glu His Gly Cys Thr Gln Gly Gly Arg Arg Glu
      180              185              190
Leu Asp Asn Ala Gln Phe Phe Thr Arg Met Gly Gln Arg Leu Ile Lys
      195              200              205
Val Leu Asp Gln Pro Thr Gln Asp Gly Phe Val Tyr Arg Val Asp Met
      210              215              220
Arg Leu Arg Pro Phe Gly Glu Ser Gly Pro Leu Val Leu Ser Phe Ala
225              230              235              240
Ala Leu Glu Asp Tyr Tyr Gln Glu Gln Gly Arg Asp Trp Glu Arg Tyr
      245              250              255
Ala Met Val Lys Ala Arg Ile Met Gly Asp Ser Glu Gly Val Tyr Ala
      260              265              270
Asn Glu Leu Arg Ala Met Leu Arg Pro Phe Val Phe Arg Arg Tyr Ile
      275              280              285
Asp Phe Ser Val Ile Gln Ser Leu Arg Asn Met Lys Gly Met Ile Ala
      290              295              300
Arg Glu Val Arg Arg Arg Gly Leu Thr Asp Asn Ile Lys Leu Gly Ala
305              310              315              320

```


Gly Gly Ile Arg Glu Ile Glu Phe Ile Val Gln Val Phe Gln Leu Ile
 325 330 335
 Arg Gly Gly Arg Glu Pro Ser Leu Gln Ser Arg Ser Leu Leu Pro Thr
 340 345 350
 Leu Ser Ala Ile Ala Glu Leu His Leu Leu Ser Glu Asn Asp Ala Glu
 355 360 365
 Gln Leu Arg Val Ala Tyr Leu Phe Leu Arg Arg Leu Glu Asn Leu Leu
 370 375 380
 Gln Ser Ile Asn Asp Glu Gln Thr Gln Thr Leu Pro Ser Asp Glu Leu
 385 390 395 400
 Asn Arg Ala Arg Leu Ala Trp Ala Met Asp Phe Ala Asp Trp Pro Gln
 405 410 415
 Leu Thr Gly Ala Leu Thr Ala His Met Thr Asn Val Arg Arg Val Phe
 420 425 430
 Asn Glu Leu Ile Gly Asp Asp Glu Ser Glu Thr Gln Glu Glu Ser Leu
 435 440 445
 Ser Glu Gln Trp Arg Glu Leu Trp Gln Asp Ala Leu Gln Glu Asp Asp
 450 455 460
 Thr Thr Pro Val Leu Ala His Leu Ser Glu Asp Asp Arg Lys Gln Val
 465 470 475 480
 Leu Thr Leu Ile Ala Asp Phe Arg Lys Glu Leu Asp Lys Arg Thr Ile
 485 490 495
 Gly Pro Arg Gly Arg Gln Val Leu Asp His Leu Met Pro His Leu Leu
 500 505 510
 Ser Asp Val Cys Ala Arg Glu Asp Ala Ala Val Thr Leu Ser Arg Ile
 515 520 525
 Thr Ala Leu Leu Val Gly Ile Val Thr Arg Thr Thr Tyr Leu Glu Leu
 530 535 540
 Leu Ser Glu Phe Pro Ala Ala Leu Lys His Leu Ile Ser Leu Cys Ala
 545 550 555 560
 Ala Ser Pro Met Ile Ala Ser Gln Leu Ala Arg Tyr Pro Leu Leu Leu
 565 570 575
 Asp Glu Leu Leu Asp Pro Asn Thr Leu Tyr Gln Pro Thr Ala Thr Asp
 580 585 590
 Ala Tyr Arg Asp Glu Leu Arg Gln Tyr Leu Leu Arg Val Pro Glu Asp
 595 600 605
 Asp Glu Glu Gln Gln Leu Glu Ala Leu Arg Gln Phe Lys Gln Ala Gln
 610 615 620
 Leu Leu Arg Ile Ala Ala Ala Asp Ile Ala Gly Thr Leu Pro Val Met
 625 630 635 640
 Lys Val Ser Asp His Leu Thr Trp Leu Ala Glu Ala Met Ile Asp Ala
 645 650 655
 Val Val Gln Gln Ala Trp Val Gln Met Val Ala Arg Tyr Gly Lys Pro
 660 665 670
 Asn His Leu Asn Glu Arg Glu Gly Arg Gly Phe Ala Val Val Gly Tyr
 675 680 685
 Gly Lys Leu Gly Gly Trp Glu Leu Gly Tyr Ser Ser Asp Leu Asp Leu
 690 695 700
 Ile Phe Leu His Asp Cys Pro Met Asp Ala Met Thr Asp Gly Glu Arg
 705 710 715 720
 Glu Ile Asp Gly Arg Gln Phe Tyr Leu Arg Leu Ala Gln Arg Ile Met
 725 730 735
 His Leu Phe Ser Thr Arg Thr Ser Ser Gly Ile Leu Tyr Glu Val Asp
 740 745 750
 Ala Arg Leu Arg Pro Ser Gly Ala Ala Gly Met Leu Val Thr Ser Ala
 755 760 765
 Glu Ala Phe Ala Asp Tyr Gln Lys Asn Glu Ala Trp Thr Trp Glu His
 770 775 780
 Gln Ala Leu Val Arg Ala Arg Val Val Tyr Gly Asp Pro Gln Leu Thr
 785 790 795 800
 Ala His Phe Asp Ala Val Arg Arg Glu Ile Met Thr Leu Pro Arg Glu

805 810 815
 Gly Lys Thr Leu Gln Thr Glu Val Arg Glu Met Arg Glu Lys Met Arg
 820 825 830
 Ala His Leu Gly Asn Lys His Arg Asp Arg Phe Asp Ile Lys Ala Asp
 835 840 845
 Glu Gly Gly Ile Thr Asp Ile Glu Phe Ile Thr Gln Tyr Leu Val Leu
 850 855 860
 Arg Tyr Ala His Glu Lys Pro Lys Leu Thr Arg Trp Ser Asp Asn Val
 865 870 875 880
 Arg Ile Leu Glu Leu Leu Ala Gln Asn Asp Ile Met Glu Glu Gln Glu
 885 890 895
 Ala Met Ala Leu Thr Arg Ala Tyr Thr Thr Leu Arg Asp Glu Leu His
 900 905 910
 His Leu Ala Leu Gln Glu Leu Pro Gly His Val Ser Glu Asp Cys Phe
 915 920 925
 Thr Ala Glu Arg Glu Leu Val Arg Ala Ser Trp Gln Lys Trp Leu Val
 930 935 940
 Glu Glu
 945

<210> 327
 <211> 433
 <212> PRT
 <213> E. Coli

<400> 327
 Met Ala Gln Glu Ile Glu Leu Lys Phe Ile Val Asn His Ser Ala Val
 1 5 10 15
 Glu Ala Leu Arg Asp His Leu Asn Thr Leu Gly Gly Glu His His Asp
 20 25 30
 Pro Val Gln Leu Leu Asn Ile Tyr Thr Glu Thr Pro Asp Asn Trp Leu
 35 40 45
 Arg Gly His Asp Met Gly Leu Arg Ile Arg Gly Glu Asn Gly Arg Tyr
 50 55 60
 Glu Met Thr Met Lys Val Ala Gly Arg Val Thr Gly Gly Leu His Gln
 65 70 75 80
 Arg Pro Glu Tyr Asn Val Ala Leu Ser Glu Pro Thr Leu Asp Leu Ala
 85 90 95
 Gln Leu Pro Thr Glu Val Trp Pro Asn Gly Glu Leu Pro Ala Asp Leu
 100 105 110
 Ala Ser Arg Val Gln Pro Leu Phe Ser Thr Asp Phe Tyr Arg Glu Lys
 115 120 125
 Trp Leu Val Ala Val Asp Gly Ser Gln Ile Glu Ile Ala Leu Asp Gln
 130 135 140
 Gly Glu Val Lys Ala Gly Glu Phe Ala Glu Pro Ile Cys Glu Leu Glu
 145 150 155 160
 Leu Glu Leu Leu Ser Gly Asp Thr Arg Ala Val Leu Lys Leu Ala Asn
 165 170 175
 Gln Leu Val Ser Gln Thr Gly Leu Arg Gln Gly Ser Leu Ser Lys Ala
 180 185 190
 Ala Arg Gly Tyr His Leu Ala Gln Gly Asn Pro Ala Arg Glu Ile Lys
 195 200 205
 Pro Thr Thr Ile Leu His Val Ala Ala Lys Ala Asp Val Glu Gln Gly
 210 215 220
 Leu Glu Ala Ala Leu Glu Leu Ala Leu Ala Gln Trp Gln Tyr His Glu
 225 230 235 240
 Glu Leu Trp Val Arg Gly Asn Asp Ala Ala Lys Glu Gln Val Leu Ala
 245 250 255
 Ala Ile Ser Leu Val Arg His Thr Leu Met Leu Phe Gly Gly Ile Val

260 265 270
 Pro Arg Lys Ala Ser Thr His Leu Arg Asp Leu Leu Thr Gln Cys Glu
 275 280 285
 Ala Thr Ile Ala Ser Ala Val Ser Ala Val Thr Ala Val Tyr Ser Thr
 290 295 300
 Glu Thr Ala Met Ala Lys Leu Ala Leu Thr Glu Trp Leu Val Ser Lys
 305 310 315 320
 Ala Trp Gln Pro Phe Leu Asp Ala Lys Ala Gln Gly Lys Ile Ser Asp
 325 330 335
 Ser Phe Lys Arg Phe Ala Asp Ile His Leu Ser Arg His Ala Ala Glu
 340 345 350
 Leu Lys Ser Val Phe Cys Gln Pro Leu Gly Asp Arg Tyr Arg Asp Gln
 355 360 365
 Leu Pro Arg Leu Thr Arg Asp Ile Asp Ser Ile Leu Leu Ala Gly
 370 375 380
 Tyr Tyr Asp Pro Val Val Ala Gln Ala Trp Leu Glu Asn Trp Gln Gly
 385 390 395 400
 Leu His His Ala Ile Ala Thr Gly Gln Arg Ile Glu Ile Glu His Phe
 405 410 415
 Arg Asn Glu Ala Asn Asn Gln Glu Pro Phe Trp Leu His Ser Gly Lys
 420 425 430
 Arg

<210> 328
 <211> 70
 <212> PRT
 <213> E. Coli

<400> 328
 Met Ser Gly Lys Met Thr Gly Ile Val Lys Trp Phe Asn Ala Asp Lys
 1 5 10 15
 Gly Phe Gly Phe Ile Thr Pro Asp Asp Gly Ser Lys Asp Val Phe Val
 20 25 30
 His Phe Ser Ala Ile Gln Asn Asp Gly Tyr Lys Ser Leu Asp Glu Gly
 35 40 45
 Gln Lys Val Ser Phe Thr Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
 50 55 60
 Gly Asn Val Thr Ser Leu
 65 70

<210> 329
 <211> 523
 <212> PRT
 <213> E. Coli

<400> 329
 Met Arg Asp Ile Val Asp Pro Val Phe Ser Ile Gly Ile Ser Ser Leu
 1 5 10 15
 Trp Asp Glu Leu Arg His Met Pro Ala Gly Gly Val Trp Trp Phe Asn
 20 25 30
 Val Asp Arg His Glu Asp Ala Ile Ser Leu Ala Asn Gln Thr Ile Ala
 35 40 45
 Ser Gln Ala Glu Thr Ala His Val Ala Val Ile Ser Met Asp Ser Asp
 50 55 60
 Pro Ala Lys Ile Phe Gln Leu Asp Asp Ser Gln Gly Pro Glu Lys Ile
 65 70 75 80

Lys Leu Phe Ser Met Leu Asn His Glu Lys Gly Leu Tyr Tyr Leu Thr
 85 90 95
 Arg Asp Leu Gln Cys Ser Ile Asp Pro His Asn Tyr Leu Phe Ile Leu
 100 105 110
 Val Cys Ala Asn Asn Ala Trp Gln Asn Ile Pro Ala Glu Arg Leu Arg
 115 120 125
 Ser Trp Leu Asp Lys Met Asn Lys Trp Ser Arg Leu Asn His Cys Ser
 130 135 140
 Leu Leu Val Ile Asn Pro Gly Asn Asn Asn Asp Lys Gln Phe Ser Leu
 145 150 155 160
 Leu Leu Glu Glu Tyr Arg Ser Leu Phe Gly Leu Ala Ser Leu Arg Phe
 165 170 175
 Gln Gly Asp Gln His Leu Leu Asp Ile Ala Phe Trp Cys Asn Glu Lys
 180 185 190
 Gly Val Ser Ala Arg Gln Gln Leu Ser Val Gln Gln Gln Asn Gly Ile
 195 200 205
 Trp Thr Leu Val Gln Ser Glu Glu Ala Glu Ile Gln Pro Arg Ser Asp
 210 215 220
 Glu Lys Arg Ile Leu Ser Asn Val Ala Val Leu Glu Gly Ala Pro Pro
 225 230 235 240
 Leu Ser Glu His Trp Gln Leu Phe Asn Asn Asn Glu Val Leu Phe Asn
 245 250 255
 Glu Ala Arg Thr Ala Gln Ala Ala Thr Val Val Phe Ser Leu Gln Gln
 260 265 270
 Asn Ala Gln Ile Glu Pro Leu Ala Arg Ser Ile His Thr Leu Arg Arg
 275 280 285
 Gln Arg Gly Ser Ala Met Lys Ile Leu Val Arg Glu Asn Thr Ala Ser
 290 295 300
 Leu Arg Ala Thr Asp Glu Arg Leu Leu Leu Ala Cys Gly Ala Asn Met
 305 310 315 320
 Val Ile Pro Trp Asn Ala Pro Leu Ser Arg Cys Leu Thr Met Ile Glu
 325 330 335
 Ser Val Gln Gly Gln Lys Phe Ser Arg Tyr Val Pro Glu Asp Ile Thr
 340 345 350
 Thr Leu Leu Ser Met Thr Gln Pro Leu Lys Leu Arg Gly Phe Gln Lys
 355 360 365
 Trp Asp Val Phe Cys Asn Ala Val Asn Asn Met Met Asn Asn Pro Leu
 370 375 380
 Leu Pro Ala His Gly Lys Gly Val Leu Val Ala Leu Arg Pro Val Pro
 385 390 395 400
 Gly Ile Arg Val Glu Gln Ala Leu Thr Leu Cys Arg Pro Asn Arg Thr
 405 410 415
 Gly Asp Ile Met Thr Ile Gly Gly Asn Arg Leu Val Leu Phe Leu Ser
 420 425 430
 Phe Cys Arg Ile Asn Asp Leu Asp Thr Ala Leu Asn His Ile Phe Pro
 435 440 445
 Leu Pro Thr Gly Asp Ile Phe Ser Asn Arg Met Val Trp Phe Glu Asp
 450 455 460
 Asp Gln Ile Ser Ala Glu Leu Val Gln Met Arg Leu Leu Ala Pro Glu
 465 470 475 480
 Gln Trp Gly Met Pro Leu Pro Leu Thr Gln Ser Ser Lys Pro Val Ile
 485 490 495
 Asn Ala Glu His Asp Gly Arg His Trp Arg Arg Ile Pro Glu Pro Met
 500 505 510
 Arg Leu Leu Asp Asp Ala Val Glu Arg Ser Ser
 515 520

<210> 330

<211> 62

<212> PRT

<213> E. Coli

<400> 330

```

Met Thr Ile Ser Asp Ile Ile Glu Ile Ile Val Val Cys Ala Leu Ile
 1           5           10           15
Phe Phe Pro Leu Gly Tyr Leu Ala Arg His Ser Leu Arg Arg Ile Arg
      20           25           30
Asp Thr Leu Arg Leu Phe Phe Ala Lys Pro Arg Tyr Val Lys Pro Ala
      35           40           45
Gly Thr Leu Arg Arg Thr Glu Lys Ala Arg Ala Thr Lys Lys
      50           55           60

```

<210> 331

<211> 559

<212> PRT

<213> E. Coli

<400> 331

```

Met Thr Gln Phe Thr Gln Asn Thr Ala Met Pro Ser Ser Leu Trp Gln
 1           5           10           15
Tyr Trp Arg Gly Leu Ser Gly Trp Asn Phe Tyr Phe Leu Val Lys Phe
      20           25           30
Gly Leu Leu Trp Ala Gly Tyr Leu Asn Phe His Pro Leu Leu Asn Leu
      35           40           45
Val Phe Ala Ala Phe Leu Leu Met Pro Leu Pro Arg Tyr Ser Leu His
      50           55           60
Arg Leu Arg His Trp Ile Ala Leu Pro Ile Gly Phe Ala Leu Phe Trp
      65           70           75           80
His Asp Thr Trp Leu Pro Gly Pro Glu Ser Ile Met Ser Gln Gly Ser
      85           90           95
Gln Val Ala Gly Phe Ser Thr Asp Tyr Leu Ile Asp Leu Val Thr Arg
      100          105          110
Phe Ile Asn Trp Gln Met Ile Gly Ala Ile Phe Val Leu Leu Val Ala
      115          120          125
Trp Leu Phe Leu Ser Gln Trp Ile Arg Ile Thr Val Phe Val Val Ala
      130          135          140
Ile Leu Leu Trp Leu Asn Val Leu Thr Leu Ala Gly Pro Ser Phe Ser
      145          150          155          160
Leu Trp Pro Ala Gly Gln Pro Thr Thr Val Thr Thr Thr Gly Gly
      165          170          175
Asn Ala Ala Ala Thr Val Ala Ala Thr Gly Gly Ala Pro Val Val Gly
      180          185          190
Asp Met Pro Ala Gln Thr Ala Pro Pro Thr Thr Ala Asn Leu Asn Ala
      195          200          205
Trp Leu Asn Asn Phe Tyr Asn Ala Glu Ala Lys Arg Lys Ser Thr Phe
      210          215          220
Pro Ser Ser Leu Pro Ala Asp Ala Gln Pro Phe Glu Leu Leu Val Ile
      225          230          235          240
Asn Ile Cys Ser Leu Ser Trp Ser Asp Ile Glu Ala Ala Gly Leu Met
      245          250          255
Ser His Pro Leu Trp Ser His Phe Asp Ile Glu Phe Lys Asn Phe Asn
      260          265          270
Ser Ala Thr Ser Tyr Ser Gly Pro Ala Ala Ile Arg Leu Leu Arg Ala
      275          280          285
Ser Cys Gly Gln Thr Ser His Thr Asn Leu Tyr Gln Pro Ala Asn Asn
      290          295          300
Asp Cys Tyr Leu Phe Asp Asn Leu Ser Lys Leu Gly Phe Thr Gln His
      305          310          315          320
Leu Met Met Gly His Asn Gly Gln Phe Gly Gly Phe Leu Lys Glu Val
      325          330          335

```

Arg Glu Asn Gly Gly Met Gln Ser Glu Leu Met Asp Gln Thr Asn Leu
 340 345 350
 Pro Val Ile Leu Leu Gly Phe Asp Gly Ser Pro Val Tyr Asp Asp Thr
 355 360 365
 Ala Val Leu Asn Arg Trp Leu Asp Val Thr Glu Lys Asp Lys Asn Ser
 370 375 380
 Arg Ser Ala Thr Phe Tyr Asn Thr Leu Pro Leu His Asp Gly Asn His
 385 390 395 400
 Tyr Pro Gly Val Ser Lys Thr Ala Asp Tyr Lys Ala Arg Ala Gln Lys
 405 410 415
 Phe Phe Asp Glu Leu Asp Ala Phe Phe Thr Glu Leu Glu Lys Ser Gly
 420 425 430
 Arg Lys Val Met Val Val Val Val Pro Glu His Gly Gly Ala Leu Lys
 435 440 445
 Gly Asp Arg Met Gln Val Ser Gly Leu Arg Asp Ile Pro Ser Pro Ser
 450 455 460
 Ile Thr Asp Val Pro Val Gly Val Lys Phe Phe Gly Met Lys Ala Pro
 465 470 475 480
 His Gln Gly Ala Pro Ile Val Ile Glu Gln Pro Ser Ser Phe Leu Ala
 485 490 495
 Ile Ser Asp Leu Val Val Arg Val Leu Asp Gly Lys Ile Phe Thr Glu
 500 505 510
 Asp Asn Val Asp Trp Lys Lys Leu Thr Ser Gly Leu Pro Gln Thr Ala
 515 520 525
 Pro Val Ser Glu Asn Ser Asn Ala Val Val Ile Gln Tyr Gln Asp Lys
 530 535 540
 Pro Tyr Val Arg Leu Asn Gly Gly Asp Trp Val Pro Tyr Pro Gln
 545 550 555

<210> 332
 <211> 127
 <212> PRT
 <213> E. Coli

<400> 332
 Met Glu Gly Ser Arg Met Lys Tyr Arg Ile Ala Leu Ala Val Ser Leu
 1 5 10 15
 Phe Ala Leu Ser Ala Gly Ser Tyr Ala Thr Thr Leu Cys Gln Glu Lys
 20 25 30
 Glu Gln Asn Ile Leu Lys Glu Ile Ser Tyr Ala Glu Lys His Gln Asn
 35 40 45
 Gln Asn Arg Ile Asp Gly Leu Asn Lys Ala Leu Ser Glu Val Arg Ala
 50 55 60
 Asn Cys Ser Asp Ser Gln Leu Arg Ala Asp His Gln Lys Lys Ile Ala
 65 70 75 80
 Lys Gln Lys Asp Glu Val Ala Glu Arg Gln Gln Asp Leu Ala Glu Ala
 85 90 95
 Lys Gln Lys Gly Asp Ala Asp Lys Ile Ala Lys Arg Glu Arg Lys Leu
 100 105 110
 Ala Glu Ala Gln Glu Glu Leu Lys Lys Leu Glu Ala Arg Asp Tyr
 115 120 125

<210> 333
 <211> 101
 <212> PRT
 <213> E. Coli

<400> 333
 Met Ser Lys Glu His Thr Thr Glu His Leu Arg Ala Glu Leu Lys Ser

```

      1           5           10           15
Leu Ser Asp Thr Leu Glu Glu Val Leu Ser Ser Ser Gly Glu Lys Ser
      20           25           30
Lys Glu Glu Leu Ser Lys Ile Arg Ser Lys Ala Glu Gln Ala Leu Lys
      35           40           45
Gln Ser Arg Tyr Arg Leu Gly Glu Thr Gly Asp Ala Ile Ala Lys Gln
      50           55           60
Thr Arg Val Ala Ala Ala Arg Ala Asp Glu Tyr Val Arg Glu Asn Pro
      65           70           75           80
Trp Thr Gly Val Gly Ile Gly Ala Ala Ile Gly Val Val Leu Gly Val
      85           90           95
Leu Leu Ser Arg Arg
      100

```

<210> 334
 <211> 134
 <212> PRT
 <213> E. Coli

```

      <400> 334
Met Ala Asp Thr His His Ala Gln Gly Pro Gly Lys Ser Val Leu Gly
      1           5           10           15
Ile Gly Gln Arg Ile Val Ser Ile Met Val Glu Met Val Glu Thr Arg
      20           25           30
Leu Arg Leu Ala Val Val Glu Leu Glu Glu Lys Ala Asn Leu Phe
      35           40           45
Gln Leu Leu Leu Met Leu Gly Leu Thr Met Leu Phe Ala Ala Phe Gly
      50           55           60
Leu Met Ser Leu Met Val Leu Ile Ile Trp Ala Val Asp Pro Gln Tyr
      65           70           75           80
Arg Leu Asn Ala Met Ile Ala Thr Thr Val Val Leu Leu Leu Ala
      85           90           95
Leu Ile Gly Gly Ile Trp Thr Leu Arg Lys Ser Arg Lys Ser Thr Leu
      100           105           110
Leu Arg His Thr Arg His Glu Leu Ala Asn Asp Arg Gln Leu Leu Glu
      115           120           125
Glu Glu Ser Arg Glu Gln
      130

```

<210> 335
 <211> 99
 <212> PRT
 <213> E. Coli

```

      <400> 335
Met Ser Ser Lys Val Glu Arg Glu Arg Arg Lys Ala Gln Leu Leu Ser
      1           5           10           15
Gln Ile Gln Gln Gln Arg Leu Asp Leu Ser Ala Ser Arg Arg Glu Trp
      20           25           30
Leu Glu Thr Thr Gly Ala Tyr Asp Arg Arg Trp Asn Met Leu Leu Ser
      35           40           45
Leu Arg Ser Trp Ala Leu Val Gly Ser Ser Val Met Ala Ile Trp Thr
      50           55           60
Ile Arg His Pro Asn Met Leu Val Arg Trp Ala Arg Arg Gly Phe Gly
      65           70           75           80
Val Trp Ser Ala Trp Arg Leu Val Lys Thr Thr Leu Lys Gln Gln Gln
      85           90           95
Leu Arg Gly

```

<210> 336
 <211> 160
 <212> PRT
 <213> E. Coli

<400> 336
 Met Ile Leu Ser Ile Asp Ser Asn Asp Ala Asn Thr Ala Pro Leu His
 1 5 10 15
 Lys Lys Thr Ile Ser Ser Leu Ser Gly Ala Val Glu Ser Met Met Lys
 20 25 30
 Lys Leu Glu Asp Val Gly Val Leu Val Ala Arg Ile Leu Met Pro Ile
 35 40 45
 Leu Phe Ile Thr Ala Gly Trp Gly Lys Ile Thr Gly Tyr Ala Gly Thr
 50 55 60
 Gln Gln Tyr Met Glu Ala Met Gly Val Pro Gly Phe Met Leu Pro Leu
 65 70 75 80
 Val Ile Leu Leu Glu Phe Gly Gly Gly Leu Ala Ile Leu Phe Gly Phe
 85 90 95
 Leu Thr Arg Thr Thr Ala Leu Phe Thr Ala Gly Phe Thr Leu Leu Thr
 100 105 110
 Ala Phe Leu Phe His Ser Asn Phe Ala Glu Gly Val Asn Ser Leu Met
 115 120 125
 Phe Met Lys Asn Leu Thr Ile Ser Gly Gly Phe Leu Leu Leu Ala Ile
 130 135 140
 Thr Gly Pro Gly Ala Tyr Ser Ile Asp Arg Leu Leu Asn Lys Lys Trp
 145 150 155 160

<210> 337
 <211> 296
 <212> PRT
 <213> E. Coli

<400> 337
 Met Ile Lys Lys Thr Thr Glu Ile Asp Ala Ile Leu Leu Asn Leu Asn
 1 5 10 15
 Lys Ala Ile Asp Ala His Tyr Gln Trp Leu Val Ser Met Phe His Ser
 20 25 30
 Val Val Ala Arg Asp Ala Ser Lys Pro Glu Ile Thr Asp Asn His Ser
 35 40 45
 Tyr Gly Leu Cys Gln Phe Gly Arg Trp Ile Asp His Leu Gly Pro Leu
 50 55 60
 Asp Asn Asp Glu Leu Pro Tyr Val Arg Leu Met Asp Ser Ala His Gln
 65 70 75 80
 His Met His Asn Cys Gly Arg Glu Leu Met Leu Ala Ile Val Glu Asn
 85 90 95
 His Trp Gln Asp Ala His Phe Asp Ala Phe Gln Glu Gly Leu Leu Ser
 100 105 110
 Phe Thr Ala Ala Leu Thr Asp Tyr Lys Ile Tyr Leu Leu Thr Ile Arg
 115 120 125
 Ser Asn Met Asp Val Leu Thr Gly Leu Pro Gly Arg Arg Val Leu Asp
 130 135 140
 Glu Ser Phe Asp His Gln Leu Arg Asn Ala Glu Pro Leu Asn Leu Tyr
 145 150 155 160
 Leu Met Leu Leu Asp Ile Asp Arg Phe Lys Leu Val Asn Asp Thr Tyr
 165 170 175

Gly His Leu Ile Gly Asp Val Val Leu Arg Thr Leu Ala Thr Tyr Leu
 180 185 190
 Ala Ser Trp Thr Arg Asp Tyr Glu Thr Val Tyr Arg Tyr Gly Gly Glu
 195 200 205
 Glu Phe Ile Ile Ile Val Lys Ala Ala Asn Asp Glu Glu Ala Cys Arg
 210 215 220
 Ala Gly Val Arg Ile Cys Gln Leu Val Asp Asn His Ala Ile Thr His
 225 230 235 240
 Ser Glu Gly His Ile Asn Ile Thr Val Thr Ala Gly Val Ser Arg Ala
 245 250 255
 Phe Pro Glu Glu Pro Leu Asp Val Val Ile Gly Arg Ala Asp Arg Ala
 260 265 270
 Met Tyr Glu Gly Lys Gln Thr Gly Arg Asn Arg Cys Met Phe Ile Asp
 275 280 285
 Glu Gln Asn Val Ile Asn Arg Val
 290 295

<210> 338
 <211> 203
 <212> PRT
 <213> E. Coli

<400> 338
 Met Arg Leu Arg Val Val Pro Gly Phe Ile Ser Pro Pro Pro Gly Phe
 1 5 10 15
 Gly Gly Leu Gly Tyr Thr Pro Thr Ala Arg Ala Cys Val Asn Ile Ser
 20 25 30
 Ile Pro Leu Gln Leu Arg Val Ile Asp Met Leu Asp Val Phe Thr Pro
 35 40 45
 Leu Leu Lys Leu Phe Ala Asn Glu Pro Leu Glu Arg Leu Met Tyr Thr
 50 55 60
 Ile Ile Ile Phe Gly Leu Thr Leu Trp Leu Ile Pro Lys Glu Phe Thr
 65 70 75 80
 Val Ala Phe Asn Ala Tyr Thr Glu Ile Pro Trp Leu Phe Gln Ile Ile
 85 90 95
 Val Phe Ala Phe Ser Phe Val Val Ala Ile Ser Phe Ser Arg Leu Arg
 100 105 110
 Ala His Ile Gln Lys His Tyr Ser Leu Leu Pro Glu Gln Arg Val Leu
 115 120 125
 Leu Arg Leu Ser Glu Lys Glu Ile Ala Val Phe Lys Asp Phe Leu Lys
 130 135 140
 Thr Gly Asn Leu Ile Ile Thr Ser Pro Cys Arg Asn Pro Val Met Lys
 145 150 155 160
 Lys Leu Glu Arg Lys Gly Ile Ile Gln His Gln Ser Asp Ser Ala Asn
 165 170 175
 Cys Ser Tyr Tyr Leu Val Thr Glu Lys Tyr Ser His Phe Met Lys Leu
 180 185 190
 Phe Trp Asn Ser Arg Ser Arg Arg Phe Asn Arg
 195 200

<210> 339
 <211> 58
 <212> PRT
 <213> E. Coli

<400> 339
 Met Leu Leu Gln Pro Ser Ala Arg Thr Ser Phe Gly Phe Lys Cys Phe

1 5 10 15
 Ala Phe Gly Ile Arg His Gly Ser Glu Arg Ser Ile Leu Val Gly Glu
 20 25 30
 His Ala Ala His Gln Gly Phe Val Val Ala Glu Val Asp Phe Leu His
 35 40 45
 Phe Ala Asn Leu Thr Ser Cys Cys Tyr Val
 50 55

<210> 340

<211> 1426

<212> PRT

<213> E. Coli

<400> 340

Met Ser Gly Lys Pro Ala Ala Arg Gln Gly Asp Met Thr Gln Tyr Gly
 1 5 10 15
 Gly Pro Ile Val Gln Gly Ser Ala Gly Val Arg Ile Gly Ala Pro Thr
 20 25 30
 Gly Val Ala Cys Ser Val Cys Pro Gly Gly Met Thr Ser Gly Asn Pro
 35 40 45
 Val Asn Pro Leu Leu Gly Ala Lys Val Leu Pro Gly Glu Thr Asp Leu
 50 55 60
 Ala Leu Pro Gly Pro Leu Pro Phe Ile Leu Ser Arg Thr Tyr Ser Ser
 65 70 75 80
 Tyr Arg Thr Lys Thr Pro Ala Pro Val Gly Val Phe Gly Pro Gly Trp
 85 90 95
 Lys Ala Pro Ser Asp Ile Arg Leu Gln Leu Arg Asp Asp Gly Leu Ile
 100 105 110
 Leu Asn Asp Asn Gly Gly Arg Ser Ile His Phe Glu Pro Leu Leu Pro
 115 120 125
 Gly Glu Ala Val Tyr Ser Arg Ser Glu Ser Met Trp Leu Val Arg Gly
 130 135 140
 Gly Lys Ala Ala Gln Pro Asp Gly His Thr Leu Ala Arg Leu Trp Gly
 145 150 155 160
 Ala Leu Pro Pro Asp Ile Arg Leu Ser Pro His Leu Tyr Leu Ala Thr
 165 170 175
 Asn Ser Ala Gln Gly Pro Trp Trp Ile Leu Gly Trp Ser Glu Arg Val
 180 185 190
 Pro Gly Ala Glu Asp Val Leu Pro Ala Pro Leu Pro Pro Tyr Arg Val
 195 200 205
 Leu Thr Gly Met Ala Asp Arg Phe Gly Arg Thr Leu Thr Tyr Arg Arg
 210 215 220
 Glu Ala Ala Gly Asp Leu Ala Gly Glu Ile Thr Gly Val Thr Asp Gly
 225 230 235 240
 Ala Gly Arg Glu Phe Arg Leu Val Leu Thr Thr Gln Ala Gln Arg Ala
 245 250 255
 Glu Glu Ala Arg Thr Ser Ser Leu Ser Ser Ser Asp Ser Ser Arg Pro
 260 265 270
 Leu Ser Ala Ser Ala Phe Pro Asp Thr Leu Pro Gly Thr Glu Tyr Gly
 275 280 285
 Pro Asp Arg Gly Ile Arg Leu Ser Ala Val Trp Leu Met His Asp Pro
 290 295 300
 Ala Tyr Pro Glu Ser Leu Pro Ala Ala Pro Leu Val Arg Tyr Thr Tyr
 305 310 315 320
 Thr Glu Ala Gly Glu Leu Leu Ala Val Tyr Asp Arg Ser Asn Thr Gln
 325 330 335
 Val Arg Ala Phe Thr Tyr Asp Ala Gln His Pro Gly Arg Met Val Ala
 340 345 350
 His Arg Tyr Ala Gly Arg Pro Glu Met Arg Tyr Arg Tyr Asp Asp Thr
 355 360 365

Gly Arg Val Val Glu Gln Leu Asn Pro Ala Gly Leu Ser Tyr Arg Tyr
 370 375 380
 Leu Tyr Glu Gln Asp Arg Ile Thr Val Thr Asp Ser Leu Asn Arg Arg
 385 390 395 400
 Glu Val Leu His Thr Glu Gly Gly Ala Gly Leu Lys Arg Val Val Lys
 405 410 415
 Lys Glu Leu Ala Asp Gly Ser Val Thr Arg Ser Gly Tyr Asp Ala Ala
 420 425 430
 Gly Arg Leu Thr Ala Gln Thr Asp Ala Ala Gly Arg Arg Thr Glu Tyr
 435 440 445
 Gly Leu Asn Val Val Ser Gly Asp Ile Thr Asp Ile Thr Thr Pro Asp
 450 455 460
 Gly Arg Glu Thr Lys Phe Tyr Tyr Asn Asp Gly Asn Gln Leu Thr Ala
 465 470 475 480
 Val Val Ser Pro Asp Gly Leu Glu Ser Arg Arg Glu Tyr Asp Glu Pro
 485 490 495
 Gly Arg Leu Val Ser Glu Thr Ser Arg Ser Gly Glu Thr Val Arg Tyr
 500 505 510
 Arg Tyr Asp Asp Ala His Ser Glu Leu Pro Ala Thr Thr Thr Asp Ala
 515 520 525
 Thr Gly Ser Thr Arg Gln Met Thr Trp Ser Arg Tyr Gly Gln Leu Leu
 530 535 540
 Ala Phe Thr Asp Cys Ser Gly Tyr Gln Thr Arg Tyr Glu Tyr Asp Arg
 545 550 555 560
 Phe Gly Gln Met Thr Ala Val His Arg Glu Glu Gly Ile Ser Leu Tyr
 565 570 575
 Arg Arg Tyr Asp Asn Arg Gly Arg Leu Thr Ser Val Lys Asp Ala Gln
 580 585 590
 Gly Arg Glu Thr Arg Tyr Glu Tyr Asn Ala Ala Gly Asp Leu Thr Ala
 595 600 605
 Val Ile Thr Pro Asp Gly Asn Arg Ser Glu Thr Gln Tyr Asp Ala Trp
 610 615 620
 Gly Lys Ala Val Ser Thr Thr Gln Gly Gly Leu Thr Arg Ser Met Glu
 625 630 635 640
 Tyr Asp Ala Ala Gly Arg Val Ile Ser Leu Thr Asn Glu Asn Gly Ser
 645 650 655
 His Ser Val Phe Ser Tyr Asp Ala Leu Asp Arg Leu Val Gln Gln Gly
 660 665 670
 Gly Phe Asp Gly Arg Thr Gln Arg Tyr His Tyr Asp Leu Thr Gly Lys
 675 680 685
 Leu Thr Gln Ser Glu Asp Glu Gly Leu Val Ile Leu Trp Tyr Tyr Asp
 690 695 700
 Glu Ser Asp Arg Ile Thr His Arg Thr Val Asn Gly Glu Pro Ala Glu
 705 710 715 720
 Gln Trp Gln Tyr Asp Gly His Gly Trp Leu Thr Asp Ile Ser His Leu
 725 730 735
 Ser Glu Gly His Arg Val Ala Val His Tyr Gly Tyr Asp Asp Lys Gly
 740 745 750
 Arg Leu Thr Gly Glu Cys Gln Thr Val Glu Asn Pro Glu Thr Gly Glu
 755 760 765
 Leu Leu Trp Gln His Glu Thr Lys His Ala Tyr Asn Glu Gln Gly Leu
 770 775 780
 Ala Asn Arg Val Thr Pro Asp Ser Leu Pro Pro Val Glu Trp Leu Thr
 785 790 795 800
 Tyr Gly Ser Gly Tyr Leu Ala Gly Met Lys Leu Gly Gly Thr Pro Leu
 805 810 815
 Val Glu Tyr Thr Arg Asp Arg Leu His Arg Glu Thr Val Arg Ser Phe
 820 825 830
 Gly Ser Met Ala Gly Ser Asn Ala Ala Tyr Glu Leu Thr Ser Thr Tyr
 835 840 845
 Thr Pro Ala Gly Gln Leu Gln Ser Gln His Leu Asn Ser Leu Val Tyr

850 855 860
 Asp Arg Asp Tyr Gly Trp Ser Asp Asn Gly Asp Leu Val Arg Ile Ser
 865 870 875 880
 Gly Pro Arg Gln Thr Arg Glu Tyr Gly Tyr Ser Ala Thr Gly Arg Leu
 885 890 895
 Glu Ser Val Arg Thr Leu Ala Pro Asp Leu Asp Ile Arg Ile Pro Tyr
 900 905 910
 Ala Thr Asp Pro Ala Gly Asn Arg Leu Pro Asp Pro Glu Leu His Pro
 915 920 925
 Asp Ser Thr Leu Thr Val Trp Pro Asp Asn Arg Ile Ala Glu Asp Ala
 930 935 940
 His Tyr Val Tyr Arg His Asp Glu Tyr Gly Arg Leu Thr Glu Lys Thr
 945 950 955 960
 Asp Arg Ile Pro Ala Gly Val Ile Arg Thr Asp Asp Glu Arg Thr His
 965 970 975
 His Tyr His Tyr Asp Ser Gln His Arg Leu Val Phe Tyr Thr Arg Ile
 980 985 990
 Gln His Gly Glu Pro Leu Val Glu Ser Arg Tyr Leu Tyr Asp Pro Leu
 995 1000 1005
 Gly Arg Arg Met Ala Lys Arg Val Trp Arg Arg Glu Arg Asp Leu Thr
 1010 1015 1020
 Gly Trp Met Ser Leu Ser Arg Lys Pro Glu Val Thr Trp Tyr Gly Trp
 1025 1030 1035 1040
 Asp Gly Asp Arg Leu Thr Thr Val Gln Thr Asp Thr Thr Arg Ile Gln
 1045 1050 1055
 Thr Val Tyr Glu Pro Gly Ser Phe Thr Pro Leu Ile Arg Val Glu Thr
 1060 1065 1070
 Glu Asn Gly Glu Arg Glu Lys Ala Gln Arg Arg Ser Leu Ala Glu Thr
 1075 1080 1085
 Leu Gln Gln Glu Gly Ser Glu Asn Gly His Gly Val Phe Pro Ala
 1090 1095 1100
 Glu Leu Val Arg Leu Leu Asp Arg Leu Glu Glu Glu Ile Arg Ala Asp
 1105 1110 1115 1120
 Arg Val Ser Ser Glu Ser Arg Ala Trp Leu Ala Gln Cys Gly Leu Thr
 1125 1130 1135
 Val Glu Gln Leu Ala Arg Gln Val Glu Pro Glu Tyr Thr Pro Ala Arg
 1140 1145 1150
 Lys Ala His Leu Tyr His Cys Asp His Arg Gly Leu Pro Leu Ala Leu
 1155 1160 1165
 Ile Ser Glu Asp Gly Asn Thr Ala Trp Ser Ala Glu Tyr Asp Glu Trp
 1170 1175 1180
 Gly Asn Gln Leu Asn Glu Glu Asn Pro His His Val Tyr Gln Pro Tyr
 1185 1190 1195 1200
 Arg Leu Pro Gly Gln Gln His Asp Glu Glu Ser Gly Leu Tyr Tyr Asn
 1205 1210 1215
 Arg His Arg Tyr Tyr Asp Pro Leu Gln Gly Arg Tyr Ile Thr Gln Asp
 1220 1225 1230
 Pro Met Gly Leu Lys Gly Gly Trp Asn Leu Tyr Gln Tyr Pro Leu Asn
 1235 1240 1245
 Pro Leu Gln Gln Ile Asp Pro Met Gly Leu Leu Gln Thr Trp Asp Asp
 1250 1255 1260
 Ala Arg Ser Gly Ala Cys Thr Gly Gly Val Cys Gly Val Leu Ser Arg
 1265 1270 1275 1280
 Ile Ile Gly Pro Ser Lys Phe Asp Ser Thr Ala Asp Ala Ala Leu Asp
 1285 1290 1295
 Ala Leu Lys Glu Thr Gln Asn Arg Ser Leu Cys Asn Asp Met Glu Tyr
 1300 1305 1310
 Ser Gly Ile Val Cys Lys Asp Thr Asn Gly Lys Tyr Phe Ala Ser Lys
 1315 1320 1325
 Ala Glu Thr Asp Asn Leu Arg Lys Glu Ser Tyr Pro Leu Lys Arg Lys
 1330 1335 1340

Cys Pro Thr Gly Thr Asp Arg Val Ala Ala Tyr His Thr His Gly Ala
 1345 1350 1355 1360
 Asp Ser His Gly Asp Tyr Val Asp Glu Phe Phe Ser Ser Ser Asp Lys
 1365 1370 1375
 Asn Leu Val Arg Ser Lys Asp Asn Asn Leu Glu Ala Phe Tyr Leu Ala
 1380 1385 1390
 Thr Pro Asp Gly Arg Phe Glu Ala Leu Asn Asn Lys Gly Glu Tyr Ile
 1395 1400 1405
 Phe Ile Arg Asn Ser Val Pro Gly Leu Ser Ser Val Cys Ile Pro Tyr
 1410 1415 1420
 His Asp
 1425

<210> 341
 <211> 122
 <212> PRT
 <213> E. Coli

<400> 341
 Met Lys Tyr Ser Ser Ile Phe Ser Met Leu Ser Phe Phe Ile Leu Phe
 1 5 10 15
 Ala Cys Asn Glu Thr Ala Val Tyr Gly Ser Asp Glu Asn Ile Ile Phe
 20 25 30
 Met Arg Tyr Val Glu Lys Leu His Leu Asp Lys Tyr Ser Val Lys Asn
 35 40 45
 Thr Val Lys Thr Glu Thr Met Ala Ile Gln Leu Ala Glu Ile Tyr Val
 50 55 60
 Arg Tyr Arg Tyr Gly Glu Arg Ile Ala Glu Glu Glu Lys Pro Tyr Leu
 65 70 75 80
 Ile Thr Glu Leu Pro Asp Ser Trp Val Val Glu Gly Ala Lys Leu Pro
 85 90 95
 Tyr Glu Val Ala Gly Gly Val Phe Ile Ile Glu Ile Asn Lys Lys Asn
 100 105 110
 Gly Cys Val Leu Asn Phe Leu His Ser Lys
 115 120

<210> 342
 <211> 236
 <212> PRT
 <213> E. Coli

<400> 342
 Met Leu Ala Leu Met Asp Ala Asp Gly Asn Ile Ala Trp Ser Gly Glu
 1 5 10 15
 Tyr Asp Glu Trp Gly Asn Gln Leu Asn Glu Glu Asn Pro His His Leu
 20 25 30
 His Gln Pro Tyr Arg Leu Pro Gly Gln Gln Tyr Asp Lys Glu Ser Gly
 35 40 45
 Leu Tyr Tyr Asn Arg Asn Arg Tyr Tyr Asp Pro Leu Gln Gly Arg Tyr
 50 55 60
 Ile Thr Gln Asp Pro Ile Gly Leu Glu Gly Gly Trp Ser Leu Tyr Ala
 65 70 75 80
 Tyr Pro Leu Asn Pro Val Asn Gly Ile Asp Pro Leu Gly Leu Ser Pro
 85 90 95
 Ala Asp Val Ala Leu Ile Arg Arg Lys Asp Gln Leu Asn His Gln Arg
 100 105 110
 Ala Trp Asp Ile Leu Ser Asp Thr Tyr Glu Asp Met Lys Arg Leu Asn
 115 120 125
 Leu Gly Gly Thr Asp Gln Phe Phe His Cys Met Ala Phe Cys Arg Val

```

      130              135              140
Ser Lys Leu Asn Asp Ala Gly Val Ser Arg Ser Ala Lys Gly Leu Gly
145              150              155              160
Tyr Glu Lys Glu Ile Arg Asp Tyr Gly Leu Asn Leu Phe Gly Met Tyr
      165              170              175
Gly Arg Lys Val Lys Leu Ser His Ser Glu Met Ile Glu Asp Asn Lys
      180              185              190
Lys Asp Leu Ala Val Asn Asp His Gly Leu Thr Cys Pro Ser Thr Thr
      195              200              205
Asp Cys Ser Asp Arg Cys Ser Asp Tyr Ile Asn Pro Glu His Lys Lys
210              215              220
Thr Ile Lys Ala Leu Gln Asp Ala Gly Tyr Leu Lys
225              230              235

```

<210> 343
 <211> 86
 <212> PRT
 <213> E. Coli

```

      <400> 343
Met Leu Ala Ile Ser Ser Asn Leu Ser Lys Met Ile Ile Phe Ile Phe
1              5              10              15
Ala Ile Ile Ile Ile Val Val Leu Cys Val Ile Thr Tyr Leu Tyr Leu
      20              25              30
Tyr Lys Asp Glu Ser Leu Val Ser Lys His Tyr Ile Asn Tyr Met Ala
      35              40              45
Ile Pro Glu Asn Asp Gly Val Phe Thr Trp Leu Pro Asp Phe Phe Pro
      50              55              60
His Val Ala Val Asp Ile Ser Ile Tyr Thr Asn Val Glu Asp Asp Tyr
65              70              75              80
Phe Phe Leu Ile Phe Pro
      85

```

<210> 344
 <211> 63
 <212> PRT
 <213> E. Coli

```

      <400> 344
Met Arg Ala Arg Glu Gln Val Ala Lys Ile Val Ser Lys Asn Asp Pro
1              5              10              15
Asp Thr Lys Lys Val Trp Cys Lys Tyr Gly Lys Ile Pro Gly Gln Gly
      20              25              30
Asp Gly Val Asn Leu Phe Phe Val Gly Glu Ile Asn Val Thr His Tyr
      35              40              45
Phe Ile Thr Asn Ile Gly Ala Gly Leu Pro Asp Ala Cys Ala Glu
50              55              60

```

<210> 345
 <211> 167
 <212> PRT
 <213> E. Coli

```

      <400> 345
Met Pro Gly Asn Ser Pro His Tyr Gly Arg Trp Pro Gln His Asp Phe
1              5              10              15

```

Thr Ser Leu Lys Lys Leu Arg Pro Gln Ser Val Thr Ser Arg Ile Gln
 20 25 30
 Pro Gly Ser Asp Val Ile Val Cys Ala Glu Met Asp Glu Gln Trp Gly
 35 40 45
 Tyr Val Gly Ala Lys Ser Arg Gln Arg Trp Leu Phe Tyr Ala Tyr Asp
 50 55 60
 Ser Leu Arg Lys Thr Val Val Ala His Val Phe Gly Glu Arg Thr Met
 65 70 75 80
 Ala Thr Leu Gly Arg Leu Met Ser Leu Leu Ser Pro Phe Asp Val Val
 85 90 95
 Ile Trp Met Thr Asp Gly Trp Pro Leu Tyr Glu Ser Arg Leu Lys Gly
 100 105 110
 Lys Leu His Val Ile Ser Lys Arg Tyr Thr Gln Arg Ile Glu Arg His
 115 120 125
 Asn Leu Asn Leu Arg Gln His Leu Ala Arg Leu Gly Arg Lys Ser Leu
 130 135 140
 Ser Phe Ser Lys Ser Val Glu Leu His Asp Lys Val Ile Gly His Tyr
 145 150 155 160
 Leu Asn Ile Lys His Tyr Gln
 165

<210> 346
 <211> 91
 <212> PRT
 <213> E. Coli

<400> 346
 Met Ala Ser Val Ser Ile Ser Cys Pro Ser Cys Ser Ala Thr Asp Gly
 1 5 10 15
 Val Val Arg Asn Gly Lys Ser Thr Ala Gly His Gln Arg Tyr Leu Cys
 20 25 30
 Ser His Cys Arg Lys Thr Trp Gln Leu Gln Phe Thr Tyr Thr Ala Ser
 35 40 45
 Gln Pro Gly Thr His Gln Lys Ile Ile Asp Met Ala Met Asn Gly Val
 50 55 60
 Gly Cys Arg Ala Thr Ala Arg Ile Met Gly Val Gly Leu Asn Thr Ile
 65 70 75 80
 Leu Arg His Leu Lys Asn Ser Gly Arg Ser Arg
 85 90

<210> 347
 <211> 138
 <212> PRT
 <213> E. Coli

<400> 347
 Met Met Thr Lys Thr Gln Ile Asn Lys Leu Ile Lys Met Met Asn Asp
 1 5 10 15
 Leu Asp Tyr Pro Phe Glu Ala Pro Leu Lys Glu Ser Phe Ile Glu Ser
 20 25 30
 Ile Ile Gln Ile Glu Phe Asn Ser Asn Ser Thr Asn Cys Leu Glu Lys
 35 40 45
 Leu Cys Asn Glu Val Ser Ile Leu Phe Lys Asn Gln Pro Asp Tyr Leu
 50 55 60
 Thr Phe Leu Arg Ala Met Asp Gly Phe Glu Val Asn Gly Leu Arg Leu
 65 70 75 80
 Phe Ser Leu Ser Ile Pro Glu Pro Ser Val Lys Asn Leu Phe Ala Val
 85 90 95

Asn Glu Phe Tyr Arg Asn Asn Asp Asp Phe Ile Asn Pro Asp Leu Gln
 100 105 110
 Glu Arg Leu Val Ile Gly Asp Tyr Ser Ile Ser Ile Phe Thr Tyr Asp
 115 120 125
 Ile Lys Gly Asp Ala Ala Asn Leu Leu Ile
 130 135

<210> 348
 <211> 392
 <212> PRT
 <213> E. Coli

<400> 348
 Met Ser Asn Ile Val Tyr Leu Thr Val Thr Gly Glu Gln Gln Gly Ser
 1 5 10 15
 Ile Ser Ala Gly Cys Gly Thr Ser Glu Ser Thr Gly Asn Arg Trp Gln
 20 25 30
 Ser Gly His Glu Asp Glu Ile Phe Thr Phe Ser Leu Leu Asn Asn Ile
 35 40 45
 Asn Asn Thr Gly Leu Gly Ser Gln Phe His Gly Ile Thr Phe Cys Lys
 50 55 60
 Leu Ile Asp Lys Ser Thr Pro Leu Phe Ile Asn Ser Ile Asn Asn Asn
 65 70 75 80
 Glu Gln Leu Phe Met Gly Phe Asp Phe Tyr Arg Ile Asn Arg Phe Gly
 85 90 95
 Arg Leu Glu Lys Tyr Tyr Tyr Ile Gln Leu Arg Gly Ala Phe Leu Ser
 100 105 110
 Ala Ile His His Gln Ile Ile Glu Asn Gln Leu Asp Thr Glu Thr Ile
 115 120 125
 Thr Ile Ser Tyr Glu Phe Ile Leu Cys Gln His Leu Ile Ala Asn Thr
 130 135 140
 Glu Phe Ser Tyr Leu Ala Leu Pro Glu Asn Tyr Asn Arg Leu Phe Leu
 145 150 155 160
 Pro Asn Ser Lys Asn Gln Thr Asn Asn Arg Phe Lys Thr Leu Asn Ser
 165 170 175
 Lys Ala Ile Gly Arg Leu Leu Ala Ala Gly Gly Val Tyr Asn Gly Asn
 180 185 190
 Ile Glu Gly Phe Arg Asp Thr Ala Glu Lys Leu Gly Gly Asp Ala Ile
 195 200 205
 Lys Gly Tyr Asp Gln Ile Leu Asn Glu Lys Thr Ala Gly Ile Ala Ile
 210 215 220
 Ala Thr Ala Ser Ile Leu Leu Thr Lys Arg Ser Asn Val Asp Thr Tyr
 225 230 235 240
 Thr Glu Ile Asn Ser Tyr Leu Gly Lys Leu Arg Gly Gln Gln Lys Leu
 245 250 255
 Leu Asp Gly Ile Asp Ile Ile Glu Ile Ile Tyr Ile Lys Arg Pro Ser
 260 265 270
 Lys Asp Leu Ala Asn Leu Arg Lys Glu Phe Asn Lys Thr Val Arg Lys
 275 280 285
 Asn Phe Leu Ile Lys Leu Ala Lys Thr Ser Glu Ala Ser Gly Arg Phe
 290 295 300
 Asn Ala Glu Asp Leu Leu Arg Met Arg Lys Gly Asn Val Pro Leu Asn
 305 310 315 320
 Tyr Asn Val His His Lys Leu Ser Leu Asp Asp Gly Gly Thr Asn Asp
 325 330 335
 Phe Glu Asn Leu Val Leu Ile Glu Asn Glu Pro Tyr His Lys Val Phe
 340 345 350
 Thr Asn Met Gln Ser Arg Ile Ala Lys Gly Ile Leu Val Gly Glu Ser
 355 360 365
 Lys Ile Thr Pro Trp Ala Ile Pro Ser Gly Ser Ile Tyr Pro Pro Met

370 375 380
 Lys Asn Ile Met Asp His Thr Lys
 385 390

<210> 349
 <211> 221
 <212> PRT
 <213> E. Coli

<400> 349
 Met Val Leu Ala Leu Asn Tyr Asn Met His Gly Val Asn Ile Arg Ser
 1 5 10 15
 Glu Asn Ala Ala Lys Pro His Thr Met Pro Ser Arg Tyr Leu Cys Glu
 20 25 30
 Tyr Ile Arg Ser Ile Glu Lys Asn Gly His Ala Leu Asp Phe Gly Cys
 35 40 45
 Gly Lys Leu Arg Tyr Ser Asp Glu Leu Ile Ser Lys Phe Asp Glu Val
 50 55 60
 Thr Phe Leu Asp Ser Lys Arg Gln Leu Glu Arg Glu Gln Ile Ile Arg
 65 70 75 80
 Gly Ile Lys Thr Lys Ile Ile Asp Tyr Val Pro Arg Tyr Tyr Lys Asn
 85 90 95
 Ala Asn Thr Val Ala Phe Glu Asp Val Asp Lys Ile Ile Gly Gly Tyr
 100 105 110
 Asp Phe Ile Leu Cys Ser Asn Val Leu Ser Ala Val Pro Cys Arg Asp
 115 120 125
 Thr Ile Asp Lys Ile Val Leu Ser Ile Lys Arg Leu Leu Lys Ser Gly
 130 135 140
 Gly Glu Thr Leu Ile Val Asn Gln Tyr Lys Ser Ser Tyr Phe Lys Lys
 145 150 155 160
 Tyr Glu Thr Gly Arg Lys His Leu Tyr Gly Tyr Ile Tyr Lys Asn Ser
 165 170 175
 Lys Ser Val Ser Tyr Tyr Gly Leu Leu Asp Glu Leu Ala Val Gln Glu
 180 185 190
 Ile Cys Ser Ser His Gly Leu Glu Ile Leu Lys Ser Trp Ser Lys Ala
 195 200 205
 Gly Ser Ser Tyr Val Thr Val Gly Ser Cys Asn Ala Ile
 210 215 220

<210> 350
 <211> 234
 <212> PRT
 <213> E. Coli

<400> 350
 Met Asn Asn Met Phe Glu Pro Pro Lys Asn Tyr Asn Glu Met Leu Pro
 1 5 10 15
 Lys Leu His Lys Ala Thr Phe Leu Asn Thr Leu Ile Tyr Cys Ile Leu
 20 25 30
 Leu Val Ile Tyr Glu Tyr Ile Pro Leu Ile Thr Leu Pro Thr Lys Tyr
 35 40 45
 Val Pro Pro Ile Lys Asp His Glu Ser Phe Ile Asn Trp Ala Leu Ser
 50 55 60
 Phe Gly Ile Leu Pro Cys Ala Phe Ala Ile Phe Ala Tyr Leu Ile Ser
 65 70 75 80
 Gly Ala Leu Asp Leu His Asn Asn Ala Ala Lys Leu Leu Arg Val Arg
 85 90 95
 Tyr Leu Trp Asp Lys His Leu Ile Ile Lys Pro Leu Ser Arg Arg Ala

100 105 110
 Gly Val Asn Arg Lys Leu Asn Lys Asp Glu Ala His Asn Val Met Ser
 115 120 125
 Asn Leu Tyr Tyr Pro Glu Val Arg Lys Ile Glu Asp Lys His Tyr Ile
 130 135 140
 Glu Leu Phe Trp Asn Lys Val Tyr Tyr Phe Trp Ile Phe Phe Glu Phe
 145 150 155 160
 Ser Ile Ile Ala Leu Ile Ser Phe Leu Ile Ile Phe Phe Cys Lys Gln
 165 170 175
 Met Asp Ile Phe His Val Glu Gly Ser Leu Leu Ser Leu Phe Phe Phe
 180 185 190
 Val Ile Leu Ser Phe Ser Val Ser Gly Ile Ile Phe Ala Leu Thr Val
 195 200 205
 Lys Pro Arg Thr Glu Ser Gln Val Gly Lys Ile Pro Asp Asp Lys Ile
 210 215 220
 Lys Glu Phe Phe Thr Lys Asn Asn Ile Asn
 225 230

<210> 351
 <211> 94
 <212> PRT
 <213> E. Coli

<400> 351
 Met Phe Thr Ile Asn Ala Glu Val Arg Lys Glu Gln Gly Lys Gly Ala
 1 5 10 15
 Ser Arg Arg Leu Arg Ala Ala Asn Lys Phe Pro Ala Ile Ile Tyr Gly
 20 25 30
 Gly Lys Glu Ala Pro Leu Ala Ile Glu Leu Asp His Asp Lys Val Met
 35 40 45
 Asn Met Gln Ala Lys Ala Glu Phe Tyr Ser Glu Val Leu Thr Ile Val
 50 55 60
 Val Asp Gly Lys Glu Ile Lys Val Lys Ala Gln Asp Val Gln Arg His
 65 70 75 80
 Pro Tyr Lys Pro Lys Leu Gln His Ile Asp Phe Val Arg Ala
 85 90

<210> 352
 <211> 658
 <212> PRT
 <213> E. Coli

<400> 352
 Met Val Leu Phe Tyr Arg Ala His Trp Arg Asp Tyr Lys Asn Asp Gln
 1 5 10 15
 Val Arg Ile Met Met Asn Leu Thr Thr Leu Thr His Arg Asp Ala Leu
 20 25 30
 Cys Leu Asn Ala Arg Phe Thr Ser Arg Glu Glu Ala Ile His Ala Leu
 35 40 45
 Thr Gln Arg Leu Ala Ala Leu Gly Lys Ile Ser Ser Thr Glu Gln Phe
 50 55 60
 Leu Glu Glu Val Tyr Arg Arg Glu Ser Leu Gly Pro Thr Ala Leu Gly
 65 70 75 80
 Glu Gly Leu Ala Val Pro His Gly Lys Thr Ala Ala Val Lys Glu Ala
 85 90 95
 Ala Phe Ala Val Ala Thr Leu Ser Glu Pro Leu Gln Trp Glu Gly Val
 100 105 110
 Asp Gly Pro Glu Ala Val Asp Leu Val Val Leu Leu Ala Ile Pro Pro

115	120	125
Asn Glu Ala Gly Thr Thr	His Met Gln Leu Leu Thr	Ala Leu Thr Thr
130	135	140
Arg Leu Ala Asp Asp Glu Ile Arg Ala Arg Ile Gln Ser Ala Thr Thr		
145	150	155
Pro Asp Glu Leu Leu Ser Ala Leu Asp Asp Lys Gly Gly Thr Gln Pro		160
165	170	175
Ser Ala Ser Phe Ser Asn Ala Pro Thr Ile Val Cys Val Thr Ala Cys		
180	185	190
Pro Ala Gly Ile Ala His Thr Tyr Met Ala Ala Glu Tyr Leu Glu Lys		
195	200	205
Ala Gly Arg Lys Leu Gly Val Asn Val Tyr Val Glu Lys Gln Gly Ala		
210	215	220
Asn Gly Ile Glu Gly Arg Leu Thr Ala Asp Gln Leu Asn Ser Ala Thr		
225	230	235
Ala Cys Ile Phe Ala Ala Glu Val Ala Ile Lys Glu Ser Glu Arg Phe		240
245	250	255
Asn Gly Ile Pro Ala Leu Ser Val Pro Val Ala Glu Pro Ile Arg His		
260	265	270
Ala Glu Ala Leu Ile Gln Gln Ala Leu Thr Leu Lys Arg Ser Asp Glu		
275	280	285
Thr Arg Thr Val Gln Gln Asp Thr Gln Pro Val Lys Ser Val Lys Thr		
290	295	300
Glu Leu Lys Gln Ala Leu Ser Gly Ile Ser Phe Ala Val Pro Leu		
305	310	315
Ile Val Ala Gly Gly Thr Val Leu Ala Val Ala Val Leu Leu Ser Gln		
325	330	335
Ile Phe Gly Leu Gln Asp Leu Phe Asn Glu Glu Asn Ser Trp Leu Trp		
340	345	350
Met Tyr Arg Lys Leu Gly Gly Gly Leu Leu Gly Ile Leu Met Val Pro		
355	360	365
Val Leu Ala Ala Tyr Thr Ala Tyr Ser Leu Ala Asp Lys Pro Ala Leu		
370	375	380
Ala Pro Gly Phe Ala Ala Gly Leu Ala Ala Asn Met Ile Gly Ser Gly		
385	390	395
Phe Leu Gly Ala Val Val Gly Gly Leu Ile Ala Gly Tyr Leu Met Arg		
405	410	415
Trp Val Lys Asn His Leu Arg Leu Ser Ser Lys Phe Asn Gly Phe Leu		
420	425	430
Thr Phe Tyr Leu Tyr Pro Val Leu Gly Thr Leu Gly Ala Gly Ser Leu		
435	440	445
Met Leu Phe Val Val Gly Glu Pro Val Ala Trp Ile Asn Asn Ser Leu		
450	455	460
Thr Ala Trp Leu Asn Gly Leu Ser Gly Ser Asn Ala Leu Leu Leu Gly		
465	470	475
Ala Ile Leu Gly Phe Met Cys Ser Phe Asp Leu Gly Gly Pro Val Asn		
485	490	495
Lys Ala Ala Tyr Ala Phe Cys Leu Gly Ala Met Ala Asn Gly Val Tyr		
500	505	510
Gly Pro Tyr Ala Ile Phe Ala Ser Val Lys Met Val Ser Ala Phe Thr		
515	520	525
Val Thr Ala Ser Thr Met Leu Ala Pro Arg Leu Phe Lys Glu Phe Glu		
530	535	540
Ile Glu Thr Gly Lys Ser Thr Trp Leu Leu Gly Leu Ala Gly Ile Thr		
545	550	555
Glu Gly Ala Ile Pro Met Ala Ile Glu Asp Pro Leu Arg Val Ile Gly		
565	570	575
Ser Phe Val Leu Gly Ser Met Val Thr Gly Ala Ile Val Gly Ala Met		
580	585	590
Asn Ile Gly Leu Ser Thr Pro Gly Ala Gly Ile Phe Ser Leu Phe Leu		
595	600	605

Leu His Asp Asn Gly Ala Gly Gly Val Met Ala Ala Ile Gly Trp Phe
 610 615 620
 Gly Ala Ala Leu Val Gly Ala Ala Ile Ser Thr Ala Ile Leu Leu Met
 625 630 635 640
 Trp Arg Arg His Ala Val Lys His Gly Asn Tyr Leu Thr Asp Gly Val
 645 650 655
 Met Pro

<210> 353
 <211> 877
 <212> PRT
 <213> E. Coli

<400> 353
 Met Lys Ala Val Ser Arg Val His Ile Thr Pro His Met His Trp Asp
 1 5 10 15
 Arg Glu Trp Tyr Phe Thr Thr Glu Glu Ser Arg Ile Leu Leu Val Asn
 20 25 30
 Asn Met Glu Glu Ile Leu Cys Arg Leu Glu Gln Asp Asn Glu Tyr Lys
 35 40 45
 Tyr Tyr Val Leu Asp Gly Gln Thr Ala Ile Leu Glu Asp Tyr Phe Ala
 50 55 60
 Val Lys Pro Glu Asn Lys Asp Arg Val Lys Lys Gln Val Glu Ala Gly
 65 70 75 80
 Lys Leu Ile Ile Gly Pro Trp Tyr Thr Gln Thr Asp Thr Thr Ile Val
 85 90 95
 Ser Ala Glu Ser Ile Val Arg Asn Leu Met Tyr Gly Met Arg Asp Cys
 100 105 110
 Leu Ala Phe Gly Glu Pro Met Lys Ile Gly Tyr Leu Pro Asp Ser Phe
 115 120 125
 Gly Met Ser Gly Gln Leu Pro His Ile Tyr Asn Gly Phe Gly Ile Thr
 130 135 140
 Arg Thr Met Phe Trp Arg Gly Cys Ser Glu Arg His Gly Thr Asp Lys
 145 150 155 160
 Thr Glu Phe Leu Trp Gln Ser Ser Asp Gly Ser Glu Val Thr Ala Gln
 165 170 175
 Val Leu Pro Leu Gly Tyr Ala Ile Gly Lys Tyr Leu Pro Ala Asp Glu
 180 185 190
 Asn Gly Leu Arg Lys Arg Leu Asp Ser Tyr Phe Asp Val Leu Glu Lys
 195 200 205
 Ala Ser Val Thr Lys Glu Ile Leu Leu Pro Asn Gly His Asp Gln Met
 210 215 220
 Pro Leu Gln Gln Asn Ile Phe Glu Val Met Asp Lys Leu Arg Glu Ile
 225 230 235 240
 Tyr Pro Gln Arg Lys Phe Val Met Ser Arg Phe Glu Glu Val Phe Glu
 245 250 255
 Lys Ile Glu Ala Gln Arg Asp Asn Leu Ala Thr Leu Lys Gly Glu Phe
 260 265 270
 Ile Asp Gly Lys Tyr Met Arg Val His Arg Thr Ile Gly Ser Thr Arg
 275 280 285
 Met Asp Ile Lys Ile Ala His Ala Arg Ile Glu Asn Lys Ile Val Asn
 290 295 300
 Leu Leu Glu Pro Leu Ala Thr Leu Ala Trp Thr Leu Gly Phe Glu Tyr
 305 310 315 320
 His His Gly Leu Leu Glu Lys Met Trp Lys Glu Ile Leu Lys Asn His
 325 330 335
 Ala His Asp Ser Ile Gly Cys Cys Ser Asp Lys Val His Arg Glu
 340 345 350
 Ile Val Ala Arg Phe Glu Leu Ala Glu Asp Met Ala Asp Asn Leu Ile

```

      355      360      365
Arg Phe Tyr Met Arg Lys Ile Ala Asp Asn Met Pro Gln Ser Asp Ala
370      375      380
Asp Lys Leu Val Leu Phe Asn Leu Met Pro Trp Pro Arg Glu Glu Val
385      390      395      400
Ile Asn Thr Thr Val Arg Leu Arg Ala Ser Gln Phe Asn Leu Arg Asp
405      410      415
Asp Arg Gly Gln Pro Val Pro Tyr Phe Ile Arg His Ala Arg Glu Ile
420      425      430
Asp Pro Gly Leu Ile Asp Arg Gln Ile Val His Tyr Gly Asn Tyr Asp
435      440      445
Pro Phe Met Glu Phe Asp Ile Gln Ile Asn Gln Ile Val Pro Ser Met
450      455      460
Gly Tyr Arg Thr Leu Tyr Ile Glu Ala Asn Gln Pro Gly Asn Val Ile
465      470      475      480
Ala Ala Lys Ser Asp Ala Glu Gly Ile Leu Glu Asn Ala Phe Trp Gln
485      490      495
Ile Ala Leu Asn Glu Asp Gly Ser Leu Gln Leu Val Asp Lys Asp Ser
500      505      510
Gly Val Arg Tyr Asp Arg Val Leu Gln Ile Glu Glu Ser Ser Asp Asp
515      520      525
Gly Asp Glu Tyr Asp Tyr Ser Pro Ala Lys Glu Glu Trp Val Ile Thr
530      535      540
Ala Ala Asn Ala Lys Pro Gln Cys Asp Ile Ile His Glu Ala Trp Gln
545      550      555      560
Ser Arg Ala Val Ile Arg Tyr Asp Met Ala Val Pro Leu Asn Leu Ser
565      570      575
Glu Arg Ser Ala Arg Gln Ser Thr Gly Arg Val Gly Val Val Leu Val
580      585      590
Val Thr Leu Ser His Asn Ser Arg Arg Ile Asp Val Asp Ile Asn Leu
595      600      605
Asp Asn Gln Ala Asp Asp His Arg Leu Arg Val Leu Val Pro Thr Pro
610      615      620
Phe Asn Thr Asp Ser Val Leu Ala Asp Thr Gln Phe Gly Ser Leu Thr
625      630      635      640
Arg Pro Val Asn Asp Ser Ala Met Asn Asn Trp Gln Gln Glu Gly Trp
645      650      655
Lys Glu Ala Pro Val Pro Val Trp Asn Met Leu Asn Tyr Val Ala Leu
660      665      670
Gln Glu Gly Arg Asn Gly Met Ala Val Phe Ser Glu Gly Leu Arg Glu
675      680      685
Phe Glu Val Ile Gly Glu Glu Lys Lys Thr Phe Ala Ile Thr Leu Leu
690      695      700
Arg Gly Val Gly Leu Leu Gly Lys Glu Asp Leu Leu Arg Pro Gly
705      710      715      720
Arg Pro Ser Gly Ile Lys Met Pro Val Pro Asp Ser Gln Leu Arg Gly
725      730      735
Leu Leu Ser Cys Arg Leu Ser Leu Leu Ser Tyr Thr Gly Thr Pro Thr
740      745      750
Ala Ala Gly Val Ala Gln Gln Ala Arg Ala Trp Leu Thr Pro Val Gln
755      760      765
Cys Tyr Asn Lys Ile Pro Trp Asp Val Met Lys Leu Asn Lys Ala Gly
770      775      780
Phe Asn Val Pro Glu Ser Tyr Ser Leu Leu Lys Met Pro Pro Val Gly
785      790      795      800
Cys Leu Ile Ser Ala Leu Lys Lys Ala Glu Asp Arg Gln Glu Val Ile
805      810      815
Leu Arg Leu Phe Asn Pro Ala Glu Ser Ala Thr Cys Asp Ala Thr Val
820      825      830
Ala Phe Ser Arg Glu Val Ile Ser Cys Ser Glu Thr Met Met Asp Glu
835      840      845

```

His Ile Thr Thr Glu Glu Asn Gln Gly Ser Asn Leu Ser Gly Pro Phe
 850 855 860
 Leu Pro Gly Gln Ser Arg Thr Phe Ser Tyr Arg Leu Ala
 865 870 875

<210> 354
 <211> 523
 <212> PRT
 <213> E. Coli

<400> 354
 Met Met Leu Asp Ile Val Glu Leu Ser Arg Leu Gln Phe Ala Leu Thr
 1 5 10 15
 Ala Met Tyr His Phe Leu Phe Val Pro Leu Thr Leu Gly Met Ala Phe
 20 25 30
 Leu Leu Ala Ile Met Glu Thr Val Tyr Val Leu Ser Gly Lys Gln Ile
 35 40 45
 Tyr Lys Asp Met Thr Lys Phe Trp Gly Lys Leu Phe Gly Ile Asn Phe
 50 55 60
 Ala Leu Gly Val Ala Thr Gly Leu Thr Met Glu Phe Gln Phe Gly Thr
 65 70 75 80
 Asn Trp Ser Tyr Tyr Ser His Tyr Val Gly Asp Ile Phe Gly Ala Pro
 85 90 95
 Leu Ala Ile Glu Gly Leu Met Ala Phe Phe Leu Glu Ser Thr Phe Val
 100 105 110
 Gly Leu Phe Phe Phe Gly Trp Asp Arg Leu Gly Lys Val Gln His Met
 115 120 125
 Cys Val Thr Trp Leu Val Ala Leu Gly Ser Asn Leu Ser Ala Leu Trp
 130 135 140
 Ile Leu Val Ala Asn Gly Trp Met Gln Asn Pro Ile Ala Ser Asp Phe
 145 150 155 160
 Asn Phe Glu Thr Met Arg Met Glu Met Val Ser Phe Ser Glu Leu Val
 165 170 175
 Leu Asn Pro Val Ala Gln Val Lys Phe Val His Thr Val Ala Ser Gly
 180 185 190
 Tyr Val Thr Gly Ala Met Phe Ile Leu Gly Ile Ser Ala Trp Tyr Met
 195 200 205
 Leu Lys Gly Arg Asp Phe Ala Phe Ala Lys Arg Ser Phe Ala Ile Ala
 210 215 220
 Ala Ser Phe Gly Met Ala Ala Val Leu Ser Val Ile Val Leu Gly Asp
 225 230 235 240
 Glu Ser Gly Tyr Glu Met Gly Asp Val Gln Lys Thr Lys Leu Ala Ala
 245 250 255
 Ile Glu Ala Glu Trp Glu Thr Gln Pro Ala Pro Ala Ala Phe Thr Leu
 260 265 270
 Phe Gly Ile Pro Asp Gln Glu Glu Thr Asn Lys Phe Ala Ile Gln
 275 280 285
 Ile Pro Tyr Ala Leu Gly Ile Ile Ala Thr Arg Ser Val Asp Thr Pro
 290 295 300
 Val Ile Gly Leu Lys Glu Leu Met Val Gln His Glu Arg Ile Arg
 305 310 315 320
 Asn Gly Met Lys Ala Tyr Ser Leu Leu Glu Gln Leu Arg Ser Gly Ser
 325 330 335
 Thr Asp Gln Ala Val Arg Asp Gln Phe Asn Ser Met Lys Lys Asp Leu
 340 345 350
 Gly Tyr Gly Leu Leu Lys Arg Tyr Thr Pro Asn Val Ala Asp Ala
 355 360 365
 Thr Glu Ala Gln Ile Gln Gln Ala Thr Lys Asp Ser Ile Pro Arg Val
 370 375 380
 Ala Pro Leu Tyr Phe Ala Phe Arg Ile Met Val Ala Cys Gly Phe Leu

```

385          390          395          400
Leu Leu Ala Ile Ile Ala Leu Ser Phe Trp Ser Val Ile Arg Asn Arg
          405          410          415
Ile Gly Glu Lys Lys Trp Leu Leu Arg Ala Ala Leu Tyr Gly Ile Pro
          420          425          430
Leu Pro Trp Ile Ala Val Glu Ala Gly Trp Phe Val Ala Glu Tyr Gly
          435          440          445
Arg Gln Pro Trp Ala Ile Gly Glu Val Leu Pro Thr Ala Val Ala Asn
          450          455          460
Ser Ser Leu Thr Ala Gly Asp Leu Ile Phe Ser Met Val Leu Ile Cys
          465          470          475          480
Gly Leu Tyr Thr Leu Phe Leu Val Ala Glu Leu Phe Leu Met Phe Lys
          485          490          495
Phe Ala Arg Leu Gly Pro Ser Ser Leu Lys Thr Gly Arg Tyr His Phe
          500          505          510
Glu Gln Ser Ser Thr Thr Thr Gln Pro Ala Arg
          515          520

```

```

<210> 355
<211> 379
<212> PRT
<213> E. Coli

```

```

<400> 355
Met Ile Asp Tyr Glu Val Leu Arg Phe Ile Trp Trp Leu Leu Val Gly
1          5          10          15
Val Leu Leu Ile Gly Phe Ala Val Thr Asp Gly Phe Asp Met Gly Val
          20          25          30
Gly Met Leu Thr Arg Phe Leu Gly Arg Asn Asp Thr Glu Arg Arg Ile
          35          40          45
Met Ile Asn Ser Ile Ala Pro His Trp Asp Gly Asn Gln Val Trp Leu
          50          55          60
Ile Thr Ala Gly Gly Ala Leu Phe Ala Ala Trp Pro Met Val Tyr Ala
65          70          75          80
Ala Ala Phe Ser Gly Phe Tyr Val Ala Met Ile Leu Val Leu Ala Ser
          85          90          95
Leu Phe Phe Arg Pro Val Gly Phe Asp Tyr Arg Ser Lys Ile Glu Glu
          100          105          110
Thr Arg Trp Arg Asn Met Trp Asp Trp Gly Ile Phe Ile Gly Ser Phe
          115          120          125
Val Pro Pro Leu Val Ile Gly Val Ala Phe Gly Asn Leu Leu Gln Gly
          130          135          140
Val Pro Phe Asn Val Asp Glu Tyr Leu Arg Leu Tyr Tyr Thr Gly Asn
145          150          155          160
Phe Phe Gln Leu Leu Asn Pro Phe Gly Leu Leu Ala Gly Val Val Ser
          165          170          175
Val Gly Met Ile Ile Thr Gln Gly Ala Thr Tyr Leu Gln Met Arg Thr
          180          185          190
Val Gly Glu Leu His Leu Arg Thr Arg Ala Thr Ala Gln Val Ala Ala
          195          200          205
Leu Val Thr Leu Val Cys Phe Ala Leu Ala Gly Val Trp Val Met Tyr
210          215          220
Gly Ile Asp Gly Tyr Val Val Lys Ser Thr Met Asp His Tyr Ala Ala
225          230          235          240
Ser Asn Pro Leu Asn Lys Glu Val Val Arg Glu Ala Gly Ala Trp Leu
          245          250          255
Val Asn Phe Asn Asn Thr Pro Ile Leu Trp Ala Ile Pro Ala Leu Gly
          260          265          270
Val Val Leu Pro Leu Leu Thr Ile Leu Thr Ala Arg Met Asp Lys Ala
          275          280          285

```

Ala Trp Ala Phe Val Phe Ser Ser Leu Thr Leu Ala Cys Ile Ile Leu
 290 295 300
 Thr Ala Gly Ile Ala Met Phe Pro Phe Val Met Pro Ser Ser Thr Met
 305 310 315 320
 Met Asn Ala Ser Leu Thr Met Trp Asp Ala Thr Ser Ser Gln Leu Thr
 325 330 335
 Leu Asn Val Met Thr Trp Val Ala Val Val Leu Val Pro Ile Ile Leu
 340 345 350
 Leu Tyr Thr Ala Trp Cys Tyr Trp Lys Met Phe Gly Arg Ile Thr Lys
 355 360 365
 Glu Asp Ile Glu Arg Asn Thr His Ser Leu Tyr
 370 375

<210> 356
 <211> 456
 <212> PRT
 <213> E. Coli

<400> 356
 Met Glu Leu Ser Ser Leu Thr Ala Val Ser Pro Val Asp Gly Arg Tyr
 1 5 10 15
 Gly Asp Lys Val Ser Ala Leu Arg Gly Ile Phe Ser Glu Tyr Gly Leu
 20 25 30
 Leu Lys Phe Arg Val Gln Val Glu Val Arg Trp Leu Gln Lys Leu Ala
 35 40 45
 Ala His Ala Ala Ile Lys Glu Val Pro Ala Phe Ala Ala Asp Ala Ile
 50 55 60
 Gly Tyr Leu Asp Ala Ile Val Ala Ser Phe Ser Glu Glu Asp Ala Ala
 65 70 75 80
 Arg Ile Lys Thr Ile Glu Arg Thr Thr Asn His Asp Val Lys Ala Val
 85 90 95
 Glu Tyr Phe Leu Lys Glu Lys Val Ala Glu Ile Pro Glu Leu His Ala
 100 105 110
 Val Ser Glu Phe Ile His Phe Ala Cys Thr Ser Glu Asp Ile Asn Asn
 115 120 125
 Leu Ser His Ala Leu Met Leu Lys Thr Ala Arg Asp Glu Val Ile Leu
 130 135 140
 Pro Tyr Trp Arg Gln Leu Ile Asp Gly Ile Lys Asp Leu Ala Val Gln
 145 150 155 160
 Tyr Arg Asp Ile Pro Leu Leu Ser Arg Thr His Gly Gln Pro Ala Thr
 165 170 175
 Pro Ser Thr Ile Gly Lys Glu Met Ala Asn Val Ala Tyr Arg Met Glu
 180 185 190
 Arg Gln Tyr Arg Gln Leu Asn Gln Val Glu Ile Leu Gly Lys Ile Asn
 195 200 205
 Gly Ala Val Gly Asn Tyr Asn Ala His Ile Ala Ala Tyr Pro Glu Val
 210 215 220
 Asp Trp His Gln Phe Ser Glu Glu Phe Val Thr Ser Leu Gly Ile Gln
 225 230 235 240
 Trp Asn Pro Tyr Thr Thr Gln Ile Glu Pro His Asp Tyr Ile Ala Glu
 245 250 255
 Leu Phe Asp Cys Val Ala Arg Phe Asn Thr Ile Leu Ile Asp Phe Asp
 260 265 270
 Arg Asp Val Trp Gly Tyr Ile Ala Leu Asn His Phe Lys Gln Lys Thr
 275 280 285
 Ile Ala Gly Glu Ile Gly Ser Ser Thr Met Pro His Lys Val Asn Pro
 290 295 300
 Ile Asp Phe Glu Asn Ser Glu Gly Asn Leu Gly Leu Ser Asn Ala Val
 305 310 315 320
 Leu Gln His Leu Ala Ser Lys Leu Pro Val Ser Arg Trp Gln Arg Asp


```

          325          330          335
Leu Thr Asp Ser Thr Val Leu Arg Asn Leu Gly Val Gly Ile Gly Tyr
          340          345          350
Ala Leu Ile Ala Tyr Gln Ser Thr Leu Lys Gly Val Ser Lys Leu Glu
          355          360          365
Val Asn Arg Asp His Leu Leu Asp Glu Leu Asp His Asn Trp Glu Val
          370          375          380
Leu Ala Glu Pro Ile Gln Thr Val Met Arg Arg Tyr Gly Ile Glu Lys
          385          390          395          400
Pro Tyr Glu Lys Leu Lys Glu Leu Thr Arg Gly Lys Arg Val Asp Ala
          405          410          415
Glu Gly Met Lys Gln Phe Ile Asp Gly Leu Ala Leu Pro Glu Glu Glu
          420          425          430
Lys Ala Arg Leu Lys Ala Met Thr Pro Ala Asn Tyr Ile Gly Arg Ala
          435          440          445
Ile Thr Met Val Asp Glu Leu Lys
          450          455

```

<210> 357
 <211> 61
 <212> PRT
 <213> E. Coli

```

          <400> 357
Met Leu Ile Leu Thr Arg Arg Val Gly Glu Thr Leu Met Ile Gly Asp
  1          5          10          15
Glu Val Thr Val Thr Val Leu Gly Val Lys Gly Asn Gln Val Arg Ile
          20          25          30
Gly Val Asn Ala Pro Lys Glu Val Ser Val His Arg Glu Glu Ile Tyr
          35          40          45
Gln Arg Ile Gln Ala Glu Lys Ser Gln Gln Ser Ser Tyr
          50          55          60

```

<210> 358
 <211> 83
 <212> RNA
 <213> E. Coli

```

          <400> 358
ggugaggugg ccgagaggcu gaaggcgcuc ccugcuaag ggaguaugcg gucaaaagcu    60
gcauccgggg uucgaauccc cgccuacccg cca                                83

```

<210> 359
 <211> 200
 <212> PRT
 <213> E. Coli

```

          <400> 359
Met Lys Asn Lys Ala Asp Asn Lys Lys Arg Asn Phe Leu Thr His Ser
  1          5          10          15
Glu Ile Glu Ser Leu Leu Lys Ala Ala Asn Thr Gly Pro His Ala Ala
          20          25          30
Arg Asn Tyr Cys Leu Thr Leu Leu Cys Phe Ile His Gly Phe Arg Ala
          35          40          45
Ser Glu Ile Cys Arg Leu Arg Ile Ser Asp Ile Asp Leu Lys Ala Lys
          50          55          60
Cys Ile Tyr Ile His Arg Leu Lys Lys Gly Phe Ser Thr Thr His Pro
          65          70          75          80

```

Leu Leu Asn Lys Glu Val Gln Ala Leu Lys Asn Trp Leu Ser Ile Arg
 85 90 95
 Thr Ser Tyr Pro His Ala Glu Ser Glu Trp Val Phe Leu Ser Arg Lys
 100 105 110
 Gly Asn Pro Leu Ser Arg Gln Gln Phe Tyr His Ile Ile Ser Thr Ser
 115 120 125
 Gly Gly Asn Ala Gly Leu Ser Leu Glu Ile His Pro His Met Leu Arg
 130 135 140
 His Ser Cys Gly Phe Ala Leu Ala Asn Met Gly Ile Asp Thr Arg Leu
 145 150 155 160
 Ile Gln Asp Tyr Leu Gly His Arg Asn Ile Arg His Thr Val Trp Tyr
 165 170 175
 Thr Ala Ser Asn Ala Gly Arg Phe Tyr Gly Ile Trp Asp Arg Ala Arg
 180 185 190
 Gly Arg Gln Arg His Ala Val Leu
 195 200

<210> 360
 <211> 198
 <212> PRT
 <213> E. Coli

<400> 360
 Met Ser Lys Arg Arg Tyr Leu Thr Gly Lys Glu Val Gln Ala Met Met
 1 5 10 15
 Gln Ala Val Cys Tyr Gly Ala Thr Gly Ala Arg Asp Tyr Cys Leu Ile
 20 25 30
 Leu Leu Ala Tyr Arg His Gly Met Arg Ile Ser Glu Leu Leu Asp Leu
 35 40 45
 His Tyr Gln Asp Leu Asp Leu Asn Glu Gly Arg Ile Asn Ile Arg Arg
 50 55 60
 Leu Lys Asn Gly Phe Ser Thr Val His Pro Leu Arg Phe Asp Glu Arg
 65 70 75 80
 Glu Ala Val Glu Arg Trp Thr Gln Glu Arg Ala Asn Trp Lys Gly Ala
 85 90 95
 Asp Arg Thr Asp Ala Ile Phe Ile Ser Arg Arg Gly Ser Arg Leu Ser
 100 105 110
 Arg Gln Gln Ala Tyr Arg Ile Ile Arg Asp Ala Gly Ile Glu Ala Gly
 115 120 125
 Thr Val Thr Gln Thr His Pro His Met Leu Arg His Ala Cys Gly Tyr
 130 135 140
 Glu Leu Ala Glu Arg Gly Ala Asp Thr Arg Leu Ile Gln Asp Tyr Leu
 145 150 155 160
 Gly His Arg Asn Ile Arg His Thr Val Arg Tyr Thr Ala Ser Asn Ala
 165 170 175
 Ala Arg Phe Ala Gly Leu Trp Glu Arg Asn Asn Leu Ile Asn Glu Lys
 180 185 190
 Leu Lys Arg Glu Glu Val
 195

<210> 361
 <211> 182
 <212> PRT
 <213> E. Coli

<400> 361
 Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
 1 5 10 15

Ser Ser Thr Ala Ala Leu Ala Ala Thr Thr Val Asn Gly Gly Thr
 20 25 30
 Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
 35 40 45
 Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
 50 55 60
 Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
 65 70 75 80
 Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
 85 90 95
 Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
 100 105 110
 Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
 115 120 125
 Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
 130 135 140
 Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
 145 150 155 160
 Phe Ala Thr Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr
 165 170 175
 Phe Lys Val Gln Tyr Gln
 180

<210> 362
 <211> 215
 <212> PRT
 <213> E. Coli

<400> 362
 Met Leu Leu Met Arg Met Arg Pro Ser Arg Phe Ser Ile Asn Asn Leu
 1 5 10 15
 Pro Arg Phe Asp Val Ile Thr Gly Arg Asp Ala His Pro Cys Ala
 20 25 30
 Ile Lys Ile Thr Met Lys Arg Lys Arg Leu Phe Leu Leu Ala Ser Leu
 35 40 45
 Leu Pro Met Phe Ala Leu Ala Gly Asn Lys Trp Asn Thr Thr Leu Pro
 50 55 60
 Gly Gly Asn Met Gln Phe Gln Gly Val Ile Ile Ala Glu Thr Cys Arg
 65 70 75 80
 Ile Glu Ala Gly Asp Lys Gln Met Thr Val Asn Met Gly Gln Ile Ser
 85 90 95
 Ser Asn Arg Phe His Ala Val Gly Glu Asp Ser Ala Pro Val Pro Phe
 100 105 110
 Val Ile His Leu Arg Glu Cys Ser Thr Val Val Ser Glu Arg Val Gly
 115 120 125
 Val Ala Phe His Gly Val Ala Asp Gly Lys Asn Pro Asp Val Leu Ser
 130 135 140
 Val Gly Glu Gly Pro Gly Ile Ala Thr Asn Ile Gly Val Ala Leu Phe
 145 150 155 160
 Asp Asp Glu Gly Asn Leu Val Pro Ile Asn Arg Pro Pro Ala Asn Trp
 165 170 175
 Lys Arg Leu Tyr Ser Gly Ser Thr Ser Leu His Phe Ile Ala Lys Tyr
 180 185 190
 Arg Ala Thr Gly Arg Arg Val Thr Gly Gly Ile Ala Asn Ala Gln Ala
 195 200 205
 Trp Phe Ser Leu Thr Tyr Gln
 210 215

<210> 363
 <211> 241
 <212> PRT
 <213> E. Coli

<400> 363

```

Met Ser Asn Lys Asn Val Asn Val Arg Lys Ser Gln Glu Ile Thr Phe
 1          5          10          15
Cys Leu Leu Ala Gly Ile Leu Met Phe Met Ala Met Met Val Ala Gly
 20          25          30
Arg Ala Glu Ala Gly Val Ala Leu Gly Ala Thr Arg Val Ile Tyr Pro
 35          40          45
Ala Gly Gln Lys Gln Glu Gln Leu Ala Val Thr Asn Asn Asp Glu Asn
 50          55          60
Ser Thr Tyr Leu Ile Gln Ser Trp Val Glu Asn Ala Asp Gly Val Lys
 65          70          75          80
Asp Gly Arg Phe Ile Val Thr Pro Pro Leu Phe Ala Met Lys Gly Lys
 85          90          95
Lys Glu Asn Thr Leu Arg Ile Leu Asp Ala Thr Asn Asn Gln Leu Pro
 100         105         110
Gln Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys Ala Ile Pro Ser
 115         120         125
Met Asp Lys Ser Lys Leu Thr Glu Asn Thr Leu Gln Leu Ala Ile Ile
 130         135         140
Ser Arg Ile Lys Leu Tyr Tyr Arg Pro Ala Lys Leu Ala Leu Pro Pro
 145         150         155         160
Asp Gln Ala Ala Glu Lys Leu Arg Phe Arg Arg Ser Ala Asn Ser Leu
 165         170         175
Thr Leu Ile Asn Pro Thr Pro Tyr Tyr Leu Thr Val Thr Glu Leu Asn
 180         185         190
Ala Gly Thr Arg Val Leu Glu Asn Ala Leu Val Pro Pro Met Gly Glu
 195         200         205
Ser Thr Val Lys Leu Pro Ser Asp Ala Gly Ser Asn Ile Thr Tyr Arg
 210         215         220
Thr Ile Asn Asp Tyr Gly Ala Leu Thr Pro Lys Met Thr Gly Val Met
 225         230         235         240
Glu

```

<210> 364
 <211> 878
 <212> PRT
 <213> E. Coli

<400> 364

```

Met Ser Tyr Leu Asn Leu Arg Leu Tyr Gln Arg Asn Thr Gln Cys Leu
 1          5          10          15
His Ile Arg Lys His Arg Leu Ala Gly Phe Phe Val Arg Leu Val Val
 20          25          30
Ala Cys Ala Phe Ala Ala Gln Ala Pro Leu Ser Ser Ala Asp Leu Tyr
 35          40          45
Phe Asn Pro Arg Phe Leu Ala Asp Asp Pro Gln Ala Val Ala Asp Leu
 50          55          60
Ser Arg Phe Glu Asn Gly Gln Glu Leu Pro Pro Gly Thr Tyr Arg Val
 65          70          75          80
Asp Ile Tyr Leu Asn Asn Gly Tyr Met Ala Thr Arg Asp Val Thr Phe
 85          90          95
Asn Thr Gly Asp Ser Glu Gln Gly Ile Val Pro Cys Leu Thr Arg Ala
 100         105         110
Gln Leu Ala Ser Met Gly Leu Asn Thr Ala Ser Val Ala Gly Met Asn

```

115	120	125
Leu Leu Ala Asp Asp Ala Cys Val Pro Leu Thr Thr Met Val Gln Asp		
130	135	140
Ala Thr Ala His Leu Asp Val Gly Gln Gln Arg Leu Asn Leu Thr Ile		
145	150	155
Pro Gln Ala Phe Met Ser Asn Arg Ala Arg Gly Tyr Ile Pro Pro Glu		
165	170	175
Leu Trp Asp Pro Gly Ile Asn Ala Gly Leu Leu Asn Tyr Asn Phe Ser		
180	185	190
Gly Asn Ser Val Gln Asn Arg Ile Gly Gly Asn Ser His Tyr Ala Tyr		
195	200	205
Leu Asn Leu Gln Ser Gly Leu Asn Ile Gly Ala Trp Arg Leu Arg Asp		
210	215	220
Asn Thr Thr Trp Ser Tyr Asn Ser Ser Asp Arg Ser Ser Gly Ser Lys		
225	230	235
Asn Lys Trp Gln His Ile Asn Thr Trp Leu Glu Arg Asp Ile Ile Pro		
245	250	255
Leu Arg Ser Arg Leu Thr Leu Gly Asp Gly Tyr Thr Gln Gly Asp Ile		
260	265	270
Phe Asp Gly Ile Asn Phe Arg Gly Ala Gln Leu Ala Ser Asp Asp Asn		
275	280	285
Met Leu Pro Asp Ser Gln Arg Gly Phe Ala Pro Val Ile His Gly Ile		
290	295	300
Ala Arg Gly Thr Ala Gln Val Thr Ile Lys Gln Asn Gly Tyr Asp Ile		
305	310	315
Tyr Asn Ser Thr Val Pro Pro Gly Pro Phe Thr Ile Asn Asp Ile Tyr		
325	330	335
Ala Ala Gly Asn Ser Gly Asp Leu Gln Val Thr Ile Lys Glu Ala Asp		
340	345	350
Gly Ser Thr Gln Ile Phe Thr Val Pro Tyr Ser Ser Val Pro Leu Leu		
355	360	365
Gln Arg Glu Gly His Thr Arg Tyr Ser Ile Thr Ala Gly Glu Tyr Arg		
370	375	380
Ser Gly Asn Ala Gln Gln Lys Thr Arg Phe Phe Gln Ser Thr Leu		
385	390	395
Leu His Gly Leu Pro Ala Gly Trp Thr Ile Tyr Gly Gly Thr Gln Leu		
405	410	415
Ala Asp Arg Tyr Arg Ala Phe Asn Phe Gly Ile Gly Lys Asn Met Gly		
420	425	430
Ala Leu Gly Ala Leu Ser Val Asp Met Thr Gln Ala Asn Ser Thr Leu		
435	440	445
Pro Asp Asp Ser Gln His Asp Gly Gln Ser Val Arg Phe Leu Tyr Asn		
450	455	460
Lys Ser Leu Asn Glu Ser Gly Thr Asn Ile Gln Leu Val Gly Tyr Arg		
465	470	475
Tyr Ser Thr Ser Gly Tyr Phe Asn Phe Ala Asp Thr Thr Tyr Ser Arg		
485	490	495
Met Asn Gly Tyr Asn Ile Glu Thr Gln Asp Gly Val Ile Gln Val Lys		
500	505	510
Pro Lys Phe Thr Asp Tyr Tyr Asn Leu Ala Tyr Asn Lys Arg Gly Lys		
515	520	525
Leu Gln Leu Thr Val Thr Gln Gln Leu Gly Arg Thr Ser Thr Leu Tyr		
530	535	540
Leu Ser Gly Ser His Gln Thr Tyr Trp Gly Thr Ser Asn Val Asp Glu		
545	550	555
Gln Phe Gln Ala Gly Leu Asn Thr Ala Phe Glu Asp Ile Asn Trp Thr		
565	570	575
Leu Ser Tyr Ser Leu Thr Lys Asn Ala Trp Gln Lys Gly Arg Asp Gln		
580	585	590
Met Leu Ala Leu Asn Val Asn Ile Pro Phe Ser His Trp Leu Arg Ser		
595	600	605

Asp Ser Lys Ser Gln Trp Arg His Ala Ser Ala Ser Tyr Ser Met Ser
 610 615 620
 His Asp Leu Asn Gly Arg Met Thr Asn Leu Ala Gly Val Tyr Gly Thr
 625 630 635 640
 Leu Leu Glu Asp Asn Asn Leu Ser Tyr Ser Val Gln Thr Gly Tyr Ala
 645 650 655
 Gly Gly Gly Asp Gly Asn Ser Gly Ser Thr Gly Tyr Ala Thr Leu Asn
 660 665 670
 Tyr Arg Gly Gly Tyr Gly Asn Ala Asn Ile Gly Tyr Ser His Ser Asp
 675 680 685
 Asp Ile Lys Gln Leu Tyr Tyr Gly Val Ser Gly Gly Val Leu Ala His
 690 695 700
 Ala Asn Gly Val Thr Leu Gly Gln Pro Leu Asn Asp Thr Val Val Leu
 705 710 715 720
 Val Lys Ala Pro Gly Ala Lys Asp Ala Lys Val Glu Asn Gln Thr Gly
 725 730 735
 Val Arg Thr Asp Trp Arg Gly Tyr Ala Val Leu Pro Tyr Ala Thr Glu
 740 745 750
 Tyr Arg Glu Asn Arg Val Ala Leu Asp Thr Asn Thr Leu Ala Asp Asn
 755 760 765
 Val Asp Leu Asp Asn Ala Val Ala Asn Val Val Pro Thr Arg Gly Ala
 770 775 780
 Ile Val Arg Ala Glu Phe Lys Ala Arg Val Gly Ile Lys Leu Leu Met
 785 790 795 800
 Thr Leu Thr His Asn Asn Lys Pro Leu Pro Phe Gly Ala Met Val Thr
 805 810 815
 Ser Glu Ser Ser Gln Ser Ser Gly Ile Val Ala Asp Asn Gly Gln Val
 820 825 830
 Tyr Leu Ser Gly Met Pro Leu Ala Gly Lys Val Gln Val Lys Trp Gly
 835 840 845
 Glu Glu Glu Asn Ala His Cys Val Ala Asn Tyr Gln Leu Pro Pro Glu
 850 855 860
 Ser Gln Gln Gln Leu Leu Thr Gln Leu Ser Ala Glu Cys Arg
 865 870 875

<210> 365

<211> 176

<212> PRT

<213> E. Coli

<400> 365

Met Arg Asn Lys Pro Phe Tyr Leu Leu Cys Ala Phe Leu Trp Leu Ala
 1 5 10 15
 Val Ser His Ala Leu Ala Ala Asp Ser Thr Ile Thr Ile Arg Gly Tyr
 20 25 30
 Val Arg Asp Asn Gly Cys Ser Val Ala Ala Glu Ser Thr Asn Phe Thr
 35 40 45
 Val Asp Leu Met Glu Asn Ala Ala Lys Gln Phe Asn Asn Ile Gly Ala
 50 55 60
 Thr Thr Pro Val Val Pro Phe Arg Ile Leu Leu Ser Pro Cys Gly Asn
 65 70 75 80
 Ala Val Ser Ala Val Lys Val Gly Phe Thr Gly Val Ala Asp Ser His
 85 90 95
 Asn Ala Asn Leu Leu Ala Leu Glu Asn Thr Val Ser Ala Ala Ser Gly
 100 105 110
 Leu Gly Ile Gln Leu Leu Asn Glu Gln Gln Asn Gln Ile Pro Leu Asn
 115 120 125
 Ala Pro Ser Ser Ala Leu Ser Trp Thr Thr Leu Thr Pro Gly Lys Pro
 130 135 140
 Asn Thr Leu Asn Phe Tyr Ala Arg Leu Met Ala Thr Gln Val Pro Val

145 150 155 160
Thr Ala Gly His Ile Asn Ala Thr Ala Thr Phe Thr Leu Glu Tyr Gln
 165 170 175

```
<210> 366
<211> 167
<212> PRT
<213> E. Coli
```

[illegible]

```
<210> 367
<211> 300
<212> PRT
<213> E. Coli
```

<400> 367																
Met	Lys	Arg	Val	Ile	Thr	Leu	Phe	Ala	Val	Leu	Leu	Met	Gly	Trp	Ser	
1				5					10				15			
Val	Asn	Ala	Trp	Ser	Phe	Ala	Cys	Lys	Thr	Ala	Asn	Gly	Thr	Ala	Ile	
			20					25					30			
Pro	Ile	Gly	Gly	Gly	Ser	Ala	Asn	Val	Tyr	Val	Asn	Leu	Ala	Pro	Val	
		35					40					45				
Val	Asn	Val	Gly	Gln	Asn	Leu	Val	Val	Asp	Leu	Ser	Thr	Gln	Ile	Phe	
	50					55					60					
Cys	His	Asn	Asp	Tyr	Pro	Glu	Thr	Ile	Thr	Asp	Tyr	Val	Thr	Leu	Gln	
65					70					75					80	
Arg	Gly	Ser	Ala	Tyr	Gly	Gly	Val	Leu	Ser	Asn	Phe	Ser	Gly	Thr	Val	
				85					90					95		
Lys	Tyr	Ser	Gly	Ser	Ser	Tyr	Pro	Phe	Pro	Thr	Thr	Ser	Glu	Thr	Pro	
			100					105					110			
Arg	Val	Val	Tyr	Asn	Ser	Arg	Thr	Asp	Lys	Pro	Trp	Pro	Val	Ala	Leu	
		115					120					125				
Tyr	Leu	Thr	Pro	Val	Ser	Ser	Ala	Gly	Gly	Val	Ala	Ile	Lys	Ala	Gly	
	130						135					140				

```

Ser Leu Ile Ala Val Leu Ile Leu Arg Gln Thr Asn Asn Tyr Asn Ser
145      150      155      160
Asp Asp Phe Gln Phe Val Trp Asn Ile Tyr Ala Asn Asn Asp Val Val
      165      170      175
Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr
      180      185      190
Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys
      195      200      205
Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr Thr Ala Asp
      210      215      220
Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln
      225      230      235      240
Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn
      245      250      255
Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly
      260      265      270
Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn
      275      280      285
Val Gln Ser Ile Ile Gly Val Thr Phe Val Tyr Gln
      290      295      300

```

<210> 368
 <211> 521
 <212> PRT
 <213> E. Coli

<400> 368

```

Met Leu Ser Lys Leu Pro Arg Arg Leu Arg Ser Phe Gln Thr Tyr Cys
1      5      10      15
Thr Ile Arg Val His Arg Gly Glu Asp Met Lys Ser Met Asp Lys Leu
      20      25      30
Thr Thr Gly Val Ala Tyr Gly Thr Ser Ala Gly Asn Ala Gly Phe Trp
      35      40      45
Ala Leu Gln Leu Leu Asp Lys Val Thr Pro Ser Gln Trp Ala Ala Ile
      50      55      60
Gly Val Leu Gly Ser Leu Val Phe Gly Leu Leu Thr Tyr Leu Thr Asn
      65      70      75      80
Leu Tyr Phe Lys Ile Lys Glu Asp Arg Arg Lys Ala Ala Arg Gly Glu
      85      90      95
Ser Asn Asp Ser Arg Leu Thr Gly Cys Glu Arg Ser Pro Phe Glu Ser
      100      105      110
Tyr Gly Asn Cys Ser Leu Thr Gly Gln Arg Thr Leu Arg Asn Phe Pro
      115      120      125
Gly Cys Arg His Gly Pro Cys Arg Ser Cys Ala Gly Val Leu Gly Ser
      130      135      140
Ser Gln Lys Glu Arg Pro Ala Ser Leu Pro Gly Ser Ser Arg Lys Ile
      145      150      155      160
Val Arg Lys Ser Val Leu Ser Ala Ala Ser Val Leu Leu Asp Lys Ser
      165      170      175
Cys Gln Ala Arg Ala Ser Ser Ser Ile Ser Met Asn Thr Lys Ile Arg
      180      185      190
Tyr Gly Leu Ser Ala Ala Val Leu Ala Leu Ile Gly Ala Gly Ala Ser
      195      200      205
Ala Pro Gln Ile Leu Asp Gln Phe Leu Asp Glu Lys Glu Gly Asn His
      210      215      220
Thr Met Ala Tyr Arg Asp Gly Ser Gly Ile Trp Thr Ile Cys Arg Gly
      225      230      235      240
Ala Thr Val Val Asp Gly Lys Thr Val Phe Pro Asn Met Lys Leu Ser
      245      250      255

```


Lys Glu Lys Cys Asp Gln Val Asn Ala Ile Glu Arg Asp Lys Ala Leu
 260 265 270
 Ala Trp Val Glu Arg Asn Ile Lys Val Pro Leu Thr Glu Pro Gln Lys
 275 280 285
 Ala Gly Ile Ala Ser Phe Cys Pro Tyr Asn Ile Gly Pro Gly Lys Cys
 290 295 300
 Phe Pro Ser Thr Phe Tyr Lys Arg Leu Asn Ala Gly Asp Arg Lys Gly
 305 310 315 320
 Ala Cys Glu Ala Ile Arg Trp Trp Ile Lys Asp Gly Gly Arg Asp Cys
 325 330 335
 Arg Ile Arg Ser Asn Asn Cys Tyr Gly Gln Val Ile Arg Arg Asp Gln
 340 345 350
 Glu Ser Ala Leu Thr Cys Trp Gly Ile Glu Gln Ile Arg Tyr Ser Trp
 355 360 365
 Phe Phe Ser Cys Cys Gln Asp Leu Ser Ser Glu Met Ser Gly Ala Thr
 370 375 380
 Glu Asp Gly Lys Lys Asn Gly Arg Asn Val Met Leu Pro His Tyr His
 385 390 395 400
 Lys Arg Met Leu Asn Leu Leu Glu Leu Asn Arg Gly Glu Leu Pro
 405 410 415
 Val Met Arg Leu Leu Lys Met Arg Asn Arg Asn Leu Leu Lys Phe Leu
 420 425 430
 Pro Gly Leu Leu Ile Cys Leu Ile Val Leu Thr Ser Cys Val Pro Lys
 435 440 445
 Gln Lys Asn Met Pro Tyr Ala Leu Thr Gln Arg Ser Ile Pro Gln Ile
 450 455 460
 Leu Pro Leu Pro Ser Glu Ala Lys Gln Pro Lys Pro Pro Lys Glu Cys
 465 470 475 480
 Ser Pro Thr Cys Ser Glu Ile Leu Gln Gln Lys Leu Ser Phe Met Leu
 485 490 495
 Lys Leu Leu Thr Asn Ala Thr Ser Gln Glu Leu Val Asn Arg Ser Met
 500 505 510
 Asn Leu Glu Ile Lys Ser Ile Lys Cys
 515 520

<210> 369
 <211> 177
 <212> PRT
 <213> E. Coli

<400> 369
 Met Asn Thr Lys Ile Arg Tyr Gly Leu Ser Ala Ala Val Leu Ala Leu
 1 5 10 15
 Ile Gly Ala Gly Ala Ser Ala Pro Gln Ile Leu Asp Gln Phe Leu Asp
 20 25 30
 Glu Lys Glu Gly Asn His Thr Met Ala Tyr Arg Asp Gly Ser Gly Ile
 35 40 45
 Trp Thr Ile Cys Arg Gly Ala Thr Val Val Asp Gly Lys Thr Val Phe
 50 55 60
 Pro Asn Met Lys Leu Ser Lys Glu Lys Cys Asp Gln Val Asn Ala Ile
 65 70 75 80
 Glu Arg Asp Lys Ala Leu Ala Trp Val Glu Arg Asn Ile Lys Val Pro
 85 90 95
 Leu Thr Glu Pro Gln Lys Ala Gly Ile Ala Ser Phe Cys Pro Tyr Asn
 100 105 110
 Ile Gly Pro Gly Lys Cys Phe Pro Ser Thr Phe Tyr Lys Arg Leu Asn
 115 120 125
 Ala Gly Asp Arg Lys Gly Ala Cys Glu Ala Ile Arg Trp Trp Ile Lys
 130 135 140

Asp Gly Gly Arg Asp Cys Arg Ile Arg Ser Asn Asn Cys Tyr Gly Gln
 145 150 155 160
 Val Ile Arg Arg Asp Gln Glu Ser Ala Leu Thr Cys Trp Gly Ile Glu
 165 170 175
 Gln

<210> 370
 <211> 103
 <212> PRT
 <213> E. Coli

<400> 370
 Met Thr Gln Asp Tyr Glu Leu Val Val Lys Gly Val Arg Asn Phe Glu
 1 5 10 15
 Asn Lys Val Thr Val Thr Val Ala Leu Gln Asp Lys Glu Arg Phe Asp
 20 25 30
 Gly Glu Ile Phe Asp Leu Asp Val Ala Met Asp Arg Val Glu Gly Ala
 35 40 45
 Ala Leu Glu Phe Tyr Glu Ala Ala Ala Arg Arg Ser Val Arg Gln Val
 50 55 60
 Phe Leu Glu Val Ala Glu Lys Leu Ser Glu Lys Val Glu Ser Tyr Leu
 65 70 75 80
 Gln His Gln Tyr Ser Phe Lys Ile Glu Asn Pro Ala Asn Lys His Glu
 85 90 95
 Arg Pro His His Lys Tyr Leu
 100

<210> 371
 <211> 96
 <212> PRT
 <213> E. Coli

<400> 371
 Met Leu Ser Lys Leu Pro Arg Arg Leu Arg Ser Phe Gln Thr Tyr Cys
 1 5 10 15
 Thr Ile Arg Val His Arg Gly Glu Asp Met Lys Ser Met Asp Lys Leu
 20 25 30
 Thr Thr Gly Val Ala Tyr Gly Thr Ser Ala Gly Asn Ala Gly Phe Trp
 35 40 45
 Ala Leu Gln Leu Leu Asp Lys Val Thr Pro Ser Gln Trp Ala Ala Ile
 50 55 60
 Gly Val Leu Gly Ser Leu Val Phe Gly Leu Leu Thr Tyr Leu Thr Asn
 65 70 75 80
 Leu Tyr Phe Lys Ile Lys Glu Asp Arg Arg Lys Ala Ala Arg Gly Glu
 85 90 95

<210> 372
 <211> 71
 <212> PRT
 <213> E. Coli

<400> 372
 Met Ser Asn Lys Met Thr Gly Leu Val Lys Trp Phe Asn Ala Asp Lys
 1 5 10 15
 Gly Phe Gly Phe Ile Ser Pro Val Asp Gly Ser Lys Asp Val Phe Val

20 25 30
 His Phe Ser Ala Ile Gln Asn Asp Asn Tyr Arg Thr Leu Phe Glu Gly
 35 40 45
 Gln Lys Val Thr Phe Ser Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
 50 55 60
 Ala Asn Val Ile Ile Thr Asp
 65 70

<210> 373
 <211> 338
 <212> PRT
 <213> E. Coli

<400> 373
 Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln
 1 5 10 15
 Leu Thr Phe Ala Asp Ser Glu Phe Ser Ser Lys Arg Arg Gln Thr Arg
 20 25 30
 Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn
 35 40 45
 Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg
 50 55 60
 Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His
 65 70 75 80
 Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile
 85 90 95
 Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro
 100 105 110
 Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln
 115 120 125
 Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala
 130 135 140
 Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu
 145 150 155 160
 Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met
 165 170 175
 His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His
 180 185 190
 Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr
 195 200 205
 Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly
 210 215 220
 Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln
 225 230 235 240
 Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg
 245 250 255
 Pro Gly Lys Val Arg Thr Leu Lys Gln His Pro Arg Lys Asn Lys Thr
 260 265 270
 Ala Ile Asn Ile Glu Tyr Met Lys Ala Ser Ile Arg Ala Arg Val Glu
 275 280 285
 His Pro Phe Arg Ile Ile Lys Arg Gln Phe Gly Phe Val Lys Ala Arg
 290 295 300
 Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr
 305 310 315 320
 Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg
 325 330 335
 Ser His

<210> 374
 <211> 157
 <212> PRT
 <213> E. Coli

<400> 374

```

Met Val Tyr Ile Ile Ile Val Ser His Gly His Glu Asp Tyr Ile Lys
 1           5           10           15
Lys Leu Leu Glu Asn Leu Asn Ala Asp Asp Glu His Tyr Lys Ile Ile
 20           25           30
Val Arg Asp Asn Lys Asp Ser Leu Leu Leu Lys Gln Ile Cys Gln His
 35           40           45
Tyr Ala Gly Leu Asp Tyr Ile Ser Gly Gly Val Tyr Gly Phe Gly His
 50           55           60
Asn Asn Asn Ile Ala Val Ala Tyr Val Lys Glu Lys Tyr Arg Pro Ala
 65           70           75           80
Asp Asp Asp Tyr Ile Leu Phe Leu Asn Pro Asp Ile Ile Met Lys His
 85           90           95
Asp Asp Leu Leu Thr Tyr Ile Lys Tyr Val Glu Ser Lys Arg Tyr Ala
 100          105          110
Phe Ser Thr Leu Cys Leu Phe Arg Asp Glu Ala Lys Ser Leu His Asp
 115          120          125
Tyr Ser Val Arg Lys Phe Pro Val Leu Ser Asp Phe Ile Val Ser Phe
 130          135          140
Met Leu Gly Ile Lys Glu Gly Ala Asn Lys Ser Leu Ile
 145          150          155

```

<210> 375
 <211> 372
 <212> PRT
 <213> E. Coli

<400> 375

```

Met Gly Lys Ser Ile Val Val Val Ser Ala Val Asn Phe Thr Thr Gly
 1           5           10           15
Gly Pro Phe Thr Ile Leu Lys Lys Phe Leu Ala Ala Thr Asn Asn Lys
 20           25           30
Glu Asn Val Ser Phe Ile Ala Leu Val His Ser Ala Lys Glu Leu Lys
 35           40           45
Glu Ser Tyr Pro Trp Val Lys Phe Ile Glu Phe Pro Glu Val Lys Gly
 50           55           60
Ser Trp Leu Lys Arg Leu His Phe Glu Tyr Val Val Cys Lys Lys Leu
 65           70           75           80
Ser Lys Glu Leu Asn Ala Thr His Trp Ile Cys Leu His Asp Ile Thr
 85           90           95
Ala Asn Val Val Thr Lys Lys Arg Tyr Val Tyr Cys His Asn Pro Ala
 100          105          110
Pro Phe Tyr Lys Gly Ile Leu Phe Arg Glu Ile Leu Met Glu Pro Ser
 115          120          125
Phe Phe Leu Phe Lys Met Leu Tyr Gly Leu Ile Tyr Lys Ile Asn Ile
 130          135          140
Lys Lys Asn Thr Ala Val Phe Val Gln Gln Phe Trp Met Lys Glu Lys
 145          150          155          160
Phe Ile Lys Lys Tyr Ser Ile Asn Asn Ile Ile Val Ser Arg Pro Glu
 165          170          175
Ile Lys Leu Ser Asp Lys Ser Gln Leu Thr Asp Asp Asp Ser Gln Phe
 180          185          190
Lys Asn Asn Pro Ser Glu Leu Thr Ile Phe Tyr Pro Ala Val Pro Arg

```

```

      195              200              205
Val Phe Lys Asn Tyr Glu Leu Ile Ile Ser Ala Ala Arg Lys Leu Lys
 210              215              220
Glu Gln Ser Asn Ile Lys Phe Leu Leu Thr Ile Ser Gly Thr Glu Asn
 225              230              235
Ala Tyr Ala Lys Tyr Ile Ile Ser Leu Ala Glu Gly Leu Asp Asn Val
      245              250              255
His Phe Leu Gly Tyr Leu Asp Lys Glu Lys Ile Asp His Cys Tyr Asn
 260              265              270
Ile Ser Asp Ile Val Cys Phe Pro Ser Arg Leu Glu Thr Trp Gly Leu
 275              280              285
Pro Leu Ser Glu Ala Lys Glu Arg Gly Lys Trp Val Leu Ala Ser Asp
 290              295              300
Phe Pro Phe Thr Arg Glu Thr Leu Gly Ser Tyr Glu Lys Lys Ala Phe
 305              310              315
Phe Asp Ser Asn Asn Asp Asp Met Leu Val Lys Leu Ile Ile Asp Phe
      325              330              335
Lys Lys Gly Asn Leu Lys Lys Asp Ile Ser Asp Ala Asn Phe Ile Tyr
 340              345              350
Arg Asn Glu Asn Val Leu Val Gly Phe Asp Glu Leu Val Asn Phe Ile
 355              360              365
Thr Glu Glu His
 370

```

```

<210> 376
<211> 196
<212> PRT
<213> E. Coli

```

```

      <400> 376
Met Ile Leu Lys Leu Ala Lys Arg Tyr Gly Leu Cys Gly Phe Ile Arg
  1              5              10              15
Leu Val Arg Asp Val Leu Leu Thr Arg Val Phe Tyr Arg Asn Cys Arg
      20              25              30
Ile Ile Arg Phe Pro Cys Tyr Ile Arg Asn Asp Gly Ser Ile Asn Phe
  35              40              45
Gly Glu Asn Phe Thr Ser Gly Val Gly Leu Arg Leu Asp Ala Phe Gly
  50              55              60
Arg Gly Val Ile Phe Phe Ser Asp Asn Val Gln Val Asn Asp Tyr Val
  65              70              75              80
His Ile Ala Ser Ile Glu Ser Val Thr Ile Gly Arg Asp Thr Leu Ile
      85              90              95
Ala Ser Lys Val Phe Ile Thr Asp His Asn His Gly Ser Phe Lys His
 100              105              110
Ser Asp Pro Met Ser Ser Pro Asn Ile Pro Pro Asp Met Arg Thr Leu
 115              120              125
Glu Ser Ser Ala Val Val Ile Gly Gln Arg Val Trp Leu Gly Glu Asn
 130              135              140
Val Thr Val Leu Pro Gly Thr Ile Ile Gly Asn Gly Val Val Val Gly
 145              150              155              160
Ala Asn Ser Val Val Arg Gly Ser Ile Pro Glu Asn Thr Val Ile Ala
 165              170              175
Gly Val Pro Ala Lys Ile Ile Lys Lys Tyr Asn His Glu Thr Lys Leu
 180              185              190
Trp Glu Lys Ala
 195

```

```

<210> 377
<211> 330
<212> PRT

```

<213> E. Coli

<400> 377

```

Met Tyr Phe Leu Asn Asp Leu Asn Phe Ser Arg Arg Asp Ala Gly Phe
 1          5          10          15
Lys Ala Arg Lys Asp Ala Leu Asp Ile Ala Ser Asp Tyr Glu Asn Ile
 20          25          30
Ser Val Val Asn Ile Pro Leu Trp Gly Gly Val Val Gln Arg Ile Ile
 35          40          45
Ser Ser Val Lys Leu Ser Thr Phe Leu Cys Gly Leu Glu Asn Lys Asp
 50          55          60
Val Leu Ile Phe Asn Phe Pro Met Ala Lys Pro Phe Trp His Ile Leu
 65          70          75          80
Ser Phe Phe His Arg Leu Leu Lys Phe Arg Ile Val Pro Leu Ile His
 85          90          95
Asp Ile Asp Glu Leu Arg Gly Gly Gly Gly Ser Asp Ser Val Arg Leu
100          105          110
Ala Thr Cys Asp Met Val Ile Ser His Asn Pro Gln Met Thr Lys Tyr
115          120          125
Leu Ser Lys Tyr Met Ser Gln Asp Lys Ile Lys Asp Ile Lys Ile Phe
130          135          140
Asp Tyr Leu Val Ser Ser Asp Val Glu His Arg Asp Val Thr Asp Lys
145          150          155          160
Gln Arg Gly Val Ile Tyr Ala Gly Asn Leu Ser Arg His Lys Cys Ser
165          170          175
Phe Ile Tyr Thr Glu Gly Cys Asp Phe Thr Leu Phe Gly Val Asn Tyr
180          185          190
Glu Asn Lys Asp Asn Pro Lys Tyr Leu Gly Ser Phe Asp Ala Gln Ser
195          200          205
Pro Glu Lys Ile Asn Leu Pro Gly Met Gln Phe Gly Leu Ile Trp Asp
210          215          220
Gly Asp Ser Val Glu Thr Cys Ser Gly Ala Phe Gly Asp Tyr Leu Lys
225          230          235          240
Phe Asn Asn Pro His Lys Thr Ser Leu Tyr Leu Ser Met Glu Leu Pro
245          250          255
Val Phe Ile Trp Asp Lys Ala Ala Leu Ala Asp Phe Ile Val Asp Asn
260          265          270
Arg Ile Gly Tyr Ala Val Gly Ser Ile Lys Glu Met Gln Glu Ile Val
275          280          285
Asp Ser Met Thr Ile Glu Thr Tyr Lys Gln Ile Ser Glu Asn Thr Lys
290          295          300
Ile Ile Ser Gln Lys Ile Arg Thr Gly Ser Tyr Phe Arg Asp Val Leu
305          310          315          320
Glu Glu Val Ile Asp Asp Leu Lys Thr Arg
325          330

```

<210> 378

<211> 388

<212> PRT

<213> E. Coli

<400> 378

```

Met Ile Tyr Leu Val Ile Ser Val Phe Leu Ile Thr Ala Phe Ile Cys
 1          5          10          15
Leu Tyr Leu Lys Lys Asp Ile Phe Tyr Pro Ala Val Cys Val Asn Ile
 20          25          30
Ile Phe Ala Leu Val Leu Leu Gly Tyr Glu Ile Thr Ser Asp Ile Tyr
 35          40          45
Ala Phe Gln Leu Asn Asp Ala Thr Leu Ile Phe Leu Leu Cys Asn Val
 50          55          60

```

Leu Thr Phe Thr Leu Ser Cys Leu Leu Thr Glu Ser Val Leu Asp Leu
 65 70 75 80
 Asn Ile Arg Lys Val Asn Asn Ala Ile Tyr Ser Ile Pro Ser Lys Lys
 85 90 95
 Val His Asn Val Gly Leu Leu Val Ile Ser Phe Ser Met Ile Tyr Ile
 100 105 110
 Cys Met Arg Leu Ser Asn Tyr Gln Phe Gly Thr Ser Leu Leu Ser Tyr
 115 120 125
 Met Asn Leu Ile Arg Asp Ala Asp Val Glu Asp Thr Ser Arg Asn Phe
 130 135 140
 Ser Ala Tyr Met Gln Pro Ile Ile Leu Thr Thr Phe Ala Leu Phe Ile
 145 150 155 160
 Trp Ser Lys Lys Phe Thr Asn Thr Lys Val Ser Lys Thr Phe Thr Leu
 165 170 175
 Leu Val Phe Ile Val Phe Ile Phe Ala Ile Ile Leu Asn Thr Gly Lys
 180 185 190
 Gln Ile Val Phe Met Val Ile Ile Ser Tyr Ala Phe Ile Val Gly Val
 195 200 205
 Asn Arg Val Lys His Tyr Val Tyr Leu Ile Thr Ala Val Gly Val Leu
 210 215 220
 Phe Ser Leu Tyr Met Leu Phe Leu Arg Gly Leu Pro Gly Gly Met Ala
 225 230 235 240
 Tyr Tyr Leu Ser Met Tyr Leu Val Ser Pro Ile Ile Ala Phe Gln Glu
 245 250 255
 Phe Tyr Phe Gln Gln Val Ser Asn Ser Ala Ser Ser His Val Phe Trp
 260 265 270
 Phe Phe Glu Arg Leu Met Gly Leu Leu Thr Gly Gly Val Ser Met Ser
 275 280 285
 Leu His Lys Glu Phe Val Trp Val Gly Leu Pro Thr Asn Val Tyr Thr
 290 295 300
 Ala Phe Ser Asp Tyr Val Tyr Ile Ser Ala Glu Leu Ser Tyr Leu Met
 305 310 315 320
 Met Val Ile His Gly Cys Ile Ser Gly Val Leu Trp Arg Leu Ser Arg
 325 330 335
 Asn Tyr Ile Ser Val Lys Ile Phe Tyr Ser Tyr Phe Ile Tyr Thr Phe
 340 345 350
 Ser Phe Ile Phe Tyr His Glu Ser Phe Met Thr Asn Ile Ser Ser Trp
 355 360 365
 Ile Gln Ile Thr Leu Cys Ile Ile Val Phe Ser Gln Phe Leu Lys Ala
 370 375 380
 Gln Lys Ile Lys
 385

<210> 379
 <211> 367
 <212> PRT
 <213> E. Coli

<400> 379
 Met Tyr Asp Tyr Ile Ile Val Gly Ser Gly Leu Phe Gly Ala Val Cys
 1 5 10 15
 Ala Asn Glu Leu Lys Lys Leu Asn Lys Lys Val Leu Val Ile Glu Lys
 20 25 30
 Arg Asn His Ile Gly Gly Asn Ala Tyr Thr Glu Asp Cys Glu Gly Ile
 35 40 45
 Gln Ile His Lys Tyr Gly Ala His Ile Phe His Thr Asn Asp Lys Tyr
 50 55 60
 Ile Trp Asp Tyr Val Asn Asp Leu Val Glu Phe Asn Arg Phe Thr Asn
 65 70 75 80

Ser Pro Leu Ala Ile Tyr Lys Asp Lys Leu Phe Asn Leu Pro Phe Asn
 85 90 95
 Met Asn Thr Phe His Gln Met Trp Gly Val Lys Asp Pro Gln Glu Ala
 100 105 110
 Gln Asn Ile Ile Asn Ala Gln Lys Lys Lys Tyr Gly Asp Lys Val Pro
 115 120 125
 Glu Asn Leu Glu Glu Gln Ala Ile Ser Leu Val Gly Glu Asp Leu Tyr
 130 135 140
 Gln Ala Leu Ile Lys Gly Tyr Thr Glu Lys Gln Trp Gly Arg Ser Ala
 145 150 155 160
 Lys Glu Leu Pro Ala Phe Ile Ile Lys Arg Ile Pro Val Arg Phe Thr
 165 170 175
 Phe Asp Asn Asn Tyr Phe Ser Asp Arg Tyr Gln Gly Ile Pro Val Gly
 180 185 190
 Gly Tyr Thr Lys Leu Ile Glu Lys Met Leu Glu Gly Val Asp Val Lys
 195 200 205
 Leu Gly Ile Asp Phe Leu Lys Asp Lys Asp Ser Leu Ala Ser Lys Ala
 210 215 220
 His Arg Ile Ile Tyr Thr Gly Pro Ile Asp Gln Tyr Phe Asp Tyr Arg
 225 230 235 240
 Phe Gly Ala Leu Glu Tyr Arg Ser Leu Lys Phe Glu Thr Glu Arg His
 245 250 255
 Glu Phe Pro Asn Phe Gln Gly Asn Ala Val Ile Asn Phe Thr Asp Ala
 260 265 270
 Asn Val Pro Tyr Thr Arg Ile Ile Glu His Lys His Phe Asp Tyr Val
 275 280 285
 Glu Thr Lys His Thr Val Val Thr Lys Glu Tyr Pro Leu Glu Trp Lys
 290 295 300
 Val Gly Asp Glu Pro Tyr Tyr Pro Val Asn Asp Asn Lys Asn Met Glu
 305 310 315 320
 Leu Phe Lys Lys Tyr Arg Glu Leu Ala Ser Arg Glu Asp Lys Val Ile
 325 330 335
 Phe Gly Gly Arg Leu Ala Glu Tyr Lys Tyr Tyr Asp Met His Gln Val
 340 345 350
 Ile Ser Ala Ala Leu Tyr Gln Val Lys Asn Ile Met Ser Thr Asp
 355 360 365

<210> 380

<211> 371

<212> PRT

<213> E. Coli

<400> 380

Met Phe Pro Lys Ile Met Asn Asp Glu Asn Phe Phe Lys Lys Ala Ala
 1 5 10 15
 Ala His Gly Glu Pro Pro Leu Thr Pro Gln Asn Glu His Gln Arg
 20 25 30
 Ser Gly Leu Arg Phe Ala Arg Val Arg Leu Pro Arg Ala Val Gly
 35 40 45
 Leu Ala Gly Met Phe Leu Pro Ile Ala Ser Thr Leu Val Ser His Pro
 50 55 60
 Pro Pro Gly Trp Trp Trp Leu Val Leu Val Gly Trp Ala Phe Val Trp
 65 70 75 80
 Pro His Leu Ala Trp Gln Ile Ala Ser Arg Ala Val Asp Pro Leu Ser
 85 90 95
 Arg Glu Ile Tyr Asn Leu Lys Thr Asp Ala Val Leu Ala Gly Met Trp
 100 105 110
 Val Gly Val Met Gly Val Asn Val Leu Pro Ser Thr Ala Met Leu Met
 115 120 125
 Ile Met Cys Leu Asn Leu Met Gly Ala Gly Gly Pro Arg Leu Phe Val


```

      130      135      140
Ala Gly Leu Val Leu Met Val Val Ser Cys Leu Val Thr Leu Glu Leu
145      150      155      160
Thr Gly Ile Thr Val Ser Phe Asn Ser Ala Pro Leu Glu Trp Trp Leu
      165      170      175
Ser Leu Pro Ile Ile Val Ile Tyr Pro Leu Leu Phe Gly Trp Val Ser
      180      185      190
Tyr Gln Thr Ala Thr Lys Leu Ala Glu His Lys Arg Arg Leu Gln Val
      195      200      205
Met Ser Thr Arg Asp Gly Met Thr Gly Val Tyr Asn Arg Arg His Trp
      210      215      220
Glu Thr Met Leu Arg Asn Glu Phe Asp Asn Cys Arg Arg His Asn Arg
      225      230      235      240
Asp Ala Thr Leu Leu Ile Ile Asp Ile Asp His Phe Lys Ser Ile Asn
      245      250      255
Asp Thr Trp Gly His Asp Val Gly Asp Glu Ala Ile Val Ala Leu Thr
      260      265      270
Arg Gln Leu Gln Ile Thr Leu Arg Gly Ser Asp Val Ile Gly Arg Phe
      275      280      285
Gly Gly Asp Glu Phe Ala Val Ile Met Ser Gly Thr Pro Ala Glu Ser
      290      295      300
Ala Ile Thr Ala Met Leu Arg Val His Glu Gly Leu Asn Thr Leu Arg
      305      310      315      320
Leu Pro Asn Thr Pro Gln Val Thr Leu Arg Ile Ser Val Gly Val Ala
      325      330      335
Pro Leu Asn Pro Gln Met Ser His Tyr Arg Glu Trp Leu Lys Ser Ala
      340      345      350
Asp Leu Ala Leu Tyr Lys Ala Lys Lys Ala Gly Arg Asn Arg Thr Glu
      355      360      365
Val Ala Ala
      370

```

<210> 381
 <211> 467
 <212> PRT
 <213> E. Coli

```

      <400> 381
Met Asp Val Asn Val Asp Gln Phe Asp Thr Glu Ala Phe Arg Thr Asp
1      5      10      15
Lys Leu Glu Leu Thr Ser Gly Asn Ile Ala Asp His Asn Gly Asn Val
      20      25      30
Val Ser Gly Val Phe Asp Ile His Ser Ser Asp Tyr Val Leu Asn Ala
      35      40      45
Asp Leu Val Asn Asp Arg Thr Trp Asp Thr Ser Lys Ser Asn Tyr Gly
      50      55      60
Tyr Gly Ile Val Ala Met Asn Ser Asp Gly His Leu Thr Ile Asn Gly
      65      70      75      80
Asn Gly Asp Val Asp Asn Gly Thr Glu Leu Asp Asn Ser Ser Val Asp
      85      90      95
Asn Val Val Ala Ala Thr Gly Asn Tyr Lys Val Arg Ile Asp Asn Ala
      100      105      110
Thr Gly Ala Gly Ala Ile Ala Asp Tyr Lys Asp Lys Glu Ile Ile Tyr
      115      120      125
Val Asn Asp Val Asn Ser Asn Ala Thr Phe Ser Ala Ala Asn Lys Ala
      130      135      140
Asp Leu Gly Ala Tyr Thr Tyr Gln Ala Glu Gln Arg Gly Asn Thr Val
      145      150      155      160
Val Leu Gln Gln Met Glu Leu Thr Asp Tyr Ala Asn Met Ala Leu Ser
      165      170      175
Ile Pro Ser Ala Asn Thr Asn Ile Trp Asn Leu Glu Gln Asp Thr Val

```

180 185 190
 Gly Thr Arg Leu Thr Asn Ser Arg His Gly Leu Ala Asp Asn Gly Gly
 195 200 205
 Ala Trp Val Ser Tyr Phe Gly Gly Asn Phe Asn Gly Asp Asn Gly Thr
 210 215 220
 Ile Asn Tyr Asp Gln Asp Val Asn Gly Ile Met Val Gly Val Asp Thr
 225 230 235 240
 Lys Ile Asp Gly Asn Asn Ala Lys Trp Ile Val Gly Ala Ala Ala Gly
 245 250 255
 Phe Ala Lys Gly Asp Met Asn Asp Arg Ser Gly Gln Val Asp Gln Asp
 260 265 270
 Ser Gln Thr Ala Tyr Ile Tyr Ser Ser Ala His Phe Ala Asn Asn Val
 275 280 285
 Phe Val Asp Gly Ser Leu Ser Tyr Ser His Phe Asn Asn Asp Leu Ser
 290 295 300
 Ala Thr Met Ser Asn Gly Thr Tyr Val Asp Gly Ser Thr Asn Ser Asp
 305 310 315 320
 Ala Trp Gly Phe Gly Leu Lys Ala Gly Tyr Asp Phe Lys Leu Gly Asp
 325 330 335
 Ala Gly Tyr Val Thr Pro Tyr Gly Ser Val Ser Gly Leu Phe Gln Ser
 340 345 350
 Gly Asp Asp Tyr Gln Leu Ser Asn Asp Met Lys Val Asp Gly Gln Ser
 355 360 365
 Tyr Asp Ser Met Arg Tyr Glu Leu Gly Val Asp Ala Gly Tyr Thr Phe
 370 375 380
 Thr Tyr Ser Glu Asp Gln Ala Leu Thr Pro Tyr Phe Lys Leu Ala Tyr
 385 390 395 400
 Val Tyr Asp Asp Ser Asn Asn Asp Asn Asp Val Asn Gly Asp Ser Ile
 405 410 415
 Asp Asn Gly Thr Glu Gly Ser Ala' Val Arg Val Gly Leu Gly Thr Gln
 420 425 430
 Phe Ser Phe Thr Lys Asn Phe Ser Ala Tyr Thr Asp Ala Asn Tyr Leu
 435 440 445
 Gly Gly Gly Asp Val Asp Gln Asp Trp Ser Ala Asn Val Gly Val Lys
 450 455 460
 Tyr Thr Trp
 465

<210> 382
 <211> 222
 <212> PRT
 <213> E. Coli

<400> 382
 Met Pro Val Lys Asp Leu Thr Gly Ile Thr Ala Lys Asp Ala Gln Met
 1 5 10 15
 Leu Ser Val Val Lys Pro Leu Gln Glu Phe Gly Lys Leu Asp Lys Cys
 20 25 30
 Leu Ser Arg Tyr Gly Thr Arg Phe Glu Phe Asn Asn Glu Lys Gln Val
 35 40 45
 Ile Phe Ser Ser Asp Val Asn Asn Glu Asp Thr Phe Val Ile Leu Glu
 50 55 60
 Gly Val Ile Ser Leu Arg Arg Glu Glu Asn Val Leu Ile Gly Ile Thr
 65 70 75 80
 Gln Ala Pro Tyr Ile Met Gly Leu Ala Asp Gly Leu Met Lys Asn Asp
 85 90 95
 Ile Pro Tyr Lys Leu Ile Ser Glu Gly Asn Cys Thr Gly Tyr His Leu
 100 105 110
 Pro Ala Lys Gln Thr Ile Thr Leu Ile Glu Gln Asn Gln Leu Trp Arg
 115 120 125

Asp Ala Phe Tyr Trp Leu Ala Trp Gln Asn Arg Ile Leu Glu Leu Arg
 130 135 140
 Asp Val Gln Leu Ile Gly His Asn Ser Tyr Glu Gln Ile Arg Ala Thr
 145 150 155 160
 Leu Leu Ser Met Ile Asp Trp Asn Glu Glu Leu Arg Ser Arg Ile Gly
 165 170 175
 Val Met Asn Tyr Ile His Gln Arg Thr Arg Ile Ser Arg Ser Val Val
 180 185 190
 Ala Glu Val Leu Ala Ala Leu Arg Lys Gly Gly Tyr Ile Glu Met Asn
 195 200 205
 Lys Gly Lys Leu Val Ala Ile Asn Arg Leu Pro Ser Glu Tyr
 210 215 220

<210> 383
 <211> 84
 <212> PRT
 <213> E. Coli

<400> 383

Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys
 1 5 10 15
 Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro
 20 25 30
 Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp
 35 40 45
 Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys
 50 55 60
 Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu
 65 70 75 80
 Lys Ala Val Leu

<210> 384
 <211> 63
 <212> PRT
 <213> E. Coli

<400> 384

Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
 1 5 10 15
 Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
 20 25 30
 Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
 35 40 45
 Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala
 50 55 60

<210> 385
 <211> 136
 <212> PRT
 <213> E. Coli

<400> 385

Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg
 1 5 10 15
 Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly
 20 25 30
 Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala

35 40 45
 Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
 50 55 60
 Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val
 65 70 75 80
 Arg Met Gly Lys Gly Lys Gly Asn Val Glu Tyr Trp Val Ala Leu Ile
 85 90 95
 Gln Pro Gly Lys Val Leu Tyr Glu Met Asp Gly Val Pro Glu Glu Leu
 100 105 110
 Ala Arg Glu Ala Phe Lys Leu Ala Ala Lys Leu Pro Ile Lys Thr
 115 120 125
 Thr Phe Val Thr Lys Thr Val Met
 130 135

<210> 386
 <211> 233
 <212> PRT
 <213> E. Coli

<400> 386
 Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys
 1 5 10 15
 Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn
 20 25 30
 Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala
 35 40 45
 Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile
 50 55 60
 Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys
 65 70 75 80
 Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly
 85 90 95
 Val Pro Ala Gln Ile Asn Ile Ala Glu Val Arg Lys Pro Glu Leu Asp
 100 105 110
 Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val
 115 120 125
 Met Phe Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu
 130 135 140
 Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala
 145 150 155 160
 Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His
 165 170 175
 Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr
 180 185 190
 Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu
 195 200 205
 Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro
 210 215 220
 Lys Lys Gln Gln Arg Lys Gly Arg Lys
 225 230

<210> 387
 <211> 110
 <212> PRT
 <213> E. Coli

<400> 387

Met Glu Thr Ile Ala Lys His Arg His Ala Arg Ser Ser Ala Gln Lys
 1 5 10 15
 Val Arg Leu Val Ala Asp Leu Ile Arg Gly Lys Lys Val Ser Gln Ala
 20 25 30
 Leu Asp Ile Leu Thr Tyr Thr Asn Lys Lys Ala Ala Val Leu Val Lys
 35 40 45
 Lys Val Leu Glu Ser Ala Ile Ala Asn Ala Glu His Asn Asp Gly Ala
 50 55 60
 Asp Ile Asp Asp Leu Lys Val Thr Lys Ile Phe Val Asp Glu Gly Pro
 65 70 75 80
 Ser Met Lys Arg Ile Met Pro Arg Ala Lys Gly Arg Ala Asp Arg Ile
 85 90 95
 Leu Lys Arg Thr Ser His Ile Thr Val Val Val Ser Asp Arg
 100 105 110

<210> 388
 <211> 92
 <212> PRT
 <213> E. Coli

<400> 388
 Met Pro Arg Ser Leu Lys Lys Gly Pro Phe Ile Asp Leu His Leu Leu
 1 5 10 15
 Met Lys Val Glu Lys Ala Val Glu Ser Gly Asp Lys Lys Pro Leu Arg
 20 25 30
 Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Met Ile Gly Leu Thr
 35 40 45
 Ile Ala Val His Asn Gly Arg Gln His Val Pro Val Phe Val Thr Asp
 50 55 60
 Glu Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Tyr
 65 70 75 80
 Arg Gly His Ala Ala Asp Lys Lys Ala Lys Lys
 85 90

<210> 389
 <211> 273
 <212> PRT
 <213> E. Coli

<400> 389
 Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val
 1 5 10 15
 Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro
 20 25 30
 Leu Leu Glu Lys Asn Ser Lys Ser Gly Gly Arg Asn Asn Asn Gly Arg
 35 40 45
 Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile
 50 55 60
 Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg
 65 70 75 80
 Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr
 85 90 95
 Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala
 100 105 110
 Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn
 115 120 125
 Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val

130 135 140
 Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr
 145 150 155 160
 Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu
 165 170 175
 Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu
 180 185 190
 Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala
 195 200 205
 Gly Ala Ala Arg Trp Arg Gly Val Arg Pro Thr Val Arg Gly Thr Ala
 210 215 220
 Met Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Arg Asn Phe
 225 230 235 240
 Gly Lys His Pro Val Thr Pro Trp Gly Val Gln Thr Lys Gly Lys Lys
 245 250 255
 Thr Arg Ser Asn Lys Arg Thr Asp Lys Phe Ile Val Arg Arg Arg Ser
 260 265 270
 Lys

<210> 390
 <211> 100
 <212> PRT
 <213> E. Coli

<400> 390
 Met Ile Arg Glu Glu Arg Leu Leu Lys Val Leu Arg Ala Pro His Val
 1 5 10 15
 Ser Glu Lys Ala Ser Thr Ala Met Glu Lys Ser Asn Thr Ile Val Leu
 20 25 30
 Lys Val Ala Lys Asp Ala Thr Lys Ala Glu Ile Lys Ala Val Gln
 35 40 45
 Lys Leu Phe Glu Val Glu Val Glu Val Val Asn Thr Leu Val Val Lys
 50 55 60
 Gly Lys Val Lys Arg His Gly Gln Arg Ile Gly Arg Arg Ser Asp Trp
 65 70 75 80
 Lys Lys Ala Tyr Val Thr Leu Lys Glu Gly Gln Asn Leu Asp Phe Val
 85 90 95
 Gly Gly Ala Glu
 100

<210> 391
 <211> 201
 <212> PRT
 <213> E. Coli

<400> 391
 Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu
 1 5 10 15
 Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val
 20 25 30
 Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr
 35 40 45
 Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly
 50 55 60
 Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser
 65 70 75 80

Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val
 85 90 95
 Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu
 100 105 110
 Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala
 115 120 125
 Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu
 130 135 140
 Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala
 145 150 155 160
 Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp
 165 170 175
 Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala
 180 185 190
 Val Lys Gln Val Glu Glu Met Leu Ala
 195 200

<210> 392
 <211> 209
 <212> PRT
 <213> E. Coli

<400> 392
 Met Ile Gly Leu Val Gly Lys Lys Val Gly Met Thr Arg Ile Phe Thr
 1 5 10 15
 Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn
 20 25 30
 Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile
 35 40 45
 Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu
 50 55 60
 Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp
 65 70 75 80
 Glu Phe Arg Leu Ala Glu Gly Glu Glu Phe Thr Val Gly Gln Ser Ile
 85 90 95
 Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr
 100 105 110
 Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg
 115 120 125
 Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly
 130 135 140
 Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys
 145 150 155 160
 Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp
 165 170 175
 Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala
 180 185 190
 Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys
 195 200 205
 Ala

<210> 393
 <211> 103
 <212> PRT
 <213> E. Coli

<400> 393

```

Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg
 1           5           10           15
Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr
           20           25           30
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg
           35           40           45
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln
           50           55           60
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr
65           70           75           80
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val
           85           90           95
Asp Val Gln Ile Ser Leu Gly
           100

```

<210> 394

<211> 118

<212> PRT

<213> E. Coli

<400> 394

```

Met Ala Arg Val Lys Arg Gly Val Ile Ala Arg Ala Arg His Lys Lys
 1           5           10           15
Ile Leu Lys Gln Ala Lys Gly Tyr Tyr Gly Ala Arg Ser Arg Val Tyr
           20           25           30
Arg Val Ala Phe Gln Ala Val Ile Lys Ala Gly Gln Tyr Ala Tyr Arg
           35           40           45
Asp Arg Arg Gln Arg Lys Arg Gln Phe Arg Gln Leu Trp Ile Ala Arg
           50           55           60
Ile Asn Ala Ala Ala Arg Gln Asn Gly Ile Ser Tyr Ser Lys Phe Ile
65           70           75           80
Asn Gly Leu Lys Lys Ala Ser Val Glu Ile Asp Arg Lys Ile Leu Ala
           85           90           95
Asp Ile Ala Val Phe Asp Lys Val Ala Phe Thr Ala Leu Val Glu Lys
           100           105           110
Ala Lys Ala Ala Leu Ala
           115

```

<210> 395

<211> 65

<212> PRT

<213> E. Coli

<400> 395

```

Met Pro Lys Ile Lys Thr Val Arg Gly Ala Ala Lys Arg Phe Lys Lys
 1           5           10           15
Thr Gly Lys Gly Gly Phe Lys His Lys His Ala Asn Leu Arg His Ile
           20           25           30
Leu Thr Lys Lys Ala Thr Lys Arg Lys Arg His Leu Arg Pro Lys Ala
           35           40           45
Met Val Ser Lys Gly Asp Leu Gly Leu Val Ile Ala Cys Leu Pro Tyr
50           55           60
Ala
65

```


<210> 396
 <211> 180
 <212> PRT
 <213> E. Coli

<400> 396
 Met Lys Gly Gly Lys Arg Val Gln Thr Ala Arg Pro Asn Arg Ile Asn
 1 5 10 15
 Gly Glu Ile Arg Ala Gln Glu Val Arg Leu Thr Gly Leu Glu Gly Glu
 20 25 30
 Gln Leu Gly Ile Val Ser Leu Arg Glu Ala Leu Glu Lys Ala Glu Glu
 35 40 45
 Ala Gly Val Asp Leu Val Glu Ile Ser Pro Asn Ala Glu Pro Pro Val
 50 55 60
 Cys Arg Ile Met Asp Tyr Gly Lys Phe Leu Tyr Glu Lys Ser Lys Ser
 65 70 75 80
 Ser Lys Glu Gln Lys Lys Gln Lys Val Ile Gln Val Lys Glu Ile
 85 90 95
 Lys Phe Arg Pro Gly Thr Asp Glu Gly Asp Tyr Gln Val Lys Leu Arg
 100 105 110
 Ser Leu Ile Arg Phe Leu Glu Glu Gly Asp Lys Ala Lys Ile Thr Leu
 115 120 125
 Arg Phe Arg Gly Arg Glu Met Ala His Gln Gln Ile Gly Met Glu Val
 130 135 140
 Leu Asn Arg Val Lys Asp Asp Leu Gln Glu Leu Ala Val Val Glu Ser
 145 150 155 160
 Phe Pro Thr Lys Ile Glu Gly Arg Gln Met Ile Met Val Leu Ala Pro
 165 170 175
 Lys Lys Lys Gln
 180

<210> 397
 <211> 642
 <212> PRT
 <213> E. Coli

<400> 397
 Met Pro Val Ile Thr Leu Pro Asp Gly Ser Gln Arg His Tyr Asp His
 1 5 10 15
 Ala Val Ser Pro Met Asp Val Ala Leu Asp Ile Gly Pro Gly Leu Ala
 20 25 30
 Lys Ala Cys Ile Ala Gly Arg Val Asn Gly Glu Leu Val Asp Ala Cys
 35 40 45
 Asp Leu Ile Glu Asn Asp Ala Gln Leu Ser Ile Ile Thr Ala Lys Asp
 50 55 60
 Glu Glu Gly Leu Glu Ile Ile Arg His Ser Cys Ala His Leu Leu Gly
 65 70 75 80
 His Ala Ile Lys Gln Leu Trp Pro His Thr Lys Met Ala Ile Gly Pro
 85 90 95
 Val Ile Asp Asn Gly Phe Tyr Tyr Asp Val Asp Leu Asp Arg Thr Leu
 100 105 110
 Thr Gln Glu Asp Val Glu Ala Leu Glu Lys Arg Met His Glu Leu Ala
 115 120 125
 Glu Lys Asn Tyr Asp Val Ile Lys Lys Lys Val Ser Trp His Glu Ala
 130 135 140
 Arg Glu Thr Phe Ala Asn Arg Gly Glu Ser Tyr Lys Val Ser Ile Leu
 145 150 155 160
 Asp Glu Asn Ile Ala His Asp Asp Lys Pro Gly Leu Tyr Phe His Glu
 165 170 175

Glu Tyr Val Asp Met Cys Arg Gly Pro His Val Pro Asn Met Arg Phe
 180 185 190
 Cys His His Phe Lys Leu Met Lys Thr Ala Gly Ala Tyr Trp Arg Gly
 195 200 205
 Asp Ser Asn Asn Lys Met Leu Gln Arg Ile Tyr Gly Thr Ala Trp Ala
 210 215 220
 Asp Lys Lys Ala Leu Asn Ala Tyr Leu Gln Arg Leu Glu Glu Ala Ala
 225 230 235 240
 Lys Arg Asp His Arg Lys Ile Gly Lys Gln Leu Asp Leu Tyr His Met
 245 250 255
 Gln Glu Glu Ala Pro Gly Met Val Phe Trp His Asn Asp Gly Trp Thr
 260 265 270
 Ile Phe Arg Glu Leu Glu Val Phe Val Arg Ser Lys Leu Lys Glu Tyr
 275 280 285
 Gln Tyr Gln Glu Val Lys Gly Pro Phe Met Met Asp Arg Val Leu Trp
 290 295 300
 Glu Lys Thr Gly His Trp Asp Asn Tyr Lys Asp Ala Met Phe Thr Thr
 305 310 315 320
 Ser Ser Glu Asn Arg Glu Tyr Cys Ile Lys Pro Met Asn Cys Pro Gly
 325 330 335
 His Val Gln Ile Phe Asn Gln Gly Leu Lys Ser Tyr Arg Asp Leu Pro
 340 345 350
 Leu Arg Met Ala Glu Phe Gly Ser Cys His Arg Asn Glu Pro Ser Gly
 355 360 365
 Ser Leu His Gly Leu Met Arg Val Arg Gly Phe Thr Gln Asp Asp Ala
 370 375 380
 His Ile Phe Cys Thr Glu Glu Gln Ile Arg Asp Glu Val Asn Gly Cys
 385 390 395 400
 Ile Arg Leu Val Tyr Asp Met Tyr Ser Thr Phe Gly Phe Glu Lys Ile
 405 410 415
 Val Val Lys Leu Ser Thr Arg Pro Glu Lys Arg Ile Gly Ser Asp Glu
 420 425 430
 Met Trp Asp Arg Ala Glu Ala Asp Leu Ala Val Ala Leu Glu Glu Asn
 435 440 445
 Asn Ile Pro Phe Glu Tyr Gln Leu Gly Glu Gly Ala Phe Tyr Gly Pro
 450 455 460
 Lys Ile Glu Phe Thr Leu Tyr Asp Cys Leu Asp Arg Ala Trp Gln Cys
 465 470 475 480
 Gly Thr Val Gln Leu Asp Phe Ser Leu Pro Ser Arg Leu Ser Ala Ser
 485 490 495
 Tyr Val Gly Glu Asp Asn Glu Arg Lys Val Pro Val Met Ile His Arg
 500 505 510
 Ala Ile Leu Gly Ser Met Glu Arg Phe Ile Gly Ile Leu Thr Glu Glu
 515 520 525
 Phe Ala Gly Phe Phe Pro Thr Trp Leu Ala Pro Val Gln Val Val Ile
 530 535 540
 Met Asn Ile Thr Asp Ser Gln Ser Glu Tyr Val Asn Glu Leu Thr Gln
 545 550 555 560
 Lys Leu Ser Asn Ala Gly Ile Arg Val Lys Ala Asp Leu Arg Asn Glu
 565 570 575
 Lys Ile Gly Phe Lys Ile Arg Glu His Thr Leu Arg Arg Val Pro Tyr
 580 585 590
 Met Leu Val Cys Gly Asp Lys Glu Val Glu Ser Gly Lys Val Ala Val
 595 600 605
 Arg Thr Arg Arg Gly Lys Asp Leu Gly Ser Met Asp Val Asn Glu Val
 610 615 620
 Ile Glu Lys Leu Gln Gln Glu Ile Arg Ser Arg Ser Leu Lys Gln Leu
 625 630 635 640
 Glu Glu

<210> 398
 <211> 450
 <212> PRT
 <213> E. Coli

<400> 398

```

Met Thr Lys His Tyr Asp Tyr Ile Ala Ile Gly Gly Gly Ser Gly Gly
 1      5      10      15
Ile Ala Ser Ile Asn Arg Ala Ala Met Tyr Gly Gln Lys Cys Ala Leu
 20      25      30
Ile Glu Ala Lys Glu Leu Gly Gly Thr Cys Val Asn Val Gly Cys Val
 35      40      45
Pro Lys Lys Val Met Trp His Ala Ala Gln Ile Arg Glu Ala Ile His
 50      55      60
Met Tyr Gly Pro Asp Tyr Gly Phe Asp Thr Thr Ile Asn Lys Phe Asn
 65      70      75      80
Trp Glu Thr Leu Ile Ala Ser Arg Thr Ala Tyr Ile Asp Arg Ile His
 85      90      95
Thr Ser Tyr Glu Asn Val Leu Gly Lys Asn Asn Val Asp Val Ile Lys
100      105      110
Gly Phe Ala Arg Phe Val Asp Ala Lys Thr Leu Glu Val Asn Gly Glu
115      120      125
Thr Ile Thr Ala Asp His Ile Leu Ile Ala Thr Gly Gly Arg Pro Ser
130      135      140
His Pro Asp Ile Pro Gly Val Glu Tyr Gly Ile Asp Ser Asp Gly Phe
145      150      155      160
Phe Ala Leu Pro Ala Leu Pro Glu Arg Val Ala Val Val Gly Ala Gly
165      170      175
Tyr Ile Ala Val Glu Leu Ala Gly Val Ile Asn Gly Leu Gly Ala Lys
180      185      190
Thr His Leu Phe Val Arg Lys His Ala Pro Leu Arg Ser Phe Asp Pro
195      200      205
Met Ile Ser Glu Thr Leu Val Glu Val Met Asn Ala Glu Gly Pro Gln
210      215      220
Leu His Thr Asn Ala Ile Pro Lys Ala Val Val Lys Asn Thr Asp Gly
225      230      235      240
Ser Leu Thr Leu Glu Leu Glu Asp Gly Arg Ser Glu Thr Val Asp Cys
245      250      255
Leu Ile Trp Ala Ile Gly Arg Glu Pro Ala Asn Asp Asn Ile Asn Leu
260      265      270
Glu Ala Ala Gly Val Lys Thr Asn Glu Lys Gly Tyr Ile Val Val Asp
275      280      285
Lys Tyr Gln Asn Thr Asn Ile Glu Gly Ile Tyr Ala Val Gly Asp Asn
290      295      300
Thr Gly Ala Val Glu Leu Thr Pro Val Ala Val Ala Ala Gly Arg Arg
305      310      315      320
Leu Ser Glu Arg Leu Phe Asn Asn Lys Pro Asp Glu His Leu Asp Tyr
325      330      335
Ser Asn Ile Pro Thr Val Val Phe Ser His Pro Pro Ile Gly Thr Val
340      345      350
Gly Leu Thr Glu Pro Gln Ala Arg Glu Gln Tyr Gly Asp Asp Gln Val
355      360      365
Lys Val Tyr Lys Ser Ser Phe Thr Ala Met Tyr Thr Ala Val Thr Thr
370      375      380
His Arg Gln Pro Cys Arg Met Lys Leu Val Cys Val Gly Ser Glu Glu
385      390      395      400
Lys Ile Val Gly Ile His Gly Ile Gly Phe Gly Met Asp Glu Met Leu
405      410      415
Gln Gly Phe Ala Val Ala Leu Lys Met Gly Ala Thr Lys Lys Asp Phe
420      425      430

```

Asp Asn Thr Val Ala Ile His Pro Thr Ala Ala Glu Glu Phe Val Thr
 435 440 445
 Met Arg
 450

<210> 399
 <211> 2894
 <212> RNA
 <213> E. Coli

<400> 399

aagguuaagc	cucacggguu	uuuaguaccg	guuagcucaa	cgcaucgcug	cgcuuacaca	60
cccggccuau	caacgucguc	gucuuaacg	uuccuucagg	acccuuaaag	ggucaggagg	120
aacucaucuc	ggggcaaguu	ucgugcuuag	augcuuucag	cacuuauuc	uuccgcuuuu	180
agcuaccggg	cagugccauu	ggcaugacaa	cccgaacacc	agugaugcgu	ccacuccggg	240
ccucucguac	uaggagcagc	ccccucagu	ucuccagcgc	ccacggcgag	uagggaccga	300
acugucucac	gacguucuaa	acccagcucg	cguaaccacu	uaaauaggcg	acagccauac	360
ccuugggacc	uacuucagcc	ccaggauug	augagccgac	aucgaggugc	caaacaccgc	420
cgucgauaug	aacucuuagg	cgguuacagc	cuguuauccc	cgagauaccu	uuuauccguu	480
gagcgauggc	ccuuccauuc	agaaccaccg	gaucacuaug	accugcuuuc	gcaccugcuc	540
gcgccguac	gcucgcaguc	aagcuggguu	augccauugc	acuaaccucc	ugauguccga	600
ccaggauuag	ccaaccuucg	ugcuccucgg	uuacucuuua	ggaggagacc	gccccaguca	660
aaacuaccac	cagacacugu	ccgcaaccgg	gauuacgggu	caacguuaga	acaucaaa	720
uuaaagggu	guuuucaa	gucggcucca	ugcagacugg	cguccacacu	ucaaagccuc	780
ccaccuaucc	uacacaucaa	ggcucaaugu	ucagugucua	gcuuauagua	agguuacagg	840
ggcuuuuccg	ucuuucccg	gguaacacug	aucuucacag	cgaguucuu	uucacugagu	900
cucgggugga	gacagccugg	ccaucauuac	gccauucgug	caggucggaa	cuuaccggac	960
aaaggauuuc	gcuaccuua	gaccguuua	guuacggcg	ccguuuaccg	gggcuucgau	1020
caagagcuuc	gcuugcgcu	accccauca	uuuacuuucc	ggcaccgggg	agggcucaca	1080
ccguauuagc	ccacuucugu	guuugcacag	ugcuguguuu	uuauuaaaca	guugcagcca	1140
gcuuguauc	ucgacugauu	ucagcuccau	ccgcgaggga	ccuacccuac	auaucagcgu	1200
gcccucuccc	gaaguuaacg	caccuuuuug	ccuaguuccu	ucaccccgag	ucucuaaag	1260
gcccugguau	ucucuaccug	accaccugug	ucgguuuugg	guacgauuu	auguuaccug	1320
augcuuagag	gcuuuuccug	gaagcagggg	auuuuguugc	ucagcaccgu	agugccucgu	1380
caucacgccc	cagccuugau	uuuccggauu	ugccuggaaa	accagccuac	acgcuuaaac	1440
cgggacaacc	gucgcccggc	caacauagcc	uucuccgucc	ccccuucgca	guuacaccaa	1500
guacaggga	uuuaaccugu	uucccaucga	cuacgcccuu	cgccucgccc	uuaggggucg	1560
acucacccug	ccccgauuua	cguuaggacg	gaacccuugg	ucuuuccggc	agcgggcuuu	1620
ucaccccgcu	uauvcguuac	uauvcagcga	uucgcacuu	ugauaccucc	agcaugccuc	1680
acagcacacc	uucgcaggcu	uacagaacgc	uccccuaccc	aaacacgcau	aagcgucgcu	1740
gccgcagcuu	cggugcagug	uuuagccccg	uuacauucuc	cgcgagggcc	gacucgacca	1800
gugagcuauu	acgcuuucuu	uaaauagugg	cugcuucuaa	gccaaacucc	uggcugucug	1860
ggccuuucca	caucguuuuc	cacuuuaaca	ugacuauugg	accuuagcug	gcggucuggg	1920
uuuuuuuccu	cuucacgagc	gacguuagca	cccgcggugu	gucucccgug	auaacaauuc	1980
ccgguaauuc	caguuugcau	cggguuggua	agucgggag	accccccugc	cgaaacagug	2040
cucuaacccc	ggagaugaa	ucacgagggc	cuaccuaaa	agcuuucggg	gagaaccagc	2100
uauucucccg	uuugauuagg	cuuucacccc	cagccacaag	ucauccgcua	auuuuucaac	2160
auuagucgg	ucggucuccc	aguuauguuu	acccaaccuu	caaccugccc	auggcuaag	2220
caccggguuu	cgggucuaaa	cccugcaacu	uaacgcccag	uuuagacucg	guuucccuuc	2280
ggcuccccua	uucgguuaac	cuugcuacag	aaauuaaguc	gcugacccau	uaucaaaaag	2340
guacgcaguc	acacgcuuaa	gcgugcuccc	acugcuugua	cguaacagg	uucaggguuc	2400
uuuuacacuc	ccucgcccgg	guuucuuucg	ccuuucccuc	acgguaucgg	uucacuaucg	2460
gucagucagg	aguauuuagc	cuuggaggau	ggucccccca	uaauacagac	ggauaccacg	2520
ugucccgccc	uacucaucga	gcucacagca	ugugcauuuu	uguguaagg	gcugucaccc	2580
uguaucggc	gccuuuccag	acgcuuccac	uaacacacac	acugauucag	gcucugggcu	2640
gcuccccguu	cgcucgccc	uacuggggga	aucucggguu	auuucuuuuc	cucggggguac	2700
uuagauguuu	caguuccccc	gguuucgguc	auuaaccuau	ggauuacagu	aaugauagug	2760
ugucgaaaca	cacugggguu	ccccauucgg	aaucgcccgg	uuauaacgg	ucauauacc	2820
uuaccgacgc	uuauvcgaga	uuagcacguc	cuuacucg	ucugacugcc	agggcaucca	2880

ccguguacgc uuagucgcuu aacc

2894

<210> 400
 <211> 120
 <212> RNA
 <213> E. Coli

<400> 400

augccuggca guucccuacu cucgcauggg gagacccac acuaccaucg gcgcuacggc	60
guuucacuuu ugaguuaggc auggggucag gugggaccac cgcgcuaagg ccgccaggca	120

<210> 401
 <211> 76
 <212> RNA
 <213> E. Coli

<400> 401

gucccuuucg ucuagaggcc caggacaccg cccuuucacg gcgguaacag ggguucgaau	60
cccuaggagg acgcca	76

<210> 402
 <211> 1549
 <212> RNA
 <213> E. Coli

<400> 402

aaauguaga guuugaucu ggcucagau gaacgcuggc ggcaggccua acacaugcaa	60
gucgaacggg aacaggaagc agcuugcugc uucgcugacg aguggcggac gggugaguaa	120
ugucugggaa gcugccugau ggggggggaa aacuaucugga aacgguaagcu aaauaccgau	180
aaugucgcaa gaccaaagag ggggaccuuc gggccucuuu ccaucggau ugcccagau	240
ggauuagcuu guugggggg uaacggcuca ccaaggcgac gaucuuagc uggucugaga	300
ggauagaccag ccacacugga acugagacac gguccagacu ccuacgggag gcagcagugg	360
ggaaauuugc acaaugggcg caagccugau gcagccaugc cgcguguaug aagaaggccu	420
ucggguugua aaguacuuc agcggggagg aaggaguaa aguuauuacc uuugcuauu	480
gacguuacc gcagaagaag caccggcuua cuccgugcca gcagccgagg aaauacggag	540
ggugcaagcg uuaaucggaa uuacggggcg uaaagcgac gcagccgggu ugguuuaguc	600
agauugaaa uccccggcu caaccuggga acugcaucg auacuggcaa gcuugagucu	660
cguagagggg gguagaauuc caggguuagc ggugaaaugc guagagaucg ggaggauuac	720
cgguggcgaa ggcggccccc uggacgaaga cugacgcuca ggugcgaaa cggggggagc	780
aaacaggauu agauaccug guaguccacg ccguaaacga ugucgacuug gaggguuguc	840
ccuugaggcg uggcuucccg agcuuacgcg uuaagucgac cgccugggga guacggccgc	900
aaggguaaaa cucaauagaa uugacggggg cccgcacaag cgguggagca ugugguuuaa	960
uucgaugcaa cgcgaagaac cuuaccuggu cuugacauc accggaaguu ucagagauga	1020
gaaugugccu ucgggaaccg ugagacaggu gcugcauggc ugucgucagc ucguguuug	1080
aaauguuggg uuaagucccg caacgagcgc aaccuuuau cuuuguugcc agcggucccg	1140
ccgggaacuc aaaggagacu gccagugaua aacuggaggga agggggggau gacgucaagu	1200
caucauggcc cuuacgacca gggcuacaca cgugcuacaa uggcgcauac aaagagaagc	1260
gaccucgcga gagcaagcgg accucauaaa gugcgucgua guccggauug gagucgcaa	1320
cucgacucca ugaagucgga aucgcuagua aucguggauc agaaugccac ggugaauacg	1380
uuuccggggc uuquacacac cgcccgucac accaugggag uggguugcaa aagaaguag	1440
uagcuuaacc uucgggaggg cgcuuaccac uuugugauuc augacuggg ugaagucgua	1500
acaagguaac cguaggggaa ccugcgguug gaucaccucc uuaccuuaa	1549

<210> 403
 <211> 17
 <212> DNA
 <213> Artificial
 <220>
 <223> Primer Oligonucleotide

<400> 403
 tgtttatcag accgctt 17

<210> 404
 <211> 18
 <212> DNA
 <213> Artificial
 <220>
 <223> Primer Oligonucleotide

<400> 404
 acaatttcac acagcctc 18

<210> 405
 <211> 159
 <212> DNA
 <213> Escherichia coli

<400> 405
 cagggtggtat ggaaacccaa aatggagacg ggaagctgaa ccagatagtt actggagggtg 60
 atcaccagca gatgaaataa cgataaccag aacaacgcct tatagcgttg agtttgcgag 120
 aaaacgttca tattgtacct ttttgattaa ccattgggg 159

<210> 406
 <211> 640
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(640)
 <223> n = A,T,C or G

<400> 406
 ggggnccaaa gtgtttgggn cgggcaactg gagccaacc ttaanttnng ggaaattttt 60
 aanaaaaggc ggggatttgt nagccacggg ngattanttt anaataaatt aagtgttgcc 120
 ataaggggac aaagngaagg aagtggntat taanggannc gccaatgcga nttagggcag 180
 accattcggc cattcgctt cttggttacc gaagtccatc cagatagccg ttgccngacc 240
 gaccagattc gcttcnggca caaagcccca gtaacggctg tccgcgctgt tgcgcgggtt 300
 gtcgccccac atgaagtatt gtcccggagg aacaatccag gttgccagtt gttgccctgg 360
 ctgctggtaa tacatcccca cctgatcctg cgcaatcggc actgtcagaa tgcggtgcgt 420
 cacatcaccc agtgtctctt tacgctcgga aagacgaatt ccattttctt tggtttcgtt 480
 ttccggcact tcaaagaatc cgctggctgc ttccccacca ttacggcgtg agaaggctctg 540
 aacgaaatcg ctcggttcca cgtttgagta ggtgaccggc agcgcgtttt cacacgcctg 600
 gccggaactg catcccgggt gaatcgtcag ctcttttgag 640

<210> 407
 <211> 682
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature

<222> (1)...(682)

<223> n = A,T,C or G

<400> 407

cctgcagggt	aatgtcgcca	ttaaactggc	gcaggcagcc	aaagagttgc	tccgctteta	60
cccagtcggc	agcgacaact	tcggttaaag	tcgcaaaatt	atcatctgca	ctcactgcgt	120
gacgtaagcg	gatggagtg	ccggaaacct	catagtgaac	gccaccaggt	tggcctgcat	180
cgctttgtag	cgtacgcgcg	gcattggcaa	taagattcag	atactcagac	tcttccgggg	240
ccttcgccag	cataaaagag	gaggatgctc	gcgtatgcag	caactgctcc	agcgcaaat	300
gcagccggcg	ttgagtatca	ctgaataaag	gatcgttttc	gtcaatcaaa	tgtggctgag	360
caaataatttc	ctgatagcta	tcggatcatg	gaaccagggt	acgccatgca	agtttcgtaa	420
tggtcaaaagt	tgatgttttt	tagtctgttg	tcaaagccgc	nattataccn	gtaaccggca	480
ctacagcaca	cgtagaaagc	acccgacaat	actcctggca	tgggcgttaa	agctcacagg	540
atggagatct	tttcttcact	ggcctaaaaa	gctgatattc	tgtaaagagt	tacacngtaa	600
cattgagatc	gctatgaaat	atcaacaact	tggaaaatct	tgnaaagcng	gttggaaaaa	660
ggaaagtatc	tggttaagaa	gc				682

<210> 408

<211> 309

<212> DNA

<213> Escherichia coli

<400> 408

ggggatccgg	cagaatttta	cgctgaccaa	tgacgcgacg	acgtggcatg	gaaatactcc	60
gttggttaatt	caggattgtc	caaaactcta	cgagtttagt	ttgacattta	agttaaaacg	120
tttggcctta	cttaacggag	aaccattaag	ccttaggacg	cttcacgcca	tacttggaac	180
gagcctgctt	acggtcttta	acgccggagc	agtcaagcgc	accacgtacg	gtgtggtaac	240
gaacaccggg	gaggtcctta	acacgaccgc	cacggatcag	gatcacggag	tgctcctgca	300
gccaaagctt						309

<210> 409

<211> 1167

<212> DNA

<213> Escherichia coli

<400> 409

gtcgacccat	ctgtccattg	agcggacagt	ttgtgcaaca	ctattttgtt	gaccggaaaa	60
tggaacactt	tccgcaatgc	ctgttgctat	cacgcttaaa	ccatttcatt	gcgatttaca	120
cagaacggac	gtcctgtcgc	agtatattaa	gtcgtcgata	gaaacaagca	ttgaaaggca	180
cagcagtagt	caaacagtgt	gaaacgctac	tggcgcctta	cagcgcaaaa	aggctgggtga	240
ctaaaaagtc	accagccatc	agcctgattt	ctcaggctgc	aaccggaaag	gttggcttat	300
ttaaactcaa	cttcagcgcc	agcttcttcc	agagcttttt	tcagtgcctc	tgcgtcgtct	360
ttgtctacgc	cttctttcag	agcagccggt	gcagattcta	ccaggctctt	agcttctttc	420
agaccagggc	cagttgcgcc	acgtactgct	ttgataacag	caactttgtt	agcgccagca	480
gctttcagaa	ttacgtcgaa	ttcagttttt	tcttcagcag	cttcaaccgg	gccagcagct	540
acagctacag	cagcagcagc	ggaaacaccg	aatttttctt	ycattgcaga	gatcaagttc	600
tacaacgtcc	attacagaca	tagctgcaac	tgcttcaatg	awttgatctt	tagtgataga	660
cattttaaak	gttcttgaat	atcagaataa	gtttatacgt	aagcgaatgc	gttaaaaaaga	720
taactgcgaw	taagcagctt	ytttcgcac	gcgtacagma	gccagagtac	gaaccagttt	780
gccagccgaa	gcttctttca	tggttgccat	caggcgtgca	attgcttctt	cgtaggtcgg	840
cagagttgcc	aggcggtcga	tctgagacgc	cgggatcagc	tcaccttcaa	aggcagcggc	900
tttgacctca	aattttgcat	tcgctttcgc	gaactctttg	aacagacgag	cagcagcgcc	960
cgggtgttcc	atagagtatg	caatcagggt	cggaccaaca	aacgcgtctt	tcaggcactc	1020
gaacggagta	ccttcaacag	cacggcgagc	cagggtgtta	cgaacaacac	gcatgtatac	1080
gccagcttcg	cgacctgctt	tacgcagttc	agtcatttta	tctacagtta	cgcccacggg	1140
aatccgcaac	tactgcaagc	caagctt				1167

<210> 410

<211> 404

<212> DNA

<213> Escherichia coli

<400> 410
 caacmctatt ttgktggacc ggaaaaakgga acactttccg cawkgcctgt tgctatcacg 60
 cttaaaccat ttcattgcga ttacacaga acggacgtcc tgctgcagta tattaagtgc 120
 tcgatagaaa caagcattga aaggcacagc agtagtcaaa cagtgtgaaa cgctactggc 180
 gccttacagc gcaaaaaggc tgggtgactaa aaagtcacca gccatcagcc tgatttctca 240
 ggctgcaacc ggaagggttg gcttatttaa cttcaacttc agcgccagct tcttccagag 300
 cttttttcag tgcttctgcg tcgtctttgc tcacgccttc tttcagagca gccggtgcag 360
 attctaccag gtcttttagct tctttcagac ccaggccagt tgcg 404

<210> 411
 <211> 152
 <212> DNA
 <213> Escherichia coli

<400> 411
 agagcttttt tcagtgtctc tgcgtcgtct ttgctcacgc cttctttcaa gaggcagccc 60
 gtgcagattc taccaggtct ttagcttctt tcagaccag gccagttgcg ccacgtactg 120
 ctttgataac agcaactttg ttgagccag ca 152

<210> 412
 <211> 825
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(825)
 <223> n = A,T,C or G

<400> 412
 gatccgtcga cccatctgtc cattgagcgg acagtttgtg caacactatt ttgttgaccg 60
 gaaaatggaa cactttccgc aatgcctgtt gctatcacgc ttaamccatt tcattgcat 120
 ttacacagaa cggacgtcct gtcgcagtat attaatgctg cgatagaaaac aagcattgaa 180
 aggcacagca gtagtcaaac agtgtgaaac gctactggcg ccttacagcg caaaaaggct 240
 ggtgactaaa aagtcaccag ccatcagcct gatttctcag gctgcaaccg gaagggttgg 300
 cttatttaac ttcaacttca gcgccagctt cttccagagc ttttttcagt gcttctgcgt 360
 cgtctttgct cagcgccttct ttcagagcag ccgggtgcag attctaccag gtcttttagct 420
 tctttcagac ccaggccagt tgcgccacgt actgctttga taacagcaac ttgtttagcg 480
 ccagcagctt tcagaattac gtcgaattca agttttttct tcagcagctt caaccggggc 540
 agcagctaca gctacagcag cagcagcggg aacaccgaat ttttcttyca ttggcagaga 600
 tcaagttcta caacgtccat tacagacata gctgcaactg cttcaatgat tkgatcttwa 660
 gtgatagaca tttaaattgt tcctgaatat cagaataagt ttatacgtaa gcgaatgcgt 720
 taaaaagata actgcgatta agcagcttct ttcgcategc gtacagcagc cagaggtcga 780
 accagtttgc cagccgaagg ttgcttttc agcctnnnn natta 825

<210> 413
 <211> 425
 <212> DNA
 <213> Escherichia coli

<400> 413
 agtagtcaaa cagggtgkgra acgctactgg cgccttacag cgcaaaaagg ctggtgacta 60
 aaaagtcacc agccatcacc ctgattttctc aggctgcaac ccggaagggt tggttattt 120
 aacttcaact tcagcgccag cttcttccag agcttttttc agtgcttctg cgtcgtcttt 180
 gctcacgcct tctttcagag cagccggtgc agattctacc aggtcttttag cttctttcag 240
 acccaggcca gttgcgccac gtactgcttt gataacagca actttgttag cgccagcagc 300
 tttcagaatt acgtcgatt cagttttttc ttcagcagct tcaaccgggc cagcagctac 360
 agctacagca gcagcagcgg aaacaccgga atttttcttc cattgcagag atcaagttct 420
 acaac 425

<210> 414
 <211> 126
 <212> DNA
 <213> Escherichia coli

<400> 414
 agagcttttt tcagtgttc tgctgtctt ttgctcacgc cttctttcag agcagccggg 60
 gcagattcta ccagggtttt agcttctttc agaccaggc cagttgcgcc acgtactgct 120
 ttrata 126

<210> 415
 <211> 264
 <212> DNA
 <213> Escherichia coli

<400> 415
 ctgcmaccgg garggggtgg cttatttaac ttcaacttca gcgccagctt cttcagagc 60
 ttttttcaag tgcttctgcy tcttctttgc tcacgccttc tttcagagca gccgggtgcag 120
 attctaccag gtcttttagct tctttcagac ccaggccagt tgcgccacgt actgctttga 180
 taacagcaac tttgttagcg ccagcagctt tcagaattac gtcgaattca gttttttctt 240
 cagcagcttc aaccgggcca gcag 264

<210> 416
 <211> 201
 <212> DNA
 <213> Escherichia coli

<400> 416
 cgcataccct gcagcatcgg cccgatggag atcagggtcgg cagaacgctg taccgctttg 60
 taggtgggtg taccgggtgt cagatccggg aagatgaaca cggtagcgcg acctgcaacc 120
 ggagagttcg gcgctttgga tttcgcaacg tcagccatta ccgcagcgtc gtactgcage 180
 ggaccgtcga tcatcaggtc a 201

<210> 417
 <211> 239
 <212> DNA
 <213> Escherichia coli

<400> 417
 aattcagcag ttgacagtgg cataaacgta actggtgact ttgcccggc atgacgccgg 60
 gcttttttta ttattccgtg acttccagcg tagtgaaggc aaactttctg ccatcaaata 120
 gccctgact ggttagtttt agcgcgggga tctctggcag agaaagaaac gccatctgaa 180
 taaacggctc atcgggtaac ggaccgcatt caggggcggc ggctttcaag gcgtcaatt 239

<210> 418
 <211> 223
 <212> DNA
 <213> Escherichia coli

<400> 418
 ttcttttttt cgtcaacggt gtccagaatc attttattta cctcgggtac ttatgctgat 60
 ttttattatt atggggaagg tgttatttat gaggttcatt tatgccgtaa cgacaatgaa 120
 ctcgggaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taatttaatt 180
 aatactattt aaatattatt ttgagcatat gcacataagg ttg 223

<210> 419
 <211> 223
 <212> DNA
 <213> Escherichia coli

<400> 419

```

ttcttttttt cgtcaacggt gtccagaatc attttattta cctcgggtac ttatgctgat 60
ttttattatt atggggaagg tgttatttat gagtttcatt tatgccgtaa cgacaatgaa 120
ctcgggaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taatttaatt 180
aatactattt aaatattatt ttgagcatat gcacataagg ttg 223

```

<210> 420
 <211> 212
 <212> DNA
 <213> Escherichia coli

```

<400> 420
aatagcgggt atgcacgcct ttcttttttt cgtcaacggt gtccagaatc attttattta 60
cctcgggtac ttatgctgat ttttattatt atggggaagg tgttatttat gagtttcatt 120
tatgccgtaa cgmcaatgaa ctcgggaatt agtataagca gcgcgagaat aataatcatt 180
gtgcaaatgc taatttaatt aatactattt aa 212

```

<210> 421
 <211> 438
 <212> DNA
 <213> Escherichia coli

```

<400> 421
cctctgtaaat tatcgcccgt ggcataaaaa ctgctgctcaa acgcccgtctt tgccagcagc 60
caggccataa atgccaccag aattatcgtc aaccaaccaa ttgctgaaac gccaaagcagc 120
agcggggcgg agagctggtt cagttcggcg ggtaaccctt caatccattt gccgccagtc 180
cacagcaaca tgatgcctct gtacaaccct aacgtgccaa ggggtggcaac aatggcaggg 240
atcttttagcc acgcgaccag gacaccgttg aaaaatcccg cgagcaaac aagcagtaaa 300
gtcgcgacac aagcaacagg tagtgaatat cctgcgttca gtaacatccc caacagcacc 360
gcgcacattc cgggtaatcg aaccccactt gaaacatcaa tattgsgsgt aagcattwcc 420
aagcgttcgs gcccatkg 438

```

<210> 422
 <211> 682
 <212> DNA
 <213> Escherichia coli

```

<400> 422
aatcccggt gatccgtcga ccgtgcgtt ccggttggtg caaccgcgca aatggcgcgg 60
cggttaagtat gccggggtta ttccttcccc gttgaggaca ccgggttgct aggttgacca 120
tacgcttaag tgacaacccc gctgcaacgc cctctgttat caattttctg gtgacgtttg 180
gcggtatcag ttttactccg tgactgctct gccgcccttt ttaaagtga ttttgatg 240
tggtgaatgc ggctgagcgc acgcggaaca gttaaaacca aaaacagtgt tatgggtgga 300
ttctctgcat ccggcggtta ttgttaactg gttaacgtca cctggaggca ccaggcactg 360
catcacaaaa ttcattgttg aggacgcgat aatgaaaaag ttattacca acgttaatac 420
gtctgaaggt tgttttga tgggtgtcac tatcagtaac ccagtattta ctgaagatgc 480
cattaacaag agaaaaaag aacgggagct attaaataa atatgcattg tttcaatgct 540
ggctcgttta cgtctgatgc caaaaggatg tgcacaatga attcagcatt tgtgcttgtt 600
ctgacagttt ttcttgtttc cggagagcca gttgatattg cagtcagtgt tcacaggaca 660
atgcaggagt gatgactgca gc 682

```

<210> 423
 <211> 600
 <212> DNA
 <213> Escherichia coli

```

<400> 423
ggggatccga ttgtgactgc tctgcgcgcc tttttaagt gaattttgtg atgtggtgaa 60
tgcgsgctgag cgcacgcgga acagttaaaa caaaaaacag tgttatgggt ggattctctg 120
tatccggcgt taattgttaa ctggttaacg tcacctggag gcaccaggca ctgcatcaca 180
aaattcattg ttgaggacgc gataatgaaa acgttattac caaacgttaa tacgtctgaa 240
gggtgttttg aaattggtgt cactatcagt aaccagtat ttactgaaga tgccattaac 300

```

```

aagagaaaac aagaacggga gctattaaat aaaatatgca ttgtttcaat gctggctcgt    360
ttacgtctga tgccaaaagg atgtgcacaa tgaattcagc atttgtgctt gttctgacag    420
tttttcttgt ttccggagag ccagttgata ttgcagtcag tgttcacagg acaatgcagg    480
agtgtatgac tgcagcaacc gaacagaaaa ttcccggtaa ctgttaccgc gtcgataaag    540
ttattcacca ggataatatc gaaatcccgg caggtcttta aacagttccg taataaataa    600

```

<210> 424
 <211> 100
 <212> DNA
 <213> Escherichia coli

```

<400> 424
gggatccagc aagaagatgc ggttgtagcg tcctcacgca gatgcgcaaa gctactcagc    60
aactgacctt tcttcgcaat aagcacgcca ttacggtcat    100

```

<210> 425
 <211> 465
 <212> DNA
 <213> Escherichia coli

```

<400> 425
tcgcgtgttt accttcaaca tcggttaactt tctggcggat agtttcacgg taagcaacct    60
gcggtttacc tacgttcgct tcaacgttga attcacgctt catacgggtca acgatgatgt    120
cgagggtgcag ttccgccata ccgcgcgatga tggctctggt agattcttcg tcagtcata    180
cacggaaaga cgggtcttct tttagccagac ggcccagagc cagaccattt tttctctggt    240
cagcttttgtt ttccggttca actgcgatgg agattaccgg ctccagggaat tccatacgtt    300
ccagaatgat cggcgcatcc gggtcacaca ggggtgtcacc agtgggttacg tctttcagac    360
cgatagcagc agcgatgtcg cccgcgcgaa cttctttgat ctcttcacgt ttgttagcgt    420
gcatctgaac gatacgaccg aaacgctcac gtgcagcttt cacggg    465

```

<210> 426
 <211> 653
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(653)
 <223> n = A,T,C or G

```

<400> 426
tgatcggtc aagcagaact ggtttcgctt tcttaaagcc ttctttaaag gcgatagaag    60
cagccagttt aaacgccagt tcagaggagt caacgtcatg gtaagaaccg aagtgcagac    120
gaatacccat gtctactacc gggtagcctg ccagcggacc tgctttcagc tgttcctgga    180
tacctttatc aacggccggg atgtattcgc cagggattac accaccttta atgtcgttga    240
tgaactcgta gcctttcggg tttgaacccg gctccagcgg gtacatgtcg ataacaacat    300
gaccatactg accacgacca ccagactgtt tcgcgtgttt accttcaaca tcggttaactt    360
tctggcggat agtttcacgg taagcaacct gcggtttacc tacgttcgct tcaacgttga    420
attcacgctt catacgggtca acgatgatgt cgagggtgcag ttccgccata ccgcgatgat    480
ggctgggttag attcttcgtc agtccataca cggnaagacg ggtcttnttt agccagacgg    540
gccagagnca gaccttttt tttctggcag ctttgnttc ggtcaactgc gatggaaata    600
cccggctcaa ggaattcata cgtttcanaa tgatcggggc attccgggtc aca    653

```

<210> 427
 <211> 268
 <212> DNA
 <213> Escherichia coli

```

<400> 427
ctttcttaaa gccttcttta aaggcgaatg aagcagccag tttaaaccgc agttcagagg    60
agtcaacgtc atggtaaaga ccgaagtgca gacgaatacc catgtctact accgggtagc    120

```

ctgccagcgg	acctgctttc	agctgttcct	ggataccttt	atcaacggcc	gggatgtatt	180
cgccagggat	tacaccacct	ttaatgtcgt	tgatgaactc	gtagcctttc	gggtttgaac	240
ccggctccag	cggttacatg	tcgataac				268

<210> 428
 <211> 330
 <212> DNA
 <213> Escherichia coli

<400> 428						
gttttgggga	gatgtaagg	ctaactctgaa	tggtgcatt	ccttggttaa	ggaaaaacga	60
atgactgatt	gccgatacct	gattaaacgg	gtcatcaaaa	tcattcattgc	tggtttacag	120
ctgactcctc	tggtcttata	acacaaggaa	acgtacttaa	gggtgcgtccg	gtgaaccagt	180
cggaacgacc	tttaataact	ataaataagt	gtctgggcag	atactatata	aattaactta	240
gtgaatgatt	atgctaattg	catcaattaa	ataaatataa	tggtcgtaag	gcttcccagt	300
aatataatta	atactctact	tccagagtag				330

<210> 429
 <211> 465
 <212> DNA
 <213> Escherichia coli

<400> 429						
gttttgggga	gatgtaagg	ctaactctgaa	tggtgcatt	ccttggttaa	ggaaaaacga	60
atgactgatt	gccgatacct	gattaaacgg	gtcatcaaaa	tcattcattgc	tggtttacag	120
ctgactcctc	tggtcttata	acacaaggaa	acgtacttaa	gggtgcgtccg	gtgaaccagt	180
cggaacgacc	tttaataact	ataaataagt	gtctgggcag	atactatata	aattaactta	240
gtgaatgatt	atgctaattg	catcaattaa	ataaatataa	tggtcgtaag	gcttcccagt	300
aatataatta	atactctact	tccagagtag	aatattaaat	tttatccgcg	tggtgcatca	360
gcacaaattt	atcccacac	tggtcttctg	tctcgacatg	cgccggatct	ttcacaatag	420
tattggggat	cgggcacacc	ttctggcagg	ttggtgtctc	gtagt		465

<210> 430
 <211> 379
 <212> DNA
 <213> Escherichia coli

<400> 430						
aactctgaatg	gctgcattcc	ttgtttaagg	aaaaacgaat	gactgattgc	cgatacctga	60
ttaaacgggt	catcaaaatc	atcattgctg	ttttacagct	gatccttctg	ttcttataac	120
acaaggaaac	gtacttaagg	tgctgccggg	gaaccagtcg	gacgcacctt	taataactat	180
aaataagtgt	ctgggcagat	actatataaa	ttactttagt	gaatgattat	gctaagtgtca	240
tcaattaaat	aaatataatg	gcgttaaggc	ttcccagtaa	tataattaat	actctacttc	300
cagagtagaa	tattaaattt	tatccgcgtg	gtgcatcagc	acaaatttat	cccacaactg	360
ttcttctgtc	tcgacatgc					379

<210> 431
 <211> 443
 <212> DNA
 <213> Escherichia coli

<400> 431						
aagatgatgt	gatgagaaag	tcaatttgaa	taagacaata	ttaagagcta	aaaaaatgtc	60
aaaaaacact	aaatcaaaaa	ataatggcat	tagaaaaatat	aatgcgaaaa	cggaggtgaa	120
attagtttat	ttcaaatgag	gaaaaatctcc	cggcgaaaaa	accgggagat	gaaagtgtga	180
tggttatcaa	ataaacaaca	gaggagaaat	ttttaacgca	gccattcagg	caaactgttt	240
aatcccatgt	cctggcggat	aagtgcggc	ttaacgccag	gaagcgtgtc	ggccagtttc	300
aaaccaatat	cacgcagcag	ttttttcgcc	ggattggtac	cggaaaaacag	atcgcggaat	360
ccctgcatac	cagccagcat	caacgccgca	ctgtgcttgc	ggctacgctc	atagcgacgc	420
agataaatgt	actgcccgat	gtc				443

<210> 432
 <211> 638
 <212> DNA
 <213> Escherichia coli

<400> 432
 caggggggttt gttgtgggca atgatgcatt taagttatcg tctgcagata gaggagatat 60
 tacaataaac aacgaatcag ggcatttgat agtcaatacc gcaattctat caggagatat 120
 agtcactcta agaggaggag aaattagggt ggtattatag cttgtgcgcg ccattgattgg 180
 cgcgcaattt aaacttagtg ctttacatcg ctattgtctt gatttctttg aattatttta 240
 taaattaaaa aaacgactgt tatgtataag caaagggtcg aacgaaaaat acattccaaa 300
 taaatgcttg cttaaatctc tatatccttc cccgaaaaat gacacataaa attgagatat 360
 tccaaaaaga gatactacaa ataaagatgc ctttatttta ttatttctaa taaaaataga 420
 agcaataaaa aataataaca atgatataaa tctaattgtt ttaaatataat tgccttttat 480
 gttagttaata gtcgttagta tgtttgatcc tccatatatt acgtgtagtt ttttatatac 540
 atggaaataa ttttctttat actgagacat cacaccatca tcaaatggaa gtttgaagat 600
 ggtgcttggt ttgctaacca ataaaaagag tgcattcg 638

<210> 433
 <211> 299
 <212> DNA
 <213> Escherichia coli

<400> 433
 ctttacctgg catgatccac ttcgccagaa taccggcaat aagcccaaaa ataattccatg 60
 acagaatgcc cattgtttcc tcacttatct gttttgcatt agcgggtag tgcgtgataa 120
 aaagcatagc acaacatcgg gagggcaaga tttgtgacga gcatcacgga ggtttttttg 180
 cgatggcgca gaaattgccc catcaacgat cagtgataat taccaaccac aaacatcatg 240
 ttcgttttcc gtgtcataag aacgtacggt attcaccaga tcttttatca cttcagccg 299

<210> 434
 <211> 388
 <212> DNA
 <213> Escherichia coli

<400> 434
 gaaaaaggag gcaatatcgg gtaaaggcat tagcccgacg aatacgtcgg gctacaaata 60
 ttattgtgct gcaggtgttt tagcgggttg ttgatccaca ggttctaact ggaagaccac 120
 atcgacctga tcatcaaaact gaatagcggc ctgctcgtaa gtttctctgg cgacaccgg 180
 cgcgccatcg gctttcatca tccgcaccat tgggtcgggc tgatagttag aaacatggta 240
 gcgcacgcta tataccggcc ccagtttacg atgaaagccg ttgcaccagt cctgcgcctg 300
 atgaatcgcg ttatcaatcg ctgccttacg cgctttgtct ttataggcat ccggctgcgc 360
 cagccccagc gacacagaac gaattccc 388

<210> 435
 <211> 351
 <212> DNA
 <213> Escherichia coli

<400> 435
 ctatccttga tgaaccgcg agcaaagata ggtgattacg tcatggtttt acagaaaatt 60
 acagaaaaag gaggaatat cgggtaaagg cattagcccg acgaatacgt cgggctacaa 120
 atattattgt gctgcagggt ttttagcggg ttgttgatcc acaggttcta actggaagac 180
 cacatcgacc tgatcatcaa actgaatagc ggccctgctc taagtttctt gggcgacac 240
 cggcgcgcca tcggctttca tcatccgcac cattgggctg ggctgatagt tggaaacatg 300
 gttagcgacg ctatataccg gccccagttt acgatgaaag ccgttcgcca g 351

<210> 436
 <211> 762
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(762)
 <223> n = A,T,C or G

<400> 436
 aattatgaaa cactgtctgg aatcgtctga atgacgggca catttgcgag cacgcaccca 60
 gtaataaacac aggaaactat tttatctacg cgtagcgat agactgcttg catggcgaaa 120
 ggaggtaaagc cgacgatttc agcgggacgc tgaacgggga aagcccctcc cgaggaaggg 180
 gccataaata aggaaagggg catgatgaag ctactcatca tcgtggtgct cttagtcata 240
 agcttccccg cttactaaga ctaccagggc gggggaaaacc ccgctctacc ctcaactctg 300
 aaagtatgcc ttacagataa gattgtcaat ccgcagggtt tgtagtctgc gatcctgcca 360
 gcaaataatc ttgcgagtc gttacgcaat aatcacagag gaaactattt tattcacgcg 420
 ttagcgatag actgcattca gggcgaaaag aggtaaagccg atgatttcag cgggacgctg 480
 aaacgggaaa gcctctcccg gagaagaggg cttttaataa ggaaaggggt atgatgaagc 540
 acgtcatcat actggtgata ctcttagtga ttagcttcca ggcttactaa gaacaccagg 600
 gggaggggga aacctcttcc taacctcac ttctgaaatt ggggtgctatg acgctggcgt 660
 tactgcttan cgctaccagt ttgtctgcc ttgctggtgt aacgccagat cggtagccgt 720
 ttggatattt taatgaaagc cgacaaatca atcancgtga cg 762

<210> 437
 <211> 292
 <212> DNA
 <213> Escherichia coli

<400> 437
 cacatttgcg agcacgcac cagtaataac acaggaaact attttatcta cgcgttagcg 60
 atagactgct tgcattggcg aaggaggtaa gccgacgatt tcagcgggac gctgaaacgg 120
 gaaagcccct cccgaggaag gggccataaa taaggaaagg gtcatgatga agctactcat 180
 catcgtggtg ctcttagtca taagcttccc cgcttactaa gactaccagg gcgggggaaa 240
 ccccgctcta ccctcactcc tgaagtatg ccttcacgat aagattgtca at 292

<210> 438
 <211> 631
 <212> DNA
 <213> Escherichia coli

<400> 438
 atttacactt ttacgaaat catgggatca ctaacaaaat atcgcttgct agttatattg 60
 tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 120
 ttaaaaaata gatgttgctg ggtgcgcttt tgctggttac cagtgcgcgc tgggccgcac 180
 cagccaccgc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 240
 ttgctgacct taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 300
 agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact 360
 ggacctatat ggggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag 420
 cctacgacgg tgagattttt tatcatcgct aaaaaagcc ccctcatcat gagggggaaa 480
 tgcagacacc ttgttatttt ttattattag ccacttgctc gtcttgcttg ttattagtgc 540
 tatttcacgt tgattaatgc ggttgccctc agtgcgccag atttaacttt gtttgatgcg 600
 tagacgtagt aactggctgt tatcggaatt g 631

<210> 439
 <211> 566
 <212> DNA
 <213> Escherichia coli

<400> 439
 tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca 60
 ttaaaaaata gatgttgctg ggtgcgcttt tgctggttac cagtgcgcgc tgggccgcac 120
 cagccaccgc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca 180
 ttgctgacct taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg 240

```

agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact    300
ggacctatat ggggtggcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag    360
cctacgacgg tgagattttt tatcatcgct aaaaaaagcc ccctcatcat gagggggaaa    420
tgcagacacc ttgttatttt ttattattag ccacttgctc gtcttgcttg ttattagtcg    480
tatttcacgt tgattaatgc ggttgccctc agtgcgccag atttaacttt gtttgatatc    540
tagacgtagt aactggctgt atcgaa                                     566

```

<210> 440
 <211> 339
 <212> DNA
 <213> *Escherichia coli*

```

<400> 440
cgtattcaca tccttttggat tgggtgataac atgcgaatcg gtattatttt tccggttgta    60
atcttcatta cagcggtcgt attttttagca tgggttttta ttggcggcta tgctgccccg    120
ggagcataaa gatgaaaaaa acaacgatta ttatgatggg tgtggcgatt attgtcgtac    180
tcggcactga gctgggatgg tggtaacgct acctctaaaa aatagcaaa gctgcctgtg    240
tgacgccttt gtgcaattta agcgtttaact tttaactctt ctgtagataa atagcacgac    300
aatcgacca ataacggcaa ccacgaagct gccaaaatt                                     339

```

<210> 441
 <211> 376
 <212> DNA
 <213> *Escherichia coli*

```

<400> 441
catgaatatt taaaaaggaa aacgacatga aaccgaagca cagaatcaac attctccaat    60
cataaaatat ttccgtggag catttttatta ttgaatatag aggtttaact ccggtaaaaa    120
acaaagaagc attgaatgca gggaaaaata atatggccat aaaaaacatc gaaagaaact    180
cttttaattt aacatgtaaa cgcattggtta atcctcatat cacgggtgga gtgttaagaa    240
catacataaa tggagtcatg ttttcctttt tccatttate aagttcctgt tgccgtttta    300
gtccatctct aattgcatat tttaattttt ctgataaatg gcattgagca tcgatttcat    360
ttaaacaac tgtaca                                     376

```

<210> 442
 <211> 446
 <212> DNA
 <213> *Escherichia coli*

```

<400> 442
ttacgatagc tattagtaaa aatataagag ttagctgtat tgttatgtct gtggcgaaat    60
tgactacctt cgtttttttg attaagaatg attttattat cgtaagtaaa attacatgaa    120
tatttaaaaa ggaacacgac atgaaaccga agcacagaat caacattctc caatcataaa    180
atatttccgt ggagcatttt attattgaat atagagggtt aactccggtg aaaaaacaaag    240
aagcattgaa tgcagggaaa aataatatgg ccataaaaaa catcgaaaaga aactctttta    300
atttaacatg taaacgcatg gttaatcctc atatcacggg tggagtgtta agaacataca    360
taaattggagt catgttttcc cttttccatt tatcaagttc ctggtgccgt tttagtccat    420
ctctaattgc atattttaat ttttct                                     446

```

<210> 443
 <211> 388
 <212> DNA
 <213> *Escherichia coli*

<220>
 <221> misc_feature
 <222> (1)...(388)
 <223> n = A,T,C or G

```

<400> 443
tcaccccggt gccgattttc aggcatactg atttaactta gcacccgcaa ctttaactaca    60

```

```

gaaaaacaaa gagataaatg tctaatactg atgcaaatcg agccgatttt ttaatcttta 120
cggaacttta cccgcctggg ttattaattg cactgtatcg cgggcggttcg cccgctttaa 180
tcacaatagg ctgtgtagcc tgggcctgtt tctctttcac ccgcgccaga gcggcgagcaa 240
tcgcattctt atctttggct gcagggtgaa cggctgcgct cttatgtcgt tcaaggcgag 300
ccgctttttc gcgctccaga cgagcctggc gcgcttcgaa acgcgctttg gcttctgcgg 360
cncgcttttc ttcctgacga atagccgc 388

```

<210> 444

<211> 209

<212> DNA

<213> Escherichia coli

<400> 444

```

aattttaata acgctatctg cggataaagc agaataagggt gttaaaccca gacataaacc 60
gaggaataata atgttattgt atttcataat ctattgttcc ttagcgacag attgctgtct 120
gctggttcag taaggtagca ggagaaactt caggaagctt gtactcgaca atacagtttg 180
agttttttatc ttgccccat gaaacctgt 209

```

<210> 445

<211> 341

<212> DNA

<213> Escherichia coli

<400> 445

```

catctcaat accgttaaat gcaaccgaa ccccggttgt ccctttgctg cattcactta 60
acgtaaatctg aaaagggagc gctggacttg tgctaccggt cgttggaat tgtctggcac 120
tggttttttg gagatctacg gtaaaattaa gcgaatccga tgagactgtg cagccataat 180
cgaggacgcg cccgctaatt ttaataacgc tatctgcgga taaagcagaa taggtggtta 240
acccagacaa taaaccgagg aaaataatgt tattgtattt cataatctat tgttccttag 300
cgacagattg ctgtctgctg gttcagtaag gtaccaggag a 341

```

<210> 446

<211> 697

<212> DNA

<213> Escherichia coli

<400> 446

```

agattttactg ccaattttccg gcagatcgga aagggttaam ccatattgat ccataagggg 60
acgaatcmcg ggctataaccg ccaggcatgg cttagagccat ggcattaaat tccgcaaatt 120
cgggcgctga ttcttccac gcggttattt tggcacacac cagatccagc aagggggttt 180
caggatcggt gagcagcaga tgatctacca gtccagcgc ctgggtgtat tgttcctcgt 240
tctgaatacc cgccagaaaaa ggtgccacag cagttagctt ttctctgct tgcaagatgt 300
cggaatcgc aatcattttt tccccttagt acgatgaaca gcggtaaaaga aatcgtattc 360
tttatgcgtc ataacttcac gtatgtagca cttttgcgat tcaaaaaaga ccattgctac 420
aacacgtaat tcattgcccc caacattgaa aacataatgc ttatccagat atttgaagtt 480
atccagagat gggaaatactg cttttaatga ctcaggtttt ttgaaatata ccttagcaat 540
cgtgktcccc agagccacca actccgtttt atgttgcggg tatttttccg cagcatcttt 600
caatgctttt tgagttatca ggtgcattct tcatcacgtc cgtkgmcaaa ttggcaatat 660
gataacatcc gttgccagat tggcacggat gaattat 697

```

<210> 447

<211> 215

<212> DNA

<213> Escherichia coli

<400> 447

```

aattaataac ttttcgttag gcagttttgg gtgtgagttg caagagggga gactactgaa 60
taactcaagt ttataatcg aggggaaaaa ggtgatggcg ttcatagcaa aacgccctca 120
accataaagg tcgagggcgc ttaagatgtt aaaaacccgc tatccgttaa aaaacaatgt 180
tcaactaagg tcagtacat tgcgctaaaa aagcg 215

```


<210> 448
 <211> 395
 <212> DNA
 <213> Escherichia coli

<400> 448
 gcattattca tgagaaatgt gtatcgtaaa tcaactgaaa ttaacgcaac catttggtat 60
 ttaagggtta attatctgtg tgtgatattt tattgaatgt tttaaatatt gtttttattg 120
 gcattgctat aatattgggtt atcatttgct gaatggattc agtcttaatg agtgggtttt 180
 taagggacag gcatagagta atgatacgta tgcataacca acatctttac tcattatgtc 240
 attgaatgtt gacgctatgt gtttatgagg gagaggtatt ttcagttgat ctggattgtt 300
 aaattcatat aatgcgcctt tgctcatgaa tggatgccag tatgtagtgg gaaattataa 360
 atattgaaat agtccaacta cttctttatt accaa 395

<210> 449
 <211> 641
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(641)
 <223> n = A,T,C or G

<400> 449
 ataatacagg aagaaaaggt gcgcggagat taccgtgtgt tgcgatatat tttttagttt 60
 cgcggtggcaa tacatcagtg gcaataaaac gacatatcca gaaaaatata cactaagtga 120
 atgatattctt ccgattttatc ttaatcggtt atggataaac gcaaagggct tcgttttttc 180
 ctataacttat tcagcactca caaataaagg aacgccaatg aaaattatac tctgggctgt 240
 attgattatt ttcctgattg ggctactggt ggtgactggc gtatttaaga tgatatttta 300
 aaatttaatta atgtcatcag gtccgaaaaat aacgagaata tttcagtcct tcacccctgt 360
 gcgctcctgt catgtgcatt gcttcatata atcactggcg caaggagcgc cgcaggcgna 420
 gnntgcncgn cgnccaccct naccccatgc cgaacttcag aantgaaaac nccntaacnc 480
 cgatngtcgg cggnggcctc cccatgcnan agtangggaa ntgccangcg ncnntataaa 540
 cgaaaggctn attncaaaga ctgggccttn cntttatctg atgtttgtcg gagaacgctc 600
 tcttgagnan gacaaatncc gccgggagcg gatttgaacn t 641

<210> 450
 <211> 314
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(314)
 <223> n = A,T,C or G

<400> 450
 gaactacgag taagaatagc tncgaattcc cgtttatgga taacggcaaa gggcttcggt 60
 ttttcctata cttattcagc actcacaat aaaggaacgc caatgaaaat tatactctgg 120
 gctgtattga ttattttcct gattgggcta ctggtggtga ctggcgattt taagatgata 180
 ttttaaaatt aattaatgtc atcaggtccg aaaataacga gaattttca gtctctcatc 240
 ctgttgcgct cctgtcatgt gcattgcttc atataatcac tggcgcaagg agcgcgcagg 300
 ggntntnnt cttt 314

<210> 451
 <211> 236
 <212> DNA
 <213> Escherichia coli

<400> 451

atatacacta	agtgaatgat	atcttccgat	ttatcttaat	cgtttatgga	taacggcaaa	60
gggcttcgtt	ttttcctata	cttattcagc	actcacaaat	aaaggaacgc	caatgaaaat	120
tatactctgg	gctgtattga	ttattttcct	gattgggcta	ctgggtggtga	ctggcgtatt	180
taagatgata	ttttaaaatt	aattaatgtc	atcaggtccg	aaaataacga	gaatat	236

<210> 452

<211> 418

<212> DNA

<213> Escherichia coli

<400> 452

cggagattac	cgtgtgttgc	gatataat	ttagtctcgc	gtggcaatac	atcagtggca	60
ataaaacgac	atatccagaa	aaatatacac	taagtgaatg	atatcttccg	atttatctta	120
atcgtttatg	gataacggca	aagggcttcg	tttttccta	tacttattca	gactcacaa	180
ataaaggaa	gccaatgaaa	attatactct	gggctgtatt	gattattttc	ctgattgggc	240
tactggtggt	gactggcgta	tttaagatga	tattttaaaa	ttaattaatg	tcatcaggtc	300
cgaaaataac	gagaatattt	cagtctctca	tcctgttgcg	ctcctgtcat	gtgcattgct	360
tcatataatc	actggcgcaa	ggagcgcgca	gggggcggcc	aatcgccgcc	gccccctg	418

<210> 453

<211> 551

<212> DNA

<213> Escherichia coli

<400> 453

aacaatttgc	ccatgcgctc	ggtcatgcgc	tgcacgcgcc	ggccattttg	sgcgtccccc	60
cgaccgccat	tgcactgtta	atgggcgaat	cttcagtact	ggtattaggt	ggacaacgcg	120
cgctgcctaa	acggctggaa	gaagcgggtt	ttgcgtttcg	ctggtagcat	ttagaagagg	180
cgctggcgga	tgctgttcgc	tgatgtggtt	tacagcaaac	atccgccagt	taactcccg	240
tgttacagga	ttagtggctt	tgccgcgata	gatcgtctgg	tgaaagtcgg	gtcaccatca	300
taactaactc	tctgtctaaa	cctctatcca	gcattctcct	agcaatacgc	agggcttctt	360
cgtgtttgcc	ctgcattgcg	ccttcttcac	gtaatctgtc	agcaatggtc	atcaagtttc	420
tccttttctt	gtggtgcgcg	ttccgctatc	tcaccaataa	atgcacgaaa	acgctgggca	480
tcccctgttt	gtaatacgta	attaaacagg	gcttttagct	gtctgtcatt	agtgtkccct	540
gtaactagca	g					551

<210> 454

<211> 93

<212> DNA

<213> Escherichia coli

<400> 454

tggcatctcg	gtgttgccga	tcttcatgat	atccagcccg	ccggaactt	cttcccaaac	60
ggttttgctg	ttatccattg	agtcacggaa	ctg			93

<210> 455

<211> 232

<212> DNA

<213> Escherichia coli

<400> 455

cgtgccgaga	tgatcctgta	accatcatca	gttgtgaagt	agtgattcac	gacttcaagg	60
cgcttttcaa	aagggatatt	tggctttgac	atattagggg	ctattccatt	tcatcgtcca	120
acaaaatggg	tgacgtacat	actcgttgga	aatcaacaca	ggaggctggg	aatgccgcag	180
aaatatagat	tactttcttt	aatagtatt	tgtttcacgc	ttttattttt	ca	232

<210> 456

<211> 713

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(713)

<223> n = A,T,C or G

<400> 456

ttagnggatn	naangccac	ancctcgang	gatctaggag	gtagaatagc	ttcgaattcc	60
ccagcagagc	gcggccttct	tcgtcagatt	tcgcagtagt	ggtaatggta	atatccaaac	120
cacgaacgcg	gtcgacttta	tcgtagtcga	tttctgggaa	gatgatctgc	tcacggacac	180
ccatgctgta	gttaccacga	ccgtcgaaag	acttagcgga	caggccacgg	aagtcacgga	240
tacgaggtac	agcaatagt	atcaggcgct	caaagaactc	ccacatgcgt	tcgccacgca	300
gaqttacttt	acagccgac	ggatagccct	gacggatttt	gaagcctgca	acagatttgc	360
gtgctttggt	gatcagcggt	ttttgaccgg	agattgctgc	caggtctgct	gctgcgttat	420
ccagcagttt	tttgtcagcg	atcgcttcac	caacacccat	gttcaggggt	atcttctcga	480
cccgagggac	ttgcatgaca	gaattgtagt	taaactcagt	catgagtttt	ttaactactt	540
cgtctttgta	gtaatcatgc	agtttcgcca	tcgtactact	ccatgtcggg	gaacgctctc	600
ctgagtagga	caaatccgcc	ggagccggat	ttaacgttgc	gaacaaccgn	cccggagggg	660
tggnngcagg	accccgccat	aactggcagc	attaaattaa	gcagaaggcc	atc	713

<210> 457

<211> 292

<212> DNA

<213> Escherichia coli

<400> 457

tgaacagcag	agatacggcc	agtgcggcca	atgttttttg	tcctttaaac	ataacagagt	60
cctttaagga	tatagaatag	gggtatagct	acgccagaat	atcgattttg	attattgcta	120
gttttttagtt	ttgcttaaaa	atattgttag	ttttattaaa	tgcaaaacta	aattattggt	180
atcatgaatt	tggtgtatga	tgaataaaat	ataggggggt	atagatagac	gtcattttca	240
taggggtata	aatgcgacta	ccatgaagtt	tttaattgaa	agtattgggt	tg	292

<210> 458

<211> 282

<212> DNA

<213> Escherichia coli

<400> 458

ttattaaatg	caaaaactaaa	ttattgggtat	catgaatttg	ttgtatgatg	aataaaatat	60
aggggggtat	agatagacgt	cattttcata	gggtataaaa	tgcgactacc	atgaagtttt	120
taattgaaag	tattgggttg	ctgataat	gagctgttct	attcttttta	aatatctata	180
taggtctgtt	aatggatttt	atttttacaa	ttttttgtgt	ttaggcatat	aaaaatcaac	240
ccgccatatg	aacggcgggt	taaaatattt	acaacttagc	aa		282

<210> 459

<211> 300

<212> DNA

<213> Escherichia coli

<400> 459

tctgcgttcc	gctaaaaggt	gcaaagtctc	aggacgttgc	agcgttttgc	gtgaccgctc	60
ggggaaggca	aaattgcctc	tgggaaagca	ttgcgcgggg	tccggcgctc	atcaacaatc	120
ggggggcagc	aaggggctga	aacgggaaag	cccctcccg	agaaggggce	ttgtataagg	180
aaagggttat	gatgaagctc	gtcatcatat	tggttgtgtt	gttactgtta	agtttcccg	240
cttactaaca	actcatcaga	ggggggagaa	atcctccctt	acccttggtc	ctttactcta	300

<210> 460

<211> 293

<212> DNA

<213> Escherichia coli

<400> 460

cgggggtccgg	cgctcatcaa	caatcggggg	gcagcaaggg	gctgaaacgg	gaaagcccct	60
cccgaagaag	gggccttgta	taaggaaagg	gttatgatga	agctcgtcat	catactgggt	120
gtgttggtac	tgtaagttt	cccgaactac	taacaactca	tcagaggggg	gagaaatcct	180
cccttaccct	tgttccctta	ctctaggttg	aaaaaacaac	agcgtcaata	ggcctgccat	240
gtacgaagcg	agatctgtga	accgctttcc	ggtagcctt	ttttatcctg	ttg	293

<210> 461

<211> 359

<212> DNA

<213> Escherichia coli

<400> 461

caacacagga	ggctgggaat	gccgcagaaa	tatagattac	tttctttaat	agtgatttgt	60
ttcacgcttt	tattttttcac	ctggatgata	agagattcac	tggtggaatt	gcatattaaa	120
caggagagtt	atgagctggc	ggcgttttta	gcctgcaaat	tgaaagagta	agagtcttcg	180
gcgggaaatt	attccccgct	tacttacggc	gttgcgcatt	ctcattgcac	ccaaatctat	240
tcttcacaaa	aataataata	gattttatta	cgcgatcgat	tattttattc	ctgaaaacaa	300
ataaaaaaat	ccccgccaaa	tggcagggat	cttagattct	gtgcttttaa	gcagagatt	359

<210> 462

<211> 673

<212> DNA

<213> Escherichia coli

<400> 462

gcaacccatg	tcttgacctg	ggttcggggg	acacaaaaac	gtgccgagat	gacctctgtaa	60
ccatcatcag	ttgtgaagta	gtgattcacg	acttcaaggc	gctttttcaa	agggattttt	120
ggcttttgaca	tattaggggc	tattccattt	catcgtccaa	caaaatgggt	gcagtacata	180
ctcgttgga	atcaacacag	gaggctggga	atgccgcaga	aatatagatt	actttcttta	240
atagtattt	gtttcacgct	tttatttttc	acctggatga	taagagattc	actgtgtgaa	300
ttgcatatta	aacaggagag	ttatgagctg	gcggcggttt	tagcctgcga	attgaaagag	360
taagagtctt	cgccgggaaa	ttattcccgc	cttacttacg	gcgttgcgca	ttctcattgc	420
acccaaattt	attcttcaca	aaaataataa	tagattttat	tacgcgatcg	attattttat	480
tctgaaaac	aaataaaaaa	atccccgccca	aatggcaggg	atcttagatt	ctgtgctttt	540
aagcagagaa	tacaggctgg	ttacggttacc	agctgccggg	cccttagcgc	cgctttcgat	600
ggtgaaggac	actttctgac	cttcgtccag	agatttgtaa	ccatcgttct	ggatagcaga	660
gaagtgtacg	aac					673

<210> 463

<211> 630

<212> DNA

<213> Escherichia coli

<400> 463

tggtggcatt	ggttgctgga	gagagaaaac	ccccgcacgt	tgagggtatg	cacctgacaa	60
caccacgggg	gctaactctg	actctagacc	actcaagaat	agccgcgaaa	cgttgtcatt	120
acaacacagg	cggtatatg	acgttcgcag	agctgggcat	ggccttcttg	catgatttag	180
cggtcccggt	cattgctggc	attcttgcca	gtatgatcgt	gaactggctg	aacaagcgga	240
agtaacgtgt	catgcgggcg	tcaggctgcc	gtaatggcaa	tttgcgcccg	gaccaggccg	300
caggggggaa	actctgcggc	ctttttcggt	cttactgcgg	gtaaggcacc	cagtcgccgc	360
cgttcaggcg	aacgtacggt	ttatcctggt	attgaataac	tactgcattt	gagttctcgg	420
agaccgggtc	tgtttggtgc	aaccactggg	tgagtttttt	ccagtcaaca	ttgtcttcgg	480
tgaaaatctt	gccatcgaga	acgcgaacca	ccagatcgga	gatagccagg	aagctgctcg	540
gttggttcgat	gacaatcggt	gccccctgat	gcgggtgcctt	catgccgaag	aatttcaccc	600
caacggggac	gtcggtgata	gacgggctag				630

<210> 464

<211> 391

<212> DNA

<213> Escherichia coli

<400> 464
 ctcaggctgc tgattgtttt tttgtgcaat ggcgcgggtat tagcgtcgtt gctgtcgtg 60
 gagagaatca taaacgtggt gaatgatgat tgttagcaag gaaactgtc aaaaatcttc 120
 aaaaaatttg agggataagg ccggaatggc tccggccaga ggaaggttaa ccgcgaagct 180
 gttgctgctt gagggtcgtt ttaaccagac gccaggcgct ccatacgcca aaaccgcgtc 240
 tggccagcg gaccagcata ttaggatggc gaatcgtcca gatcgccatc acgctactgc 300
 caaccagcgc ccaggagcgc agacttagca gcatattcca gcgacgatcg taagcgccctg 360
 ttgtctccag ccattcacga cgactggcgg a 391

<210> 465
 <211> 625
 <212> DNA
 <213> Escherichia coli

<400> 465
 aacacaccac accataaacg gaggcaata atgctgggta atatgaatgt ttaaatggcc 60
 gtactgggaa taattttatt ttctggtttt ctggccgcgt atttcagcca caaatgggat 120
 gactaatgaa cggagataat ccctcaccta accggccctt tggtacagtt gtgtacaagg 180
 ggcctgattt ttatgacggc gaaaaaaac cgccagtaaa ccggcgggtga atgcttgcac 240
 ggatagattt gtgttttctt ttacgctaa caggcatttt cctgcactga taacgaatcg 300
 ttgacacagt agcatcagtt ttctcaatga atgttaaagc gagcttaaac tcggttaatc 360
 acattttgtt cgtcaataaa catgcagcga tttcttccgg tttgcttacc ctcatcatt 420
 gcccggtccg ctcttccaat gaccacatcc agaggctctt caggaaatgc gcgactcaca 480
 cctgctgtca cggtaatgtt gatatgccct tcagaatgtg tgatggcatg gttatcgact 540
 aactggcaaa ttctgacacc tgcacgacat gcttcttcat cattagccgc ttgacaata 600
 atgataaatt cttcgccccc gtagc 625

<210> 466
 <211> 623
 <212> DNA
 <213> Escherichia coli

<400> 466
 tgcttttgaa tatgtgctcg caatcttgag aaggaaatgg cgaccacgaa agaaaaggca 60
 aaaaacgataa tctgaaagag ccaaggtatt tcagtataag cattgaatgc gacagtaaac 120
 tcttttcggta tcagccagag agtgagacca aaaatgataa tcgtatacat aagtctttcg 180
 agtggctcgt tagcaaaaag tttcaacaat ggagtaataa catccaacat atcaataact 240
 ctcaactgta agggatttga aatgttaaca caagctctcg ctgtaggggt atagccgaga 300
 ccaccgaagc ccggagggtg tgaataaaaa ccgggcacaa cacgaaggcg catttccgat 360
 atccataaag agtcgggtctt gtctgttaaa tttaaatggt gggagtgcgc ctccggttgt 420
 aaataacgac attgctgtgt gtagtcctgg cgcatcagt tttttcttg aagttcggtc 480
 gatgtccgcc ctttttaaa tgaattttgt gatgcggtga atgcgctaa gcgcacgtgg 540
 cacagttaaa agtcatgtta gtccttattg gtttgggtgg gaaagccgac tgtaattgtt 600
 aactggttgc agtcaacctgg agg 623

<210> 467
 <211> 234
 <212> DNA
 <213> Escherichia coli

<400> 467
 tgtttactta caagagattc atctttgtat aaataaagat aagtaattac gcataaaaca 60
 acaatgatta taatagcaaa aataaatatt atcatctttg atagattact tgagatagcc 120
 agcatcttgt aaagccttta tcgttttttt atgctctgga ttaataataat cactacatct 180
 atctgagcaa tctgttggtg atggacatgt caacccatgg tcatttacag ccaa 234

<210> 468
 <211> 529
 <212> DNA
 <213> Escherichia coli

<400> 468
 attagctatt tcggctaaaa tagagactac atgtcttcgg tccatctcac ttaaggagtg 60
 tagttccggt gtaagttttt ccatagcttg cactgctaaa tttcgaacaa ggaattttct 120
 gctggtaatc tctaaaaaga tggcatgggt tacaatgatt tttgtttcct tttgattatt 180
 atgaacaact gtccatgatt tcgtttaaga atgaagagaa atcactaaac gaactgaata 240
 tatttctgt gccaatatta tctctaattt caaaaaagtt acttttaatg tcggtaatga 300
 ctccaactta ttgatagtgt tttatgttca gataatgcc gatgactttg tcatgcagct 360
 ccaccgattt tgagaacgac agcgacttcc gtcccagcgg tgccagggtc tgcctcagat 420
 tcagggttat cgcgtcaatt cgctgcgtat atcgcttttc cttatcagtt cgttgatgtc 480
 agtgggtttg accacgaggg agcttcacgc gagttattga aaacctga 529

<210> 469
 <211> 261
 <212> DNA
 <213> Escherichia coli

<400> 469
 caaagaacct tcaacatgaa aaatatccat ttgtttgcaa aaaaagatta ttaggaagga 60
 aattaatgca attatcgaaa attcaaaaaa tatccaaaaa tagtatactt tattccagaa 120
 gagttcaata taatgtttgt cttcaatttt tcttacttca gggtaatata gattgctcat 180
 tacattgtga gcttcacttt tatttaattt tctgttgact ccagctctcc gtgataacgg 240
 ttttataatt agatgcttat c 261

<210> 470
 <211> 98
 <212> DNA
 <213> Escherichia coli

<400> 470
 agatgattgc cgggaacttg ttagcggcac gcaggcggcg gctcgcaccc ttacctgtct 60
 ctttacgtac ttctgcgttg atagtaaaca tttctttc 98

<210> 471
 <211> 259
 <212> DNA
 <213> Escherichia coli

<400> 471
 agcgcgaacg aagtcgatgt gctgcagctt cggttgttac gggtagcgt gtacgtcctg 60
 agctttaact ttgatttctt taccgtcaac aacgatggtc agaacttcgc ttagaattc 120
 agctttagct tgcattgtca tgactttgtc gtgatccagc tcgatagcca gcggcgcttc 180
 tttgccaccg tagatgattg ccgggaactt gttagcggca cgcaggcggc ggctcgcacc 240
 cttacctgc tctttacgt 259

<210> 472
 <211> 94
 <212> DNA
 <213> Escherichia coli

<400> 472
 aaaaacggcg taaagaaagg atgcaaacat gttaataaaa actcaaattg atcccacgta 60
 tatattacgc cgcaaaatcc ttacaataaa cagg 94

<210> 473
 <211> 174
 <212> DNA
 <213> Escherichia coli

<400> 473
 ttaattatta aaatagtga acgcgattat gtggttatgg gggtaaacat taaataaacc 60
 agcggggagg ggaggtaag tgaaaaata aaaagcgat aatcttaata agcaggccgg 120

acagcatcgc catccggcac tgatacgagg tttatttcag ctcatcaacc atcg 174

<210> 474
<211> 138
<212> DNA
<213> Escherichia coli

<400> 474
ctgtaaaaac gtcaaaaaga gtgttttatac aacagaagaa tggagggtctg acagatagta 60
gtaattgcaaa aaaatggaga cttaagtga atgaacggga gtaaagcgaa aagactatag 120
agtgaaggag aaattccc 138

<210> 475
<211> 191
<212> DNA
<213> Escherichia coli

<400> 475
tttgttggct taatattcta ttgttatctt tatttataga tgtttatatt gcatgagggtg 60
gtttttggag agaagaatga ggaagatgag tcgagccaca gaaacgttag ctttacatat 120
agcggagggtg atgtgaaatt aatttacaat agaaataatt tacatatcaa acagtttagat 180
gctttttgtc g 191

<210> 476
<211> 245
<212> DNA
<213> Escherichia coli

<400> 476
cggccattta tacaggaaaa gcctatgtca gaacgtaaaa actcaaaatc acgccgtaat 60
tatctcggtta aatgttcctg cccaaactgc acccaagagt cagaacacag tttttcaaga 120
gtacaaaaag gtgccctttt gatctgccct cattgcaaca aagtattcca gacaaatctt 180
aaagctgtag cctgattgat ttatttagta acaagtattt ttatatattt aataatatat 240
ttaa 245

<210> 477
<211> 319
<212> DNA
<213> Escherichia coli

<400> 477
aaattttcag gtaccttgtc accatacttt tttttctgag cattaatgat attttgagct 60
tcttgaggat ctttaactcc ccacatttgg tggaaagtat tcatattaaa aggaagggtg 120
aataatttgt ctttataaat cgccagtggg gaattagtaa aacgattaaa ttctactaaa 180
tcattaacgt aatcccatat atatttatca ttggtatgaa aaatatgtgc accatattta 240
tgaatctgga taccctcaca gtcctctgtg tacgcatttc caccgatatg atttcttttc 300
tcaatcacta aaacttttt 319

<210> 478
<211> 149
<212> DNA
<213> Escherichia coli

<400> 478
gcagtgtatc aagcgatgac gaagtgtatg gaaaaatcag aaaaactcag caaatcctga 60
tgactttcgc cggacgtcag gccgccactt cgggtcgggt acgtccgggt ttctttgctt 120
tgtaaagcgc caaatctgcc gatttcaac 149

<210> 479
<211> 330
<212> DNA

<213> Escherichia coli

<400> 479

gaaagtatct	tcgttattga	catcactgga	aaatataact	tgcttttcat	tattaaactc	60
gaagcgcgta	ccgtatctgg	acaaacattt	atcgagctta	ccaaattcct	gaagagggtt	120
aactacagat	aacatttgcg	cgctccttgc	agtaatgccc	gtcaaactct	tgacggggcat	180
tatttagatt	aaattaccag	tatttcttcg	gagtgaagaa	tattaccagg	tatatttaac	240
acccacgttc	gcggaccagt	cttgatctac	gtcaccacca	ccgaggtagt	tagcatcggt	300
ataggcgctg	aagttcttgg	tgaagctaaa				330

<210> 480

<211> 191

<212> DNA

<213> Escherichia coli

<400> 480

tttttttcca	gcaacggagc	aaaaggtttg	cccttggtga	gttcagggtt	aaccacttta	60
actacgtggc	gacgacccgg	agatgtcggt	ttacatttaa	caactgccat	tgtattactc	120
ctccgactta	ctcagcgccg	ccaacgaagt	ccagattctg	gccttctttc	agggtgacgt	180
aagctttttt	c					191

<210> 481

<211> 188

<212> DNA

<213> Escherichia coli

<400> 481

tccctttaac	taccagggtg	ttaacgactt	cgacttcgac	ttcaaacagt	ttctgcacag	60
cagctttgat	ttctgctttg	gtcgcgtctt	tagcaacttt	gagtacgatg	gtgttggtat	120
tttccatcgc	agtagacgct	ttttcagaaa	cgtgcggtgc	acgcagcacc	ttcagcagac	180
gttcttca						188

<210> 482

<211> 172

<212> DNA

<213> Escherichia coli

<400> 482

caaaggcgaa	caaagcctgt	gaagcccgaa	ggctccacag	acagtgtctac	ttgaaggcct	60
tactgtttct	tcttaggagc	gagcaccatg	atcatctggc	ggccttcgat	cttcggttggg	120
aaggattcga	ccactgccag	ttcttgcaaa	tcgtctttca	cgcgattaag	ca	172

<210> 483

<211> 266

<212> DNA

<213> Escherichia coli

<400> 483

tggagaaaaac	gggtgattga	taaagcaatc	atcgttctag	gggcgttaat	tgcgctgctg	60
gaactgatcc	gcttctgct	tcagcttctg	aactgatagc	ggaaacgtaa	tttagggcta	120
agagcacact	actcttagcc	ctttaacatt	taacgcattg	tcacgaactc	ttctgccgcc	180
gttgggtgaa	tgccgacggt	attgtcgaag	tcttttttgg	ttgcccccat	cttcagcgcc	240
accgcgaagc	cctgcaacat	ttcgtc				266

<210> 484

<211> 259

<212> DNA

<213> Escherichia coli

<400> 484

cgcaggcagc	tgatggtcaa	caggatgaga	gaaacccaga	gacaggttaa	tcacattgcc	60
------------	------------	------------	------------	------------	------------	----

WO 00/44906

PCT/US00/02200

ttaaccgct	gcacggtaac	ctacaccaac	cagctgcagc	ttcttagtga	agccttcggt	120
aacaccgata	accattgagt	tcagcagggc	acgcgcggta	ccagcctgtg	cccaaccgtc	180
tgcgtaacca	tcacgcggac	cgaaggtcag	ggtattatct	gcatgtttaa	cttcaacagc	240
atcgttgaga	gtacgagtc					259

<210> 485

<211> 73

<212> DNA

<213> Escherichia coli

<400> 485

caggtcggaa	cttaccgcac	aaggaatttc	gctaccttag	gaccgttata	gttacggccg	60
ccgtttaccg	ggg					73